




VERIFICATION OF TRANSLATION

I, Norio Ohmori, registered Patent Attorney, having my business place at Fukuoka Building, 9th Floor 8-7, Yaesu 2-Chome, Chuo-ku, Tokyo 104-0028 Japan, do hereby declare that I am conversant in the Japanese and the English language and that I am the translator of the documents attached and certify that to the best of my knowledge and belief the following is a true and correct English translation of the specification contained in the Application No. JP2001-395196.

Signature : 
Norio Ohmori

This 24th day of June, 2005

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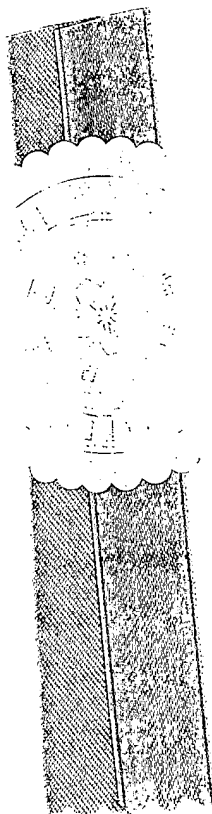
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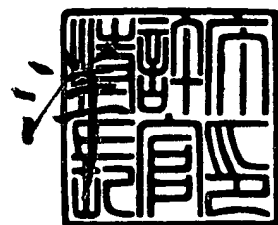
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[Name of Document] SPECIFICATION

[Title of the Invention] METHOD OF DETECTING GENE POLYMORPHISM

[Scope of Claims]

1. A method for detecting a genetic polymorphism(s), comprising creating
5 oligonucleotide probes and/or oligonucleotide primers so that the probes and/or primers
contain a polymorphic site(s) present in a gene encoding a drug metabolizing enzyme or so
that the polymorphic site(s) is/are contained in the amplified fragment when at least one of
said gene encoding the drug metabolizing enzyme is amplified; and detecting at least one
genetic polymorphism in a gene of a subject encoding the drug metabolizing enzyme using
10 the resultant oligonucleotide probes and/or oligonucleotide primers.

2. The method according to claim 1, wherein the oligonucleotide probe and/or
oligonucleotide primer containing a gene polymorphic site is created so that the nucleotide
positioned at its 5' or 3' end or its central part is the polymorphic site.

3. The method according to claim 1, wherein the oligonucleotide probe
15 containing a gene polymorphic site is composed of two fragments being linked to each other,
one fragment being hybridizable to the gene encoding a drug metabolizing enzyme and the
other fragment being not hybridizable thereto, and said polymorphic site is positioned at the
5' or 3' end of the hybridizable fragment.

4. The method according to claim 1, wherein the oligonucleotide probes and/or
20 oligonucleotide primers containing a gene polymorphic site comprising an at least 13
nucleotide sequence within any of the nucleotide sequences as shown in SEQ ID NOS: 1
through 4309, said at least 13 nucleotide sequence containing the 21st nucleotide, or a
sequence complementary to said at least 13 nucleotide sequence.

5. The method according to any one of claims 1 to 4 wherein the polymorphism
25 is a single-nucleotide polymorphism, a polymorphism caused by deletion, substitution or
insertion of a plurality of nucleotides, or a VNTR or microsatellite polymorphism.

6. A method for evaluating a drug, wherein the effectiveness and safety of a drug
metabolized by the drug metabolizing enzyme are evaluated based on the results obtained by
the detection method according to any one of claims 1 to 5.

7. A method for screening a drug, wherein the drug to be used is selected based
30 on the results obtained in the evaluation method according to claim 6.

8. A method for screening a drug, wherein the genetic polymorphism data
associated with the gene encoding a drug metabolizing enzyme in a control subject is
compared to the genetic polymorphism data associated with the same gene in a test subject,
35 and wherein a drug to be used is selected from the results of an analysis of the effectiveness

and/or safety of the drugs metabolized by the drug metabolizing enzyme.

9. The method according to any one of claims 1 to 8 wherein information of the polymorphic site is as shown in Table 1.

10. The method according to any one of claims 1 to 9, wherein the drug
5 metabolizing enzyme is at least one selected from the group consisting of epoxide hydrolase, methyltransferase, N-acetyltransferase, sulfotransferase, quinone oxidoreductase, glutathione S-transferase, UDP-glycosyltransferase, aldehyde dehydrogenase, alcohol dehydrogenase, esterase, NDUF, cytochrome P450 (CYP) and ATP-binding cassette/transporter.

11. An oligonucleotide selected from the group consisting of the nucleotide
10 sequences as shown in SEQ ID NOS: 1 through 4309 and sequences complementary thereto.

12. An oligonucleotide created so that it contains information of the polymorphic site present in a gene encoding a drug metabolizing enzyme.

13. The oligonucleotide according to claim 12, which is created so that the nucleotide positioned at its 5' or 3' end or its central part is the polymorphic site.

14. The oligonucleotide according to claim 12, wherein the oligonucleotide
15 containing a polymorphic site is composed of two fragments being linked to each other, one fragment being hybridizable to the gene encoding a drug metabolizing enzyme and the other fragment being not hybridizable thereto, and said polymorphic site is positioned at the 5' or 3' end of the hybridizable fragment.

15. The oligonucleotide according to any one of claims 12 to 14, wherein the
20 oligonucleotide comprising an at least 13 nucleotide sequence within any of the nucleotide sequences as shown in SEQ ID NOS: 1 through 4309, said at least 13 nucleotide sequence containing the 21st nucleotide, or a sequence complementary to said at least 13 nucleotide sequence.

16. A genetic polymorphism detection kit comprising the oligonucleotide according to any
25 one of claims 11 to 15.

[Detailed Description of the Invention]

[Technical Field to which the Invention Pertains]

The present invention relates to information on genetic polymorphisms; a method
30 for detecting information on genetic polymorphisms; a method for evaluating drugs using genetic polymorphisms; and a method for screening for drugs.

[Background Art]

As physical appearances of human individuals vary infinitely, the human genetic
code consisting of three billion (3,000,000,000) base pairs vary at a considerably large
35 number of sites when compared among individuals. These differences in the genetic code

are called genetic polymorphisms, and single nucleotide polymorphism is known as a representative polymorphism.

Single nucleotide polymorphism (SNP) means a difference in one DNA letter among individuals. As faces and shapes of human individuals vary infinitely, nucleotide sequences (i.e. genetic code) of individuals vary at a considerably large number of sites. SNPs are classified into cSNP (coding SNP) and gSNP (genome SNP) depending on their locations; cSNP is further classified into sSNP (silent SNP), rSNP (regulatory SNP) and iSNP (intron SNP).

These SNPs are useful as polymorphic markers in searching for those genes which are associated in the development or worsening of diseases; finally, these SNPs directly relates to risk diagnosis of diseases or selection and use of therapeutic drugs in the clinical field. Also, drug development on the basis of evidence obtained using causative substances as target molecules has become the trend of the world. When a drug is administered to patients with the same disease, their responsiveness is diverse. Some patients show remarkable effect; some patients show low effect; and some patients show no effect. Thus, responsiveness to a drug varies greatly depending on the patient. Even if the conditions of patients are the same and diagnosed as the same disease, the routes which have caused that disease may be different; or the metabolizing rate of the drug may vary greatly among patients. Therefore, it is desired to select an appropriate drug and develop an appropriate therapeutic method against a target disease based on genetic polymorphisms such as SNPs (i.e. the so-called personalized medicine is desired).

In addition to responsiveness to drugs, the problem of strong side effect which sometimes might be lethal is also one of the major problems that medical staffs should address. Even if there is no excessive administration caused by prescription error or the like, unexpected, lethal side effect might occur. Therefore, with respect to responsiveness to a drug, it is desired that the metabolism and delivery of the drug, the responsiveness of the drug's receptor and the sensitivities of those receptors associated with side effect should be determined taking into account genetic polymorphisms such as SNPs.

[Problem to be Solved by the Invention]

It is an object of the present invention to provide a method for detecting information on genetic polymorphism; a method for evaluating the efficacy and safety of drugs based on the information; and a method for screening for drugs.

[Means for Solving Problem]

As a result of extensive and intensive researches toward the solution of the above problem, the present inventors have succeeded in establishing a method which comprises

detecting genetic polymorphisms in a gene encoding a drug metabolizing enzyme and evaluating with the resultant information the relationship between a drug and a disease. Thus, the present invention has been achieved.

The present invention is as described below.

5 (1) A method for detecting a genetic polymorphism(s), comprising creating oligonucleotide probes and/or oligonucleotide primers so that the probes and/or primers contain a gene polymorphic site(s) present in a gene encoding a drug metabolizing enzyme or so that the polymorphic site(s) is/are contained in the amplified fragment when at least one of said gene encoding the drug metabolizing enzyme is amplified; and detecting at least one
10 genetic polymorphism in a gene of a subject encoding the drug metabolizing enzyme using the resultant oligonucleotide probes and/or oligonucleotide primers.

 The oligonucleotide probe and/or oligonucleotide primer containing a gene polymorphic site is created so that the nucleotide positioned at its 5' or 3' end or its central part is the polymorphic site. The oligonucleotide probe containing a gene polymorphic site
15 is composed of two fragments being linked to each other, one fragment being hybridizable to the gene encoding a drug metabolizing enzyme and the other fragment being not hybridizable thereto, and said polymorphic site is positioned at the 5' or 3' end of the hybridizable fragment. The oligonucleotide probes and/or oligonucleotide primers containing a gene polymorphic site include an oligonucleotide comprising an at least 13 nucleotide
20 sequence within any of the nucleotide sequences as shown in SEQ ID NOS: 1 through 4309, said at least 13 nucleotide sequence containing the 21st nucleotide, or a sequence complementary to said at least 13 nucleotide sequence. The types of genetic polymorphisms include single-nucleotide polymorphism, polymorphism caused by deletion, substitution or insertion of a plurality of nucleotides, or VNTR or microsatellite
25 polymorphism.

 (2) A method for evaluating a drug, wherein the effectiveness and safety of a drug metabolized by the drug metabolizing enzyme are evaluated based on the results obtained by the detection method according to the above method.

 (3) A method for screening a drug, wherein the drug to be used is selected based
30 on the results obtained in the above evaluation method.

 (4) A method for screening a drug, wherein the genetic polymorphism data associated with the gene encoding a drug metabolizing enzyme in a control subject is compared to the genetic polymorphism data associated with the same gene in a test subject, and wherein a drug to be used is selected from the results of an analysis of the effectiveness
35 and/or safety of the drugs metabolized by the drug metabolizing enzyme.

In the above detecting method, evaluating method or screening method, information of the genetic polymorphism includes polymorphic site is as shown in Table 1. Example of the drug metabolizing enzyme includes at least one, selected from the group consisting of epoxide hydrolase, methyltransferase, N-acetyltransferase, sulfotransferase, quinone oxidoreductase, glutathione S-transferase, UDP-glycosyltransferase, aldehyde dehydrogenase, alcohol dehydrogenase, esterase, NDUF, cytochrome P450 (CYP) and ATP-binding cassette/transporter.

(5) An oligonucleotide selected from the group consisting of the nucleotide sequences as shown in SEQ ID NOS: 1 through 4309 and sequences complementary thereto.

(6) An oligonucleotide created so that it contains information of the polymorphic site present in a gene encoding a drug metabolizing enzyme.

The above oligonucleotide is created so that the nucleotide positioned at its 5' or 3' end or its central part is the polymorphic site. The oligonucleotide is composed of two fragments being linked to each other, one fragment being hybridizable to the gene encoding a drug metabolizing enzyme and the other fragment being not hybridizable thereto, and said polymorphic site is positioned at the 5' or 3' end of the hybridizable fragment. Example of the oligonucleotide includes an oligonucleotide comprising an at least 13 nucleotide sequence within any of the nucleotide sequences as shown in SEQ ID NOS: 1 through 4309, said at least 13 nucleotide sequence containing the 21st nucleotide, or a sequence complementary to said at least 13 nucleotide sequence.

(7) A genetic polymorphism detection kit comprising the oligonucleotide described above.

[Mode for Carrying Out the Invention]

The present invention relates to a method for detecting a genetic polymorphism in a test subject using the genetic polymorphism data related to a drug metabolizing enzyme. The present invention analyzes the effectiveness, safety and strength of drugs metabolized by a drug metabolizing enzyme. The relationship between a disease and the drug to be evaluated is based on the results of the analysis. The genetic polymorphism data for the drug metabolizing enzyme is different for each patient with a given disease. Therefore, the effectiveness and safety of a specific drug depends on drug metabolism in the presence of certain genetic polymorphism data and the side effects in the presence of certain genetic polymorphism data. As a result, a physician can determine whether a certain drug should be used by a certain patient and can tailor drugs for use by a certain patient based on the genetic polymorphism data (so-called "made-to-order" treatments).

1. Genetic Polymorphism

Genetic polymorphism includes single nucleotide polymorphism, insertion/deletion polymorphism, and polymorphism caused by difference in the number of repetition of a nucleotide sequence. Generally, single nucleotide polymorphism (SNP) means a polymorphism caused by substitution of one specific nucleotide with other nucleotide in a gene or its complementary strand (complementary sequence) region. In the present invention, however, the term SNP also includes the polymorphism caused by substitution above as well as a polymorphism caused by deletion of the nucleotide and a polymorphism caused by addition of one more nucleotide to the nucleotide.

Insertion/deletion type polymorphism means a polymorphism caused by deletion or insertion of a plurality of nucleotides (e.g. two to several ten nucleotides). Sometimes, several hundred to several thousand nucleotides may be deleted or inserted. The polymorphism caused by difference in the number of repetition of a nucleotide sequence has repetition of a sequence of two to several ten nucleotides, and the number of this repetition varies among individuals. Those polymorphisms where the repeat unit consists of several to several ten nucleotides are called VNTR (variable number of tandem repeats) polymorphism, and those polymorphisms where the repeat unit consists of about two to four nucleotides are called microsatellite polymorphism. In VNTR or microsatellite polymorphisms, the number of such repetition is different among individuals' alleles, which results in acquisition of variation.

2. Drug Metabolizing Enzyme

"Drug metabolizing enzymes" refer to a group of enzymes that catalyze *in vivo* structural changes in exogenous materials including drugs. When used for clinical purposes, the group of metabolizing enzymes includes some endogenous materials. Because drug-metabolizing enzymes absorb, metabolize and secrete drugs, the polymorphism of an enzyme depends on the amount of enzyme expressed (transcription and translation) and the amount of activity. As a result, there are blood serum concentrations of both unchanged materials and metabolites.

Drug metabolizing enzymes expressed by the genes that are targeted for genetic polymorphism analysis in the present invention include, but are not limited to the following classes of enzymes:

Epoxide hydrolases

Methyltransferases

N-acetyltransferases

Sulfotransferases

Quinone oxidoreductases

Glutathione S-transferases

UDP-glycosyltransferases

5 Aldehyde dehydrogenases

Alcohol dehydrogenases

Esterases

Ubiquinone dehydrogenases : NDUF

Cytochrome P450s (CYPs)

10 ATP-binding cassettes

ATP-binding cassettes / Transporters

Other enzymes

(1) Epoxide hydrolases are enzymes that hydrolyze epoxide using a
15 trans-cleavage mechanism to produce 1,2-glycol. Examples include microsomal epoxide
hydrolase 1 and cytoplasmic epoxide hydrolase 2.

(2) Methyltransferases are enzymes that catalyze transmethylation in amino
groups, hydroxyl groups and thiol groups. Examples include the following.

Catechol-O-methyltransferase

20 Histamin-N-methyltransferase

Phenylethanolamine-N-methyltransferase

Phosphatidylethanolamine-N-methyltransferase

Nicotinamide-N-methyltransferase

Guanidinoacetate-N- methyltransferase

25 Acetylserotonin-O-methyltransferase

(3) N-acetyltransferases are enzymes that catalyze transacetylation in amino
groups, sulfonamide groups and hydrazine groups. Examples include the following.

Arylamine-N-acetyltransferase 1, 2

Arylalkylamine-N-acetyltransferase

30 N-acetyltransferase homologues of *Saccharomyces cerevisiae*

LI intracellular adhesion molecules

(4) Sulfotransferases are enzymes that contribute to sulfate conjugation and
catalyzes trans-sulfonylation in phenols, steroids, arylamines and biliary acid. Examples
include the following.

35 Sulfotransferase 1A1, 1A2, 1A3, 1C1, 1C2, 2A1, 2B1

Thyroid hormone sulfotransferase
 Tyrosyl protein sulfotransferase 1, 2
 Sulfotransferase-opening protein 3
 Estrogen sulfotransferase
 5 Cerebroside sulfotransferase
 HNK-sulfotransferase 1
 Carbohydrate sulfotransferase 2, 4, 5
 Carbohydrate sulfotransferase 1, 3

(5) Quinone oxidoreductases are enzymes that catalyze the reduction of
 10 quinones such as o-quinone and p-quinone. Examples include the following.

NAD(P)H: Quinone oxidoreductase 1
 NRH: Quinone oxidoreductase 2
 p53-induced gene 3 (PIG3) of a quinone oxide transferase homologue

(6) Glutathione S-transferases are enzymes that catalyze the conjugation of
 15 glutathione. Examples include the following.

Glutathione S-transferase Mu1, Mu2, Mu3, Mu4, Mu5
 Glutathione S-transferase Z1 (zeta)
 Glutathione S-transferase Π (pi)
 Glutathione S-transferase T1 (zeta)
 20 Glutathione S-transferase 1 Theta 1, Theta 2
 Microsomal Glutathione S-transferase 1
 Microsomal Glutathione S-transferase 1-like 1
 Microsomal Glutathione S-transferase T2, T3
 Glutathione S-transferase A1, A4

25 Glutathione S-transferase M1, M2, M3, M4

(7) UDP-glycosyltransferases are enzymes that catalyze the contribution of
 glucuronic acid to functional groups such as hydroxyl groups, carboxyl groups, amino
 groups and thiol groups after their introduction in the 1st drug metabolism route. Examples
 include the following.

30 UDP-glycosyltransferase 1 Family Polypeptide A1
 UDP-glycosyltransferase 2 Family Polypeptide A1, B7, B10, B4, B11, B15, B17
 UDP-glycosyltransferase 8
 Dolichyl-diphospho-oligosaccharide protein glycosyl transferase

(8) Aldehyde dehydrogenases are enzyme that converts aldehydes into
 35 carboxylic acids. Examples include the following.

Aldehyde dehydrogenase 1 family member A1, A2, A3

Aldehyde dehydrogenase 1 family member B1

Formyltetrahydroforate dehydrogenase

Aldehyde dehydrogenase 2

5 Aldehyde dehydrogenase 3 family member A1, A2

Aldehyde dehydrogenase 3 family member B1, B2

Aldehyde dehydrogenase 5 family member A1

Aldehyde dehydrogenase 6 family member A1

Aldehyde dehydrogenase 8 family member A1

10 Aldehyde dehydrogenase 9 family member A1

(9) Alcohol dehydrogenases are enzymes that convert alcohols into aldehydes or ketones. Examples include the following.

Alcohol dehydrogenase 1 through 7

Hydroxy-CoA-dehydrogenase

15 Short-chain alcohol dehydrogenase family genes

(10) Esterases are enzymes that hydrolyze some esters. Examples include the following.

Arylacetoamide deacetylase

Granzyme A

20 Granzyme B

Interleukin 17 (Cytotoxic T lymphocyte associate serine esterase 8)

Ubiquitin carboxyl-terminal esterase L1, 3

Carboxyl esterase 1

Lipase A

25 Esterase D-formylglutathione hydrolase

Carboxylester lipase (bile acetic acid-induced lipase)

Dolichyl-diphosphooligosaccharide-protein glycosyltransferase (DDOST)

Neuropathy target esterase

(11) Ubiquinone dehydrogenases (NDUF) are enzymes that support energy metabolism, *e.g.*, as in the mitochondrial respiratory chain. Examples include following.

NADH-dehydrogenase (ubiquinone)1 α -subcomplex 1 through 3 and 5 through 10

NADH-dehydrogenase (ubiquinone)1 α / β -subcomplex 1

NADH-dehydrogenase (ubiquinone)1 β -subcomplex 3, 5, 7

NADH-dehydrogenase (ubiquinone) Fe-S protein 1, 3, 4, 5, 6, 8

35 NADH-dehydrogenase (ubiquinone) flavoprotein 1 through 3

(12) Cytochrome P450s (CYPs) are enzymes that regulate 1st drug metabolism and introduce oxygen atoms to the drug. Examples include following.

Cytochrome P450 (CYP) 1A1, CYP 1A2, CYP1B1, CYP 2A6, CYP 2B6, CYP 2C8, CYP 2C18, CYP 2C9, CYP 2C19, CYP 2E1, CYP 2D6, CYP 2E1, CYP 2F1, CYP 3A3, CYP 3A4, CYP 3A5, CYP 3A7, CYP 3A43, CYP 4A11, CYP 4B1, CYP 4F2, CYP 4F3, CYP 4F8, CYP 11B1, CYP 17, CYP 19, CYP 21A2, CYP 27A1, CYP 27B1.

(13) ATP-binding cassettes/transporter absorb the drug and adjust the interstitial concentration with a transporter. Examples include the following.

ATP-Binding Cassette Subfamily A Members 1, 4, 7, 8

ATP-Binding Cassette Subfamily B Members 1, 4, 7, 8, 9, 10, 11

ATP-Binding Cassette Subfamily C Members 1, 2, 3, 4, 5, 7, 8, 9

ATP-Binding Cassette Subfamily D Members 1, 3, 4

ATP-Binding Cassette Subfamily G Members 1, 2, 4, 8

ATP-Binding Cassette Subfamily E Members 1

ATP-Binding Cassette Subfamily F Member 1

Organic anion transporters 1, 2, 3

Organic anion transporter polypeptides 1, 2, 8

Transporter 1 ATP-binding cassette subfamily B

Transporter 2 ATP-binding cassette subfamily B

SLC22A4 solute carrier family 22 (organic cation transporter) member 4

SLC22A5 solute carrier family 22 (organic cation transporter) member 5

SLC22A1 solute carrier family 22 (organic cation transporter) member 1

SLC22A2 solute carrier family 22 (organic cation transporter) member 2

SLC10A2 solute carrier family 10 (sodium/bile acid cotransporter family) member 2

SLC15A1 solute carrier family 15 (oligopeptide transporter) member 1

(14) Other enzymes include gamma glutamyl transferase 1 and transglutaminase 1.

3. Information on Genetic Polymorphisms

Genetic polymorphism data can be obtained using any general genetic polymorphism detection method. Examples include PCR methods hybridization methods using an allele-specific oligonucleotide matrix (e.g., TaqMan PCR method, Invader assay method), primer extension reaction methods, sequencing methods, MALDI-TOF/MS methods and the DNA chip methods, etc. PCR methods or sequencing methods are applicable to detection of any genetic polymorphisms and the other methods are applicable

to detection of SNP.

TaqMan PCR is a method using PCR reaction with a fluorescence-labeled, allele-specific oligo(s) and Taq DNA polymerase (Livak, K.J. Genet. Anal. 14, 143 (1999); Morris T. et al., J. Clin. Microbiol. 34, 2933 (1996)). The invader method is a method in which the hybridization of two reporter probes specific to respective alleles of SNP and one invader probe to the template DNA is combined with DNA cleavage by an enzyme having a special endonuclease activity of cleaving upon recognition of DNA structure (for example, see Livak, K. J. Biomol. Eng. 14, 143-149 (1999); Morris T. et al., J. Clin. Microbiol. 34, 2933 (1996); Lyamichev, V. et al., Science, 260, 778-783 (1993)).

As methods using primer extension reaction, SniPer method may be employed, for example. The basic principle of SniPer method is a technique called RCA (rolling circle amplification) method in which DNA polymerase moves on a circular single-stranded DNA as a template to thereby synthesize a complementary strand thereto continuously. According to this method, SNP may be judged by detecting the presence or absence of a coloring reaction that occurs when DNA amplification takes place (Lizardi, P. M. et al., Nature Genet., 19, 225-232 (1998); Piat, A. S. et al., Nature Biotech., 16, 359-363 (1998)).

The sequencing method refers to methods in which polymorphism-containing areas are amplified by PCR and the DNA sequences of the amplified products are sequenced with Dye Terminator or the like to thereby analyze the frequency of genetic polymorphisms (especially SNPs).

MALDI-TOF/MS method is a method using a mass spectrometer. Basically, this is a method for SNP genotyping utilizing the difference in mass of different nucleotides. There are methods using PCR amplification and methods using multiplex (Haff, L.A., Smimov, I.P., Genome Res., 7, 378- (1997); Little, D.P. et al. Eur. J. Clinica. Chem. Clin. Biochem., 35, 545- (1997); Ross, P., et al. Nat Biotechnol., 16, 1347- (1998)).

The DNA chip method is a method in which a large variety of DNA probes are aligned and immobilized on a baseboard such as glass; then, hybridization of a labeled DNA is performed thereon; and perfect match and one-nucleotide-mismatch are detected discriminably by using a method of detecting the label signal (such as fluorescence) on the probe.

The information on genetic polymorphisms, in particular information on SNPs, which may be used in the method of the present invention is as shown in Table 1 below.
[Table 1]

In Table 1, the "Designation of Gene" column shows the designations of the genes

encoding receptors. The nucleotides expressed with capital letters in the "Sequence" column are the SNP information. The two nucleotides on both sides of the mark "/" represent a homozygous or heterozygous SNP of the nucleotide. For example, "A/G" means that the allele is A/A or G/G homozygote or A/G heterozygote. The sequences in this Table basically represent 20 nucleotides each before and after the SNP. However, the nucleotide in parentheses [e.g. (T) in No. 27 of ABCB4: SEQ ID NO: 555] represents a polymorphism caused by insertion. The mark of open triangle (e.g. see No. 10 of NAT2: SEQ ID NO: 4255) means a polymorphism caused by deletion of one nucleotide. The nucleotide in parentheses provided with a number means that the nucleotide in the parentheses is repeated that number of times. For example, "(T) 9-12" appearing in SEQ ID NO: 689 (Table 1, No. 55 of ABCB11) means a sequence where T is repeated from 9 to 12 times.

The "Location" shows the location of SNP in the genome. The locations of SNPs in 5' flanking region, intron regions and 3' flanking region are counted taking the first nucleotide located immediately to the exon/intron junction as position 1 of the nucleotide sequence of the intron. The locations of SNPs in exon region are counted taking the first nucleotide located immediately to the exon/intron junction as position 1 of the nucleotide sequence of the exon. Numbers with "+" mark or without any mark mean that they are counted toward the 3' end of the gene; numbers with "-" mark mean that they are counted toward the 5' end of the gene. The numbers appearing in the "No." column correspond to the numbers appearing in respective gene maps (Figs. 9-177) which show the locations of SNPs.

4. Preparation of Oligonucleotide Probes or Oligonucleotide Primers

Oligonucleotides which are used in the detection method of the present invention as primers and/or probes may be prepared based on the nucleotide sequences described in Table 1 (SEQ ID NOS: 1-4309), for example, when SNPs are to be detected, and these sequences *per se* may be synthesized, or primers and/or probes may be designed and synthesized so that they contain a part of these sequences. However, it should be noted here that the nucleotide sequences of such primers or probes must contain an SNP (the portion indicated in capital letters in the "Sequence" column in Table 1). The present invention also includes complementary strands to such sequences.

Taking SNP as an example for the purpose of illustration, a primer or probe is designed so that an SNP site is located at the 3' or 5' end of the nucleotide sequence of the primer or probe; or a primer or probe is designed so that an SNP site is located at the 3' or 5'

end of the sequence complementary to its nucleotide sequence; or a primer or probe is designed so that an SNP site is located within four nucleotides, preferably two nucleotides, from the 3' or 5' end of its nucleotide sequence or the sequence complementary thereto. Alternatively, a primer or probe is designed so that an SNP site is located at the center of the full-length nucleotide sequence of the oligonucleotide. The "center" refers to a central region where the number of nucleotides counted from there toward the 5' end and the number of nucleotides counted from there toward the 3' end are almost equal. If the number of nucleotides of the oligonucleotide is an odd number, the "center" is the central five nucleotides, preferably the central three nucleotides, more preferably the single nucleotide at the very center. For example, if the oligonucleotide consists of 41 nucleotides, the "center" is from position 19 to position 23 nucleotides, preferably from position 20 to position 22 nucleotides, more preferably the nucleotide at position 21. If the number of nucleotides of the oligonucleotide is an even number, the "center" refers to the central four nucleotides, preferably the central two nucleotides. For example, if the oligonucleotide consists of 40 nucleotides, the "center" is from position 19 to position 22 nucleotides, preferably the nucleotide at position 20.

If the polymorphism consists of a plurality of bases, the probe/primer is designed so the full polymorphism sequence is contained in the probe/primer. In some preferred embodiments, it is designed so one of the bases 1 through 4 on the 5' end or 3' end complementing the primer DNA corresponds to the base at the very end of the polymorphism bases. (This is called the "corresponding base"; ideally, it is the base at the 5' or 3' end). For example, in the INVADER assay, if a probe and INVADER oligonucleotide are prepared to detect a genetic polymorphism (CAGAGGCT) in No. 12 of NDUFA7 in Table 1 (SEQ ID NO: 3411), the position of the corresponding base in the probe in FIG 4a (a "T" base in the figure) is designed to become "C" at the far left of sequence CAGAGGCT, and the N base in the INVADER oligonucleotide shown in FIG 4b is designed to replace the "C" at the far left of CAGAGGCT with A, T, C or G). Conversely, if designed so the position of the corresponding base in the INVADER oligonucleotide is the far right "T" in CAGAGGCT, the "N" base is such that the corresponding base in the probe is "T." Further, the corresponding base of the INVADER oligonucleotide and the allele probe can be set anywhere in the CAGAGGCT sequence.

The length of the nucleotide sequence is designed so that at least 13 nucleotides, preferably 13 to 60 nucleotides, more preferably 15 to 40 nucleotides, and most preferably 18-30 nucleotides are contained. This oligonucleotide sequence may be used as a probe for detecting a target gene, and it may be used as either a forward (sense) primer or a reverse

(antisense) primer.

The oligonucleotide used in the invention may be an oligonucleotide composed of two regions connected in tandem, one region being hybridizable to the genomic DNA and the other region being not hybridizable thereto. The order of connection is not particularly limited; either region may be located upstream or downstream. The hybridizable region of this oligonucleotide is designed based on the information on SNP-containing sequences described in Table 1. The oligonucleotide is prepared so that the nucleotide located at the 5' or 3' utmost end of the region hybridizable to the genomic DNA corresponds to an SNP of interest. The region of the above oligonucleotide not hybridizable to the genomic DNA is designed at random so that it does not hybridize to the SNP-containing sequence described in Table 1. This oligonucleotide may be used as a probe mainly for detecting SNPs in the invader method.

Further, the primer used in the present invention is designed so that a nucleotide sequence given in Table 1 contains a SNP when amplified by PCR for the purposes of examining functional changes resulted from the SNP, judging the efficacy or non-efficacy, and examining the occurrence of side effect. The length of the primer is designed so that at least 15 nucleotides, preferably 15 to 30 nucleotides, more preferably 18 to 24 nucleotides are contained in the primer. The primer sequence is appropriately selected from the template DNA so that the amplified fragment has a length of 500 bp or less, preferably 100 to 300 bp, more preferably 100 to 150 bp.

The thus designed oligonucleotide primers or probes may be synthesized chemically according to known techniques. Usually, such primers or probes are synthesized with a commercial chemical synthesizer.

It is also possible to label probes with fluorescent substances (e.g. FAM, VIC, Cy3, etc.) in advance to thereby automate detection procedures.

The above-described oligonucleotide may be included in a genetic polymorphism detection kit together with polymerases (e.g. Taq polymerase), buffers (e.g. Tris buffer), dNTPs and fluorescent dyes such as VIC, FAM.

5. Detection

Using the oligonucleotides prepared as described above as primers, a gene encoding a drug metabolizing enzyme (template DNA) is amplified with a DNA polymerase. Alternatively, the probe prepared as described above is hybridized to template DNAs to thereby detect those DNAs having the genetic polymorphism of interest. The template DNA may be prepared according to conventional methods, e.g. cesium chloride gradient

centrifugation, the SDS lysis method, or phenol/chloroform extraction.

(1) Detection by PCR

Amplification may be performed by polymerase chain reaction (PCR). Specific examples of useful DNA polymerase include LA Taq DNA polymerase (Takara), Ex Taq polymerase (Takara), Gold Taq polymerase (Perkin Elmer), AmpliTaq (Perkin Elmer), Pfu DNA polymerase (Stratagene) and the like.

Amplification conditions are as follows. Denaturation step at 85-105°C for 10-40 seconds, preferably at 94°C for 20-30 seconds; annealing step at 50-72°C for 30 seconds to 1 minute, preferably at 60°C for 20 seconds to 1 minutes; and extension step at 65-75°C for 1-4 minutes, preferably at 72°C for 2-3 minutes constitute one cycle, and 30 to 40 cycles are performed. However, in order to denature the template DNA and the primers sufficiently, a denaturation step of at 95°C for 1-5 minutes [if Gold Taq polymerase (Perkin Elmer) is used, at least 8-15 minutes, preferably 10-12 minutes] may be added before the start of the above-described amplification cycles. Also, in order to extend the amplified DNA completely, an extension step of at 72°C for 1-10 minutes may be added after the above amplification cycles. Moreover, if the detection of the amplified product is not performed immediately, it is desirable to add a step of storing the amplified product at 4°C to avoid unspecific amplification. Thus, a gene encoding a receptor can be amplified.

Subsequently, the amplified product is subjected to agarose gel electrophoresis, followed by staining with ethidium bromide, SYBR Green solution or the like to thereby detect the amplified product as a band or two to three bands (DNA fragments). Thus, a part of a gene encoding a drug metabolizing enzyme, containing a genetic polymorphism can be detected as a DNA fragment. Instead of agarose gel electrophoresis, polyacrylamide gel electrophoresis or capillary electrophoresis may be performed. It is also possible to perform PCR using primers labeled in advance with a substance such as fluorescent dye and to detect the amplified product. A detection method which does not require electrophoresis may also be employed; in such a method, the amplified product is bound to a solid support such as a microplate, and a DNA fragment of interest is detected by means of fluorescence, enzyme reaction, or the like.

(2) Detection by TaqMan PCR

TaqMan PCR is a method using PCR reaction with fluorescently labeled allele-specific oligos and Taq DNA polymerase. The allele-specific oligo used in TaqMan PCR (called "TaqMan probe") may be designed based on the SNP information described above. The 5' end of TaqMan probe is labeled with fluorescence reporter dye R (e.g. FAM or VIC), and at the same time, the 3' end thereof is labeled with quencher Q (quenching

substance) (Fig. 1). Thus, under these conditions, fluorescence is not detectable since the quencher absorbs fluorescence energy. Since the 3' end of TaqMan probe is phosphorylated, no extension reaction occurs from TaqMan probe during PCR reaction (Fig. 1). However, when PCR reaction is performed using this TaqMan probe together with Taq DNA polymerase and primers designed so that an SNP-containing region is amplified, the reaction described below occurs.

First, a TaqMan probe hybridizes to a specific sequence in the template DNA (Fig. 2a), and at the same time, an extension reaction occurs from a PCR primer (Fig. 2b). At this time, Taq DNA polymerase having 5' nuclease activity cleaves the hybridized TaqMan probe as the extension reaction of PCR primer proceeds. When the TaqMan probe has been cleaved, the fluorescent dye becomes free from the influence of the quencher. Then, fluorescence can be detected (Fig. 2c).

For example, as shown in Fig. 3, two alleles are supposed: one allele has A at the SNP site (allele 1) and the other allele has G at the SNP site (allele 2). A TaqMan probe specific to allele 1 is labeled with FAM and another TaqMan probe specific to allele 2 is labeled with VIC (Fig. 3). These two allele specific oligos are added to PCR reagents, and then TaqMan PCR is performed with a template DNA whose SNP is to be detected. Subsequently, fluorescence intensities of FAM and VIC are determined with a fluorescence detector. When the SNP site of the allele is complementary to the site within TaqMan probe corresponding to the SNP, the probe hybridizes to the allele; and Taq polymerase cleaves the fluorescent dye of the probe, which becomes free from the influence of the quencher. As a result, fluorescence intensity is detected.

If the template is a homozygote of allele 1, strong fluorescence intensity of FAM is recognized but the fluorescence of VIC is hardly recognized. If the template is a heterozygote of allele 1 and allele 2, fluorescence of both FAM and VIC can be detected.

(3) SNP Detection by the Invader Method

The invader method is a method for detecting SNPs by hybridizing allele-specific oligos to the template. In the invader method, two unlabeled oligos and one fluorescently labeled oligo are used. One of the two unlabeled oligos is called an "allele probe". The allele probe is composed of a region which hybridizes to the genomic DNA (template DNA) to form a complementary double strand, and a region (called "flap") which has a sequence entirely unrelated to the sequence of the template DNA and thus does not hybridize to the genomic DNA. A nucleotide located at the 5' or 3' utmost end of the hybridizable region corresponds to the SNP (Fig. 4a). The above-described flap sequence is an oligonucleotide having a sequence complementary to a FRET probe described later. The other oligo is

called an “invader probe”. This oligo is designed so that it hybridizes complementarily from the SNP site toward the 3’ end of the genomic DNA (Fig. 4b). However, the nucleotide corresponding to the SNP (“N” in Fig. 4b) may be any nucleotide. Thus, when the genomic DNA (the template) is hybridized to the above-described two probes, one
 5 nucleotide (N) of the invader probe invades into the SNP position (Fig. 4c) forming a triple strand at the SNP site.

On the other hand, the fluorescently labeled oligo has a sequence completely unrelated to the allele. This sequence is common regardless of the types of SNPs. This probe is called a “FRET” probe (fluorescence resonance energy transfer probe) (Fig. 5).
 10 The nucleotide at the 5’ end of FRET probe (reporter) is labeled with fluorescent dye R, while quencher Q is linked upstream of the reporter. Therefore, under these conditions, the quencher absorbs the fluorescent dye and no fluorescence is detectable. A certain region of the FRET probe starting from the 5’ end reporter nucleotide (designated “region 1”) is also designed so that it is complementary to a certain region of the probe located 3’ to region 1
 15 (designated “region 2”) when region 1 and region 2 are faced with each other. Therefore, region 1 and region 2 form a complementary strand within the FRET probe (Fig. 5). Also, the region located toward 3’ end of this complementary strand forming region is designed so that it hybridizes to the flap of the allele probe to thereby form a complementary strand (Fig. 5).

20 In the invader method, an enzyme called cleavase is used which is one of enzymes (5’ nucleotidases) having a unique endonuclease activity of cleaving upon recognition of a special structure of DNA. Cleavase is an enzyme which cleaves the allele probe at a point immediately 3’ to the SNP site when the genomic DNA, the allele probe and the invader probe form a triple strand at the SNP site. Therefore, when three nucleotides form a triple
 25 strand as shown in Fig. 4c, cleavase recognizes the 5’ flap and cuts off this flap. As a result, the structure of this SNP site is recognized by cleavage (Fig. 6a), and the allele probe is cut at the site of its flap to liberate the flap (Fig. 6b). Subsequently, the flap liberated from the allele probe complementarily binds to the FRET probe since it has a sequence complementary to the FRET probe (Fig. 6c). At this time, the SNP site of the flap invades
 30 into the portion of the FRET probe which has already formed a complementarily bound region. Cleavase again recognizes this structure and cuts off the nucleotide labeled with the fluorescent dye. The thus cleaved fluorescent dye becomes free from the influence of the quencher and emits fluorescence (Fig. 6d). When the SNP does not match the nucleotide corresponding to the SNP in the allele probe, a specific DNA structure recognizable by
 35 cleavase is not formed as seen in Fig. 7. Thus, the probe is not cleaved and no fluorescence

is detected.

For example, when an SNP is T/C, an invader probe and an allele probe for T, and a FRET probe with a FAM-linked reporter corresponding to the SNP are prepared. Separately, an invader probe and an allele probe for C, and a FRET probe with a VIC-linked reporter corresponding to the SNP are also prepared. Then, all of them are mixed to carry out SNP detection. As a result, if the SNP is T/T homozygous, the fluorescence of FAM is emitted; if the SNP is C/C homozygous, the fluorescence of VIC is emitted; and if the SNP is T/C heterozygous, the fluorescence of both FAM and VIC is emitted. Since FAM and VIC have different fluorescent wavelengths, they can be discriminated.

(4) Detection by SniPer Method

In order to detect SNPs by SniPer method, it is possible to discriminate alleles by examining the presence or absence of amplification by RCA. Briefly, the genomic DNA to be used as a template is linearized. Then, a probe is hybridized to this genomic DNA. When the probe sequence and the sequence of the genomic DNA as a template are complementary to each other and form a complementary strand, the genomic DNA can be converted into a circular DNA through ligation reaction. As a result, RCA of the circular DNA proceeds. On the other hand, when the ends of the probe do not match with the genomic DNA, the DNA is not ligated to become a circular DNA. Thus, RCA reaction does not proceed. Therefore, in SniPer method, a single-stranded probe which anneals with the genomic DNA and is circularizable is designed. This single-stranded probe is called a padlock probe. The sequences of the two ends of this padlock probe are designed so that they correspond to the SNP to be detected. Then, this padlock probe and the genomic DNA are mixed for ligation. If the two ends of the padlock probe and the SNP site of the genomic DNA are complementary to each other, the two ends of the padlock probe are joined by ligation, yielding a circular probe. If the two ends of the padlock probe and the SNP site of the genomic DNA are not complementary to each other, the probe does not become circular. Therefore, only those padlock probes which are complementary to the SNP to be detected become circular and are amplified by DNA polymerase. By detecting the presence or absence of this amplification, SNP may be detected. For the detection, synthetic oligonucleotides which have a fluorescent dye and a quencher at their respective ends and also have a hairpin structure are used.

(5) Detection by MALDI-TOF/MS Method

MALDI-TOF/MS (Matrix Assisted Laser Desorption-Time of Flight/Mass Spectrometry) is a method using a mass spectrometer in SNP typing. This method is composed of the following steps.

(i) PCR Amplification and Purification of SNP-Containing DNA Fragments

PCR primers are designed so that there is no overlapping between them and the nucleotides of SNP site. Then, DNA fragments are amplified. The amplified fragments are purified from the amplification reaction product by treatment with exonuclease, alkaline phosphatase, etc. to remove primers, dNTPs, etc.

(ii) Primer Extension (Thermal Cycling) and Purification

Ten-fold or more primers are added to the template of the target region (which is the PCR product), and primer extension is performed by thermal cycling. The primers used here are designed so that their 3' ends are adjacent to the nucleotide of the SNP site. The length of the primer is 15 to 30 nucleotides, preferably 20 to 25 nucleotides. When multiplex reaction is performed, a sequence not complementary to the template is added to the 5' end. Thermal cycling is performed between the two temperatures of at 85-105°C (preferably 94°C) and at 35-40°C (preferably 37°C) for 20 to 30 cycles (preferably 25 cycles). The resultant reaction products are purified with a purification kit or the like to make them fit for mass spectrometer.

(iii) Mass Spectrometry of DNA with Mass Spectrometer

The purified extension reaction product is applied to a mass spectrometer to determine the mass of the objective product. Briefly, the purified product is mixed with a matrix, and 0.5-1.0 µl of the mixture is spotted on MALDI plate. After drying the plate, laser light is applied to the sample to prepare spectrograms.

(6) Detection by DNA Sequencing Method

In the present invention, polymorphisms may be detected by using single nucleotide extension reactions. Briefly, four types of dideoxynucleotides labeled with different fluorescent compounds are added to a reaction system containing a gene of interest. Then, single nucleotide extension reactions are performed. In this case, the nucleotide to be extended is the polymorphic site. Also, two reactions of DNA synthesis termination and the fluorescent labeling of the 3' end of DNA molecules are operated. Four types of reaction solutions are subjected to electrophoresis on the same lane of a sequencing gel or on capillary. Difference in the fluorescent dyes used for labeling is detected with a fluorescence detector to thereby sequence the DNA band. Alternatively, the one-nucleotide extended oligonucleotide is examined with a fluorescence detection system or a mass spectrometry system or the like to thereby determine which nucleotide was extended using the difference in the fluorescent dyes. Instead of fluorescently labeled dideoxynucleotides, primers may be fluorescently labeled and used with unlabeled dideoxynucleotides.

6. Evaluation of Drugs

In the present invention, it is possible to evaluate the efficacy and safety of a drug intermediated by the receptor, from the results of detection of SNP and like that obtained as described above.

5 Evaluation of drugs may be performed by typing system. Briefly, according to any one of the detection methods described above, allele frequencies between toxicity (side effect) occurrence group and non-occurrence group are compared. A polymorphism which brings about difference in allele frequencies between the two groups is selected as a marker for recognizing the occurrence of toxicity. As a statistical test, usually chi square test is
10 carried out, but other statistical processing such as Fisher test may also be used. The active components (altered and metabolized drug components) in the drug will be reflected in blood and tissue concentrations. With respect to all genetic polymorphisms, the relation of cause and effect with the action or toxicity is examined. Then, only those genetic polymorphism sites that show correlation with the action or toxicity are selected. Allele pattern can be
15 examined by preparing in advance all probes or primers for analyzing the genetic polymorphisms and reagents necessary for each technique in reaction plates, cards, glass baseboards or the like, and adding thereto the genomic DNA of a human subject for reaction. When the subject has a genetic polymorphism which has correlation with the toxicity, it is possible to predict whether the drug exhibits toxicity in that subject. The efficacy of a drug
20 may be evaluated in a similar manner. Also, genetic polymorphisms which correlate with side effect or efficacy vary depending on drugs. Therefore, by conducting typing using correlating genetic polymorphisms for each drug, it becomes possible to predict the efficacy or side effect of the relevant drug.

Using this, the frequency of the relevant genetic polymorphism is compared with
25 efficacy/non-efficacy or presence/absence of side effect. When there is difference in allele frequency, a judgment on the relevant drug can be made.

For example, if the results of analysis of an SNP in persons who showed toxicity (side effect) upon administration of drug A have revealed statistically that 90% of those persons have T/T (e.g. fluorescence intensity of FAM was detected), and if the results of
30 analysis of the SNP in persons who did not show toxicity (side effect) have revealed that only 10% of those persons have T/T and 90% of them have C/C, drug A can be evaluated that it should not be administered to persons with T/T.

7. Screening for Drugs.

35 In the present invention, the genetic polymorphism data obtained as described

above is compared to genetic polymorphism data from genes encoding certain drug metabolizing enzymes to indicate the safety and effectiveness of drugs metabolized by these drug metabolizing enzymes. Therefore, the genetic polymorphism data obtained using the method of the present invention can be used to determine the likely effectiveness of certain drug therapies and to select the appropriate drug.

As a method, the evaluation method described in “5. Evaluation of Drugs” may be used. Genetic polymorphisms with correlations to side-effects and effectiveness are said to be influenced by the activation, transfer and translation of certain enzymes. The cause and effect relationship with the side-effect or effectiveness expression mechanism may be indirect. The metabolization of drugs is being studied by pharmaceutical companies in laboratory and clinical testing. If there are genetic polymorphisms in enzyme genes correlating with severe side-effects, they can be removed and used under different conditions. The same is true of effectiveness. Drugs can be screened, therefore, using side-effects and effectiveness data.

Further, by conducting genetic polymorphism frequency analysis on cases of volunteers with side effect occurrence and cases without side effect occurrence in clinical tests (from phase I to phase III tests), it becomes possible to detect new genetic polymorphisms other than the above-mentioned polymorphism which correlate with side effect or efficacy. By examining such polymorphisms in the same manner as described above, drug screening becomes possible.

[Examples]

Hereinbelow, the present invention will be described more specifically with reference to the following Example. However, the technical scope of the present invention is not limited to the Example.

[EXAMPLE 1] Obtaining SNP Information

(1) DNA Extraction

Blood samples were collected in the presence of EDTA from 48 individuals who have no kinship relation with one another. DNA extraction was carried as described below according to the method described in “Genome Analysis Laboratory Manual” (Yusuke Nakamura (ed.), Springer Verlag Tokyo).

Blood sample (10 ml) was transferred to a 50 ml Falcon tube and centrifuged at room temperature at 3000 rpm for 5 minutes. After removal of the supernatant (serum) with a pipette, 30 ml of RBC lysis buffer (10mM NH_4HCO_3 , 144mM NH_3Cl) was added and mixed until the precipitate became loosened. Then, the mixture was left at room

temperature for 20 minutes. After centrifugation at room temperature at 3000 rpm for 5 minutes, the supernatant (serum) was discarded with a pipette to obtain a pellet of white blood cells. RBC lysis buffer (30 ml) was added thereto, and the above-described operations were repeated twice. To the resultant white blood cell pellet, 4 ml of Proteinase K buffer (50mM Tris-HCl (pH7.4), 100mM NaCl, 1mM EDTA (pH8.0)), 200 µl of 10% SDS, and 200 µl of 10 mg/ml Proteinase K were added and mixed by inversion. The resultant mixture was left overnight stationary at 37°C. Subsequently, 4 ml of phenol was added to the mixture, which was then mixed slowly by inversion for 4 hours in a rotator (Rotator T-50, Taitec). After centrifugation at room temperature at 3000 rpm for 10 minutes, the resultant upper layer was collected into a fresh tube. Four milliliters of phenol/chloroform/isoamyl alcohol (25:24:1 in volume ratio) was added to the tube and mixed by inversion for 2 hours in the same manner as described above. Then, the mixture was centrifuged. The resultant upper layer was collected into a fresh tube, to which 4 ml of chloroform/isoamyl alcohol (24:1 in volume ratio) was added and mixed by inversion for 30b minutes in the same manner as described above. Then, the mixture was centrifuged. The resultant upper layer was collected into a fresh tube, to which 400 µl of 8M ammonium acetate and 4 ml of isopropanol were added and mixed by inversion. Thread-like white deposit (DNA) was recovered into a 2 ml tube, to which 70% ethanol (1 ml) was added and mixed by inversion. The DNA was recovered into a fresh 2 ml tube and air-dried. Then, 500 µl of TE solution (10mM Tris-HCl (pH7.4), 1mM EDTA (pH7.4)) was added for lysis, to thereby obtain a genomic DNA sample.

(2) PCR

Genomic sequences were obtained from GenBank DNA database. After removal of repeat sequences using RepMask computer program, PCR primers were designed so that PCR products have a length of about 1 kb. As genomic DNA, DNA samples obtained from 48 individuals who have no kinship relation with one another and prepared to have the same concentration were used. DNA samples derived from three individuals each were mixed in a tube in equal amounts. Of this mixture, 60 ng was used in PCR. PCR was performed with Ex-Taq (2.5 U; Takara) using GeneAmp PCR System 9700 (PE Applied Biosystems). Following a reaction at 94°C for 2 minutes, 35 cycles of denaturation at 94°C for 30 seconds, annealing at 60°C or 55°C for 30 seconds and extension at 72°C for 1 minute were performed.

(3) Sequencing

PCR products were purified with ArrayIt (Telechem) and subjected to sequencing reaction using BigDye Terminator RR Mix (PE Applied Biosystems). Briefly, following a

reaction at 96°C for 2 minutes, 25 cycles of denaturation at 96°C for 20 seconds, annealing at 50°C for 30 seconds and extension at 60°C for 4 minutes were performed using GeneAmp PCR System 9700 (PE Applied Biosystems). After the sequencing reaction, sequences were analyzed with ABI PRISM 3700 DNA Analyzer.

5 (4) Detection of SNPs

PolyPhred computer program (Nickerson et al., 1997, *Nucleic Acids Res.*, 25, 2745-2751) was used for the detection and analysis of SNPs.

(5) Results

10 The results as shown in Table 1 were obtained on SNPs. Figs. 9 to 177 show the designations, abbreviations and GenBank database Accession Nos. of the analyzed drug metabolizing enzyme, the structures of the genes encoding them, and the locations of SNPs. In Figs. 9 to 177, exons are indicated as open boxes or black lines on the relevant gene expressed as a horizontal line. The locations of SNPs are indicated above the gene with solid lines provided with numbers.

15

[Example 2]

Typing was performed on two different groups of patients using the INVADER assay. Results are shown in FIG 178. In FIG 178, the x-axis (Allele 1) indicates the intensity of the FAM fluorescent light corresponding to T, and the x-axis (Allele 2) indicates the intensity of the VIC fluorescent light corresponding to C. The slanted line indicates the SNP pattern for T/T, the black circles denote the pattern for C/C, and the white circles denote the pattern for T/C. The black squares indicate the background values. The x marks indicate where the detection failed. The group of patients in the graph for panel A (top) had many C/C SNP patterns and the group of patients in the graph for panel B (bottom) had many T/T SNP patterns.

25

[Exmple 3] SNP Detection

Genome DNA was extracted from five unrelated people using the method described in Example 1, and the SNPs in three different drug metabolizing enzyme genes (EPHX1, ABCB2, AANAT) were detected using the INVADER assay method. The INVADER oligonucleotides and probes were designed using base sequence No. 3 (SEQ ID NO: 1965) and No. 17 (SEQ ID NO: 1979) in the case of EPHX1, base sequence No. 4 (SEQ ID NO: 4276) and No. 11 (SEQ ID NO: 4283) in the case of ABCB2, and base sequence No. 3 (SEQ ID NO: 4326) in the case of AANAT. The positions of the SNPs are shown in Table 1.

35 The results are shown in Table 2.

Table 2

Drug Metabolizing Enzyme Gene	EPHX1		ABCB2		AANAT
	No. 3	No. 17	No. 4	No. 11	No. 3
	SEQ. ID No. 1965	SEQ. ID No. 1979	SEQ. ID No. 4276	SEQ. ID No. 4283	SEQ. ID No. 4236
SNP	(T/G)	(A/G)	(G/T)	(G/A)	(T/A)
Subject I	T/T	A/G	T/T	G/A	T/T
Subject II	T/T	A/A	G/G	G/G	T/A
Subject III	T/G	A/A	G/G	A/A	T/T
Subject IV	G/G	A/G	G/T	G/G	T/T
Subject V	T/G	A/G	G/T	G/A	T/A

As shown in Table 2, the SNPs in the drug metabolizing genes of patients can be detected and the patterns determined using the method of the present invention.

5

[Example 4] Correlation between SNP genotypes and optimal amounts of a medicament for treatment validity and safety

In this example, validity and safety of medicaments were investigated using SNP analysis.

10

Thiopurine S-methyltransferase (TPMT) is an enzyme that transfers a methyl group to a sulfur atom attached to a purine ring, and is one of the major enzymes for metabolizing drugs such as the anti-cancer agents 6-mercaptopurine and 6-thioguanine, and thiopurine derivatives such as the immunosuppressive agent azathioprine. This example shows a correlation between optimal amounts of azathioprine and various combinations of the alleles at the 868th SNP of intron 3 of TPMT(Accession No. AB045146.1) (G or T alleles) and the 2682nd SNP of intron 3 (C or A alleles)(Table 3 and Table 4).

15

Table 3

868	2682	High	Low
TT	AA	2	0
TT	AT	3	0
TT	TT	1	0
GT	AA	0	2
GT	AT	1	7
GT	TT	4	1
GG	AA	1	0
GG	AT	0	1
GG	TT	1	0

Optimal amounts of azathioprine were determined by adopting suppression of rejection after renal transplantation as an index. A group of patients in which the validity of treatment with 100 mg/day of azathioprine was confirmed was designated as a high dose group, and a group of patients in which side effects developed with treatment of 100 mg/day, but in which validity was confirmed with a treatment of 50 mg/day was designated as a low dose group. Table 3 indicates the number of patients having each combination of alleles, with the columns labeled "High" and "Low" representing the numbers of patients of each genotype in the high dose and the low dose groups, respectively. Side effects include leukopenia, anthema, angiitis, nausea/vomiting, anorexia, diarrhea, malaise, myalgia, arthralgia, fever, chill, and dizziness. More serious side effects include, for example, blood disorders, shock-like symptoms, infectious diseases, and hepatic disorders, and renal disorders.

Investigation of a correlation between the high dose and low dose groups and the two types of SNPs indicated above revealed that when G is present in at least one allele at the 868th SNP of intron 3 (G/G homozygous or G/T heterozygous) and A is present in at least one allele at the 2682nd SNP of intron 3 (A/A homozygous or A/T heterozygous), side effects were developed with 100 mg/day and 50 mg/day was an optimal amount for 10 out of 12 patients (low dose group), while 100 mg/day was an optimal amount for 11 out of 12 patients with other allele combinations (high dose group) (Table 4). Investigation of this combination of two SNP loci in patients enables prediction of optimal amounts of azathioprine for treatment prior to the administration of the drug, for improved validity and safety. These results indicate that the validity and safety of medicaments can be predicted using analysis of SNPs associated with medicament metabolic enzymes.

Table 4

Genotype	Optimal amount	
	100 mg/day	50 mg/day
G as the 868 th SNP and A as the 2682 nd	2	10
Other combinations	11	1

(Fisher exact test: p=0.0003)

[Effect of the Invention]

According to the present invention, methods for analyzing SNPs are provided. According to the methods of the invention, it becomes possible to select appropriate drugs for target diseases. Thus, the methods of the invention are extremely useful.

[SEQUENCE LISTING FREE TEXT]

SEQ ID NO 150 : n represents at or deletion (Location 21).
 SEQ ID NO 152 : n represents c or deletion (Location 21).
 SEQ ID NO 153 : n represents t or deletion (Location 21).
 5 SEQ ID NO 154 : n represents t or deletion (Location 21).
 SEQ ID NO 155 : n represents g or deletion (Location 21).
 SEQ ID NO 157 : n represents c or deletion (Location 21).
 SEQ ID NO 159 : n represents t or deletion (Location 21).
 SEQ ID NO 161 : n represents c or deletion (Location 21).
 10 SEQ ID NO 289 : n represents 14 to 16 repeats of tca (from Location 21).
 SEQ ID NO 290 : n represents 8 to 10 repeats of a (from Location 21).
 SEQ ID NO 291 : n represents cacagtcac or deletion (Location 21).
 SEQ ID NO 292 : n represents tt or deletion (Location 21).
 SEQ ID NO 293 : n represents 10 to 12 repeats of a (from Location 21).
 15 SEQ ID NO 294 : n represents c or deletion (Location 21).
 SEQ ID NO 295 : n represents 16 to 18 repeats of a (from Location 21).
 SEQ ID NO 296 : n represents g or deletion (Location 21).
 SEQ ID NO 298 : n represents c or deletion (Location 21).
 SEQ ID NO 299 : n represents t or deletion (Location 21).
 20 SEQ ID NO 300 : n represents a or deletion (Location 21).
 SEQ ID NO 301 : n represents tg or deletion (Location 21).
 SEQ ID NO 303 : n represents 10 to 13 repeats of t (from Location 21).
 SEQ ID NO 304 : n represents 11 to 13 repeats of gt (from Location 21).
 SEQ ID NO 305 : n represents a or deletion (Location 21).
 25 SEQ ID NO 306 : n represents g or deletion (Location 21).
 SEQ ID NO 307 : n represents g or deletion (Location 21).
 SEQ ID NO 308 : n represents 9 to 11 repeats of t (from Location 21).
 SEQ ID NO 309 : n represents g or deletion (Location 21).
 SEQ ID NO 311 : n represents tt or deletion (Location 21).
 30 SEQ ID NO 312 : n represents 7 to 9 repeats of a (from Location 21).
 SEQ ID NO 313 : n represents 9 to 11 repeats of t (from Location 21).
 SEQ ID NO 314 : n represents 9 to 10 repeats of a (from Location 21).
 SEQ ID NO 315 : n represents gt or deletion (Location 21).
 SEQ ID NO 316 : n represents a or deletion (Location 21).
 35 SEQ ID NO 317 : n represents t or deletion (Location 21).

	SEQ ID NO 319 : n represents a or deletion (Location 21).
	SEQ ID NO 320 : n represents ct or deletion (Location 21).
	SEQ ID NO 321 : n represents g or deletion (Location 21).
	SEQ ID NO 322 : n represents a or deletion (Location 21).
5	SEQ ID NO 323 : n represents a or deletion (Location 21).
	SEQ ID NO 324 : n represents a or deletion (Location 21).
	SEQ ID NO 325 : n represents c or deletion (Location 21).
	SEQ ID NO 326 : n represents aaag or deletion (Location 21).
	SEQ ID NO 391 : n represents 22 to 26 repeats of t (from Location 21).
10	SEQ ID NO 392 : n represents 8 to 10 repeats of g (from Location 21).
	SEQ ID NO 393 : n represents 6 to 7 repeats of c (from Location 21).
	SEQ ID NO 394 : n represents 12 to 14 repeats of a (from Location 21).
	SEQ ID NO 473 : n represents tt or deletion (Location 21).
	SEQ ID NO 474 : n represents 9 to 11 repeats of a (from Location 21).
15	SEQ ID NO 475 : n represents 8 to 12 repeats of a (from Location 21).
	SEQ ID NO 476 : n represents t or deletion (Location 21).
	SEQ ID NO 477 : n represents t or deletion (Location 21).
	SEQ ID NO 478 : n represents t or deletion (Location 21).
	SEQ ID NO 479 : n represents a or deletion (Location 21).
20	SEQ ID NO 480 : n represents t or deletion (Location 21).
	SEQ ID NO 481 : n represents t or deletion (Location 21).
	SEQ ID NO 482 : n represents 11 to 15 repeats of t (from Location 21).
	SEQ ID NO 483 : n represents cat or deletion (Location 21).
	SEQ ID NO 484 : n represents t or deletion (Location 21).
25	SEQ ID NO 485 : n represents a or deletion (Location 21).
	SEQ ID NO 486 : n represents a or deletion (Location 21).
	SEQ ID NO 487 : n represents t or deletion (Location 21).
	SEQ ID NO 488 : n represents a or deletion (Location 21).
	SEQ ID NO 497 : n represents g or deletion (Location 21).
30	SEQ ID NO 519 : n represents a or deletion (Location 21).
	SEQ ID NO 525 : n represents aaag or deletion (Location 21).
	SEQ ID NO 555 : n represents t or deletion (Location 21).
	SEQ ID NO 558 : n represents a or deletion (Location 21).
	SEQ ID NO 566 : n represents at or deletion (Location 21).
35	SEQ ID NO 573 : n represents a or deletion (Location 21).

	SEQ ID NO 590 :	n represents c or deletion (Location 21).
	SEQ ID NO 593 :	n represents gg or deletion (Location 21).
	SEQ ID NO 602 :	n represents gtc or deletion (Location 21).
	SEQ ID NO 624 :	n represents t or deletion (Location 21).
5	SEQ ID NO 631 :	n represents tt or deletion (Location 21).
	SEQ ID NO 634 :	n represents 9 to 12 repeats of t (from Location 21).
	SEQ ID NO 636 :	n represents a or deletion (Location 21).
	SEQ ID NO 638 :	n represents 10 to 13 repeats of a (from Location 21).
	SEQ ID NO 641 :	n represents ct or deletion (Location 21).
10	SEQ ID NO 644 :	n represents cagatcttcttcagctaatttagaaatgt or deletion (Location
	21).	
	SEQ ID NO 670 :	n represents a or deletion (Location 21).
	SEQ ID NO 677 :	n represents c or deletion (Location 21).
	SEQ ID NO 682 :	n represents t or deletion (Location 21).
15	SEQ ID NO 689 :	n represents 9 to 12 repeats of t (from Location 21).
	SEQ ID NO 692 :	n represents t or deletion (Location 21).
	SEQ ID NO 694 :	n represents g (a) ⁴ , a (a) ⁴ or a (Location 21).
	SEQ ID NO 698 :	n represents t or deletion (Location 21).
	SEQ ID NO 707 :	n represents c or deletion (Location 21).
20	SEQ ID NO 709 :	n represents a or deletion (Location 21).
	SEQ ID NO 710 :	n represents c or deletion (Location 21).
	SEQ ID NO 717 :	n represents g or deletion (Location 21).
	SEQ ID NO 719 :	n represents 18 to 20 repeats of t (from Location 21).
	SEQ ID NO 724 :	n represents 11 to 13 repeats of a (from Location 21).
25	SEQ ID NO 725 :	n represents gaaa or deletion (Location 21).
	SEQ ID NO 729 :	n represents 10 to 12 repeats of a (from Location 21).
	SEQ ID NO 732 :	n represents c or deletion (Location 21).
	SEQ ID NO 742 :	n represents ca or deletion (Location 21).
	SEQ ID NO 749 :	n represents at or deletion (Location 21).
30	SEQ ID NO 753 :	n represents ctt or deletion (Location 21).
	SEQ ID NO 755 :	n represents g or deletion (Location 21).
	SEQ ID NO 757 :	n represents ggggct or deletion (Location 21).
	SEQ ID NO 761 :	n represents 19 to 22 repeats of t (from Location 21).
	SEQ ID NO 766 :	n represents 6 to 7 repeats of t (from Location 21).
35	SEQ ID NO 769 :	n represents 11 to 13 repeats of t (from Location 21).

	SEQ ID NO 813 :	n represents 7 to 8 repeats of c (from Location 21).
	SEQ ID NO 815 :	n represents 10 to 12 repeats of a (from Location 21).
	SEQ ID NO 823 :	n represents c or deletion (Location 21).
	SEQ ID NO 828 :	n represents aaga or deletion (Location 21).
5	SEQ ID NO 830 :	n represents 9 to 11 repeats of a (from Location 21).
	SEQ ID NO 833 :	n represents ct or deletion (Location 21).
	SEQ ID NO 838 :	n represents 8 to 9 repeats of t (from Location 21).
	SEQ ID NO 858 :	n represents g or deletion (Location 21).
	SEQ ID NO 864 :	n represents cttt or deletion (Location 21).
10	SEQ ID NO 869 :	n represents t or deletion (Location 21).
	SEQ ID NO 874 :	n represents c or deletion (Location 21).
	SEQ ID NO 875 :	n represents a or deletion (Location 21).
	SEQ ID NO 878 :	n represents gtt or deletion (Location 21).
	SEQ ID NO 879 :	n represents t or deletion (Location 21).
15	SEQ ID NO 899 :	n represents at or deletion (Location 21).
	SEQ ID NO 913 :	n represents g or deletion (Location 21).
	SEQ ID NO 920 :	n represents 15 to 17 repeats of a (from Location 21).
	SEQ ID NO 934 :	n represents t or deletion (Location 21).
	SEQ ID NO 938 :	n represents t or deletion (Location 21).
20	SEQ ID NO 950 :	n represents t or deletion (Location 21).
	SEQ ID NO 954 :	n represents a or deletion (Location 21).
	SEQ ID NO 955 :	n represents 13 to 15 repeats of t (from Location 21).
	SEQ ID NO 956 :	n represents 12 to 13 repeats of a (from Location 21).
	SEQ ID NO 957 :	n represents t or deletion (Location 21).
25	SEQ ID NO 959 :	n represents t or deletion (Location 21).
	SEQ ID NO 960 :	n represents 13 to 15 repeats of a (from Location 21).
	SEQ ID NO 965 :	n represents a or deletion (Location 21).
	SEQ ID NO 971 :	n represents 5 to 11 repeats of t (from Location 21).
	SEQ ID NO 973 :	n represents 8 to 9 repeats of t (from Location 21).
30	SEQ ID NO 974 :	n represents t or deletion (Location 21).
	SEQ ID NO 985 :	n represents 9 to 10 repeats of t (from Location 21).
	SEQ ID NO 988 :	n represents 10 to 11 repeats of a (from Location 21).
	SEQ ID NO 994 :	n represents a or deletion (Location 21).
	SEQ ID NO 1001 :	n represents a or deletion (Location 21).
35	SEQ ID NO 1012 :	n represents ct or deletion (Location 21).

	SEQ ID NO 1031 : n represents t or deletion (Location 21).
	SEQ ID NO 1037 : n represents a or deletion (Location 21).
	SEQ ID NO 1038 : n represents at or deletion (Location 21).
	SEQ ID NO 1048 : n represents tgtccaaaggaaggacacg or deletion (Location 21).
5	SEQ ID NO 1054 : n represents 6 to 8 repeats of tc (from Location 21).
	SEQ ID NO 1056 : n represents c or deletion (Location 21).
	SEQ ID NO 1059 : n represents t or deletion (Location 21).
	SEQ ID NO 1064 : n represents t or deletion (Location 21).
	SEQ ID NO 1065 : n represents c or deletion (Location 21).
10	SEQ ID NO 1073 : n represents a or deletion (Location 21).
	SEQ ID NO 1075 : n represents t or deletion (Location 21).
	SEQ ID NO 1082 : n represents 6 to 7 repeats of gatt (from Location 21).
	SEQ ID NO 1083 : n represents t or deletion (Location 21).
	SEQ ID NO 1088 : n represents t or deletion (Location 21).
15	SEQ ID NO 1089 : n represents gt or deletion (Location 21).
	SEQ ID NO 1092 : n represents a or deletion (Location 21).
	SEQ ID NO 1093 : n represents a or deletion (Location 21).
	SEQ ID NO 1097 : n represents t or deletion (Location 21).
	SEQ ID NO 1100 : n represents at or deletion (Location 21).
20	SEQ ID NO 1106 : n represents a or deletion (Location 21).
	SEQ ID NO 1109 : n represents t or deletion (Location 21).
	SEQ ID NO 1112 : n represents at or deletion (Location 21).
	SEQ ID NO 1113 : n represents a or deletion (Location 21).
	SEQ ID NO 1114 : n represents 12 to 14 repeats of t (from Location 21).
25	SEQ ID NO 1117 : n represents t or deletion (Location 21).
	SEQ ID NO 1119 : n represents cac or deletion (Location 21).
	SEQ ID NO 1126 : n represents cca or deletion (Location 21).
	SEQ ID NO 1154 : n represents t or deletion (Location 21).
	SEQ ID NO 1184 : n represents c or deletion (Location 21).
30	SEQ ID NO 1192 : n represents aaaa or deletion (Location 21).
	SEQ ID NO 1205 : n represents c or deletion (Location 21).
	SEQ ID NO 1215 : n represents 8 to 9 repeats of t (from Location 21).
	SEQ ID NO 1216 : n represents a or deletion (Location 21).
	SEQ ID NO 1228 : n represents taac or deletion (Location 21).
35	SEQ ID NO 1229 : n represents ctcttt or deletion (Location 21).

	SEQ ID NO 1230 : n represents ct or deletion (Location 21).
	SEQ ID NO 1237 : n represents a or deletion (Location 21).
	SEQ ID NO 1240 : n represents t or deletion (Location 21).
	SEQ ID NO 1243 : n represents g or deletion (Location 21).
5	SEQ ID NO 1246 : n represents aattagaa or deletion (Location 21).
	SEQ ID NO 1247 : n represents tttaaaa or tttaa (Location 21).
	SEQ ID NO 1250 : n represents t or deletion (Location 21).
	SEQ ID NO 1255 : n represents t or deletion (Location 21).
	SEQ ID NO 1267 : n represents c or deletion (Location 21).
10	SEQ ID NO 1292 : n represents 11 to 14 repeats of t (from Location 21).
	SEQ ID NO 1293 : n represents t or deletion (Location 21).
	SEQ ID NO 1294 : n represents 10 to 13 repeats of t (from Location 21).
	SEQ ID NO 1295 : n represents t or deletion (Location 21).
	SEQ ID NO 1297 : n represents t or deletion (Location 21).
15	SEQ ID NO 1298 : n represents ta or deletion (Location 21).
	SEQ ID NO 1300 : n represents 13 to 15 repeats of t (from Location 21).
	SEQ ID NO 1301 : n represents c or deletion (Location 21).
	SEQ ID NO 1302 : n represents 17 to 20 repeats of a (from Location 21).
	SEQ ID NO 1303 : n represents 11 to 13 repeats of t (from Location 21).
20	SEQ ID NO 1304 : n represents 8 to 9 repeats of t (from Location 21).
	SEQ ID NO 1305 : n represents 10 to 11 repeats of a (from Location 21).
	SEQ ID NO 1306 : n represents 16 to 19 repeats of a (from Location 21).
	SEQ ID NO 1398 : n represents g or deletion (Location 21).
	SEQ ID NO 1400 : n represents 6 to 7 repeats of a (from Location 21).
25	SEQ ID NO 1401 : n represents c or deletion (Location 21).
	SEQ ID NO 1403 : n represents tcctcaggg or deletion (Location 21).
	SEQ ID NO 1404 : n represents 8 to 10 repeats of cgc (from Location 21).
	SEQ ID NO 1405 : n represents 10 to 12 repeats of a (from Location 21).
30	SEQ ID NO 1406 : n represents caccaggcagcagactctgatgaggaggggagggg or deletion (Location 21).
	SEQ ID NO 1408 : n represents g or deletion (Location 21).
	SEQ ID NO 1448 : n represents tcac or deletion (Location 21).
	SEQ ID NO 1449 : n represents t or deletion (Location 21).
	SEQ ID NO 1450 : n represents 9 to 11 repeats of t (from Location 21).
35	SEQ ID NO 1451 : n represents 7 to 8 repeats of a (from Location 21).

	SEQ ID NO 1487 : n represents agg or deletion (Location 21).
	SEQ ID NO 1488 : n represents taacatt or deletion (Location 21).
	SEQ ID NO 1489 : n represents 10 to 12 repeats of a (from Location 21).
	SEQ ID NO 1490 : n represents 15 to 17 repeats of t (from Location 21).
5	SEQ ID NO 1491 : n represents 11 to 13 repeats of a (from Location 21).
	SEQ ID NO 1517 : n represents 11 to 13 repeats of t (from Location 21).
	SEQ ID NO 1518 : n represents t or deletion (Location 21).
	SEQ ID NO 1519 : n represents t or deletion (Location 21).
	SEQ ID NO 1520 : n represents 10 to 12 repeats of a (from Location 21).
10	SEQ ID NO 1521 : n represents t or deletion (Location 21)
	SEQ ID NO 1523 : n represents 7 to 9 repeats of c (from Location 21).
	SEQ ID NO 1524 : n represents a or deletion (Location 21)
	SEQ ID NO 1531 : n represents 13 to 16 repeats of t (from Location 21).
	SEQ ID NO 1532 : n represents 9 to 10 repeats of t (from Location 21).
15	SEQ ID NO 1533 : n represents 14 to 16 repeats of t (from Location 21).
	SEQ ID NO 1534 : n represents 13 to 17 repeats of t (from Location 21).
	SEQ ID NO 1535 : n represents t or deletion (Location 21).
	SEQ ID NO 1537 : n represents 8 to 9 repeats of a (from Location 21).
	SEQ ID NO 1538 : n represents 8 to 9 repeats of t (from Location 21).
20	SEQ ID NO 1539 : n represents gcagtattactgtagt or deletion (Location 21).
	SEQ ID NO 1540 : n represents 13 to 14 repeats of t (from Location 21).
	SEQ ID NO 1541 : n represents 9 to 10 repeats of t (from Location 21).
	SEQ ID NO 1542 : n represents 10 to 11 repeats of t (from Location 21).
	SEQ ID NO 1547 : n represents 10 to 14 repeats of a (from Location 21).
25	SEQ ID NO 1548 : n represents 13 to 15 repeats of a (from Location 21).
	SEQ ID NO 1549 : n represents a or deletion (Location 21).
	SEQ ID NO 1550 : n represents t or deletion (Location 21).
	SEQ ID NO 1558 : n represents 13 to 15 repeats of a (from Location 21).
	SEQ ID NO 1559 : n represents 12 to 15 repeats of a (from Location 21).
30	SEQ ID NO 1576 : n represents g or deletion (Location 21).
	SEQ ID NO 1578 : n represents aa or deletion (Location 21).
	SEQ ID NO 1623 : n represents a or deletion (Location 21).
	SEQ ID NO 1625 : n represents aa or deletion (Location 21).
	SEQ ID NO 1626 : n represents ca or deletion (Location 21).
35	SEQ ID NO 1627 : n represents t or deletion (Location 21).

	SEQ ID NO 1628 :	n represents tgtgtg or deletion (Location 21).
	SEQ ID NO 1716 :	n represents a or deletion (Location 21).
	SEQ ID NO 1718 :	n represents g or deletion (Location 21).
	SEQ ID NO 1720 :	n represents actt or deletion (Location 21).
5	SEQ ID NO 1721 :	n represents ttta or deletion (Location 21).
	SEQ ID NO 1722 :	n represents 11 to 13 repeats of a (from Location 21).
	SEQ ID NO 1723 :	n represents 8 to 10 repeats of t (from Location 21).
	SEQ ID NO 1724 :	n represents 12 to 14 repeats of a (from Location 21).
	SEQ ID NO 1725 :	n represents ctgtta or deletion (Location 21).
10	SEQ ID NO 1726 :	n represents 9 to 10 repeats of a (from Location 21).
	SEQ ID NO 1727 :	n represents ctt or deletion (Location 21).
	SEQ ID NO 1728 :	n represents ctt or deletion (Location 21).
	SEQ ID NO 1730 :	n represents a or deletion (Location 21).
	SEQ ID NO 1731 :	n represents 9 to 11 repeats of a (from Location 21)
15	SEQ ID NO 1732 :	n represents tgt or deletion (Location 21).
	SEQ ID NO 1733 :	n represents 24 to 27 repeats of a (from Location 21)
	SEQ ID NO 1734 :	n represents 10 to 21 repeats of ta (from Location 21)
	SEQ ID NO 1735 :	n represents 8 to 10 repeats of a (from Location 21)
	SEQ ID NO 1736 :	n represents 11 to 13 repeats of a (from Location 21)
20	SEQ ID NO 1737 :	n represents 8 to 10 repeats of a (from Location 21)
	SEQ ID NO 1795 :	n represents ctat or deletion (Location 21).
	SEQ ID NO 1796 :	n represents atattcacttggtatctg or deletion (Location 21).
	SEQ ID NO 1797 :	n represents ttta or deletion (Location 21).
	SEQ ID NO 1798 :	n represents t or deletion (Location 21).
25	SEQ ID NO 1800 :	n represents g or deletion (Location 21).
	SEQ ID NO 1801 :	n represents a or deletion (Location 21).
	SEQ ID NO 1802 :	n represents 9 to 11 repeats of a (from Location 21).
	SEQ ID NO 1803 :	n represents g or deletion (Location 21).
	SEQ ID NO 1804 :	n represents 4 to 5 repeats of at (from Location 21).
30	SEQ ID NO 1805 :	n represents 7 to 8 repeats of t (from Location 21).
	SEQ ID NO 1806 :	n represents 19 to 23 repeats of t (from Location 21).
	SEQ ID NO 1807 :	n represents t or deletion (Location 21).
	SEQ ID NO 1808 :	n represents tgat or deletion (Location 21).
	SEQ ID NO 1809 :	n represents 8 to 10 repeats of t (from Location 21).
35	SEQ ID NO 1810 :	n represents a or deletion (Location 21).

	SEQ ID NO 1827 :	n represents gtg or deletion (Location 21).
	SEQ ID NO 1829 :	n represents gg or tgggtgggtgga (Location 21).
	SEQ ID NO 1849 :	n represents acaaca or deletion (Location 21).
	SEQ ID NO 1850 :	n represents 11 to 13 repeats of t (from Location 21).
5	SEQ ID NO 1852 :	n represents 15 to 18 repeats of ac (from Location 21).
	SEQ ID NO 1858 :	n represents 18 to 26 repeats of t (from Location 21).
	SEQ ID NO 1867 :	n represents tc or deletion (Location 21).
	SEQ ID NO 1871 :	n represents 16 to 18 repeats of t (from Location 21).
	SEQ ID NO 1886 :	n represents 18 to 20 repeats of t (from Location 21).
10	SEQ ID NO 1887 :	n represents tggtaagt or deletion (Location 21).
	SEQ ID NO 1889 :	n represents t or deletion (Location 21).
	SEQ ID NO 1895 :	n represents g or deletion (Location 21).
	SEQ ID NO 1896 :	n represents g or deletion (Location 21).
	SEQ ID NO 1897 :	n represents c or deletion (Location 21).
15	SEQ ID NO 1898 :	n represents ctct or deletion (Location 21).
	SEQ ID NO 1901 :	n represents a or deletion (Location 21).
	SEQ ID NO 1904 :	n represents t or deletion (Location 21).
	SEQ ID NO 1911 :	n represents 14 to 17 repeats of t (from Location 21).
	SEQ ID NO 1916 :	n represents 12 to 15 repeats of t (from Location 21).
20	SEQ ID NO 1917 :	n represents 10 to 13 repeats of a (from Location 21).
	SEQ ID NO 1918 :	n represents 25 to 27 repeats of a (from Location 21).
	SEQ ID NO 1939 :	n represents c or deletion (Location 21).
	SEQ ID NO 1948 :	n represents 20 to 24 repeats of t (from Location 21).
	SEQ ID NO 1951 :	n represents t or deletion (Location 21).
25	SEQ ID NO 1952 :	n represents t or deletion (Location 21).
	SEQ ID NO 1954 :	n represents g or deletion (Location 21).
	SEQ ID NO 1960 :	n represents 18 to 23 repeats of t (from Location 21).
	SEQ ID NO 1980 :	n represents c or deletion (Location 21).
	SEQ ID NO 2040 :	n represents a or deletion (Location 21).
30	SEQ ID NO 2044 :	n represents a or deletion (Location 21).
	SEQ ID NO 2047 :	n represents tt or deletion (Location 21).
	SEQ ID NO 2050 :	n represents at or deletion (Location 21).
	SEQ ID NO 2076 :	n represents tgt or deletion (Location 21).
	SEQ ID NO 2085 :	n represents t or deletion (Location 21).
35	SEQ ID NO 2190 :	n represents t or deletion (Location 21).

	SEQ ID NO 2196 :	n represents g or deletion (Location 21).
	SEQ ID NO 2197 :	n represents 11 to 13 repeats of t (from Location 21).
	SEQ ID NO 2199 :	n represents a or deletion (Location 21).
	SEQ ID NO 2201 :	n represents 9 to 11 repeats of t (from Location 21).
5	SEQ ID NO 2204 :	n represents t or deletion (Location 21).
	SEQ ID NO 2206 :	n represents t or deletion (Location 21).
	SEQ ID NO 2210 :	n represents t or deletion (Location 21).
	SEQ ID NO 2215 :	n represents aaga or deletion (Location 21).
	SEQ ID NO 2219 :	n represents aaaa or deletion (Location 21).
10	SEQ ID NO 2223 :	n represents 9 to 11 repeats of t (from Location 21).
	SEQ ID NO 2231 :	n represents a or deletion (Location 21).
	SEQ ID NO 2254 :	n represents 11 to 13 repeats of t (from Location 21).
	SEQ ID NO 2270 :	n represents acta or deletion (Location 21).
	SEQ ID NO 2276 :	n represents gtg or deletion (Location 21).
15	SEQ ID NO 2281 :	n represents 11 to 12 repeats of t (from Location 21).
	SEQ ID NO 2291 :	n represents tta or deletion (Location 21).
	SEQ ID NO 2305 :	n represents g or deletion (Location 21).
	SEQ ID NO 2307 :	n represents a or deletion (Location 21).
	SEQ ID NO 2309 :	n represents cct or deletion (Location 21).
20	SEQ ID NO 2320 :	n represents gga or deletion (Location 21).
	SEQ ID NO 2330 :	n represents 12 to 14 repeats of t (from Location 21).
	SEQ ID NO 2335 :	n represents 16 to 17 repeats of t (from Location 21).
	SEQ ID NO 2347 :	n represents g or deletion (Location 21).
	SEQ ID NO 2380 :	n represents c or deletion (Location 21).
25	SEQ ID NO 2440 :	n represents ag or deletion (Location 21).
	SEQ ID NO 2446 :	n represents g or deletion (Location 21).
	SEQ ID NO 2447 :	n represents a or deletion (Location 21).
	SEQ ID NO 2475 :	n represents g or deletion (Location 21).
	SEQ ID NO 2479 :	n represents c or deletion (Location 21).
30	SEQ ID NO 2484 :	n represents ct or deletion (Location 21).
	SEQ ID NO 2486 :	n represents gc or deletion (Location 21).
	SEQ ID NO 2489 :	n represents c or deletion (Location 21).
	SEQ ID NO 2524 :	n represents c or deletion (Location 21).
	SEQ ID NO 2530 :	n represents tc or deletion (Location 21).
35	SEQ ID NO 2542 :	n represents c or deletion (Location 21).

	SEQ ID NO 2544 :	n represents g or deletion (Location 21).
	SEQ ID NO 2557 :	n represents a or deletion (Location 21).
	SEQ ID NO 2561 :	n represents ca or deletion (Location 21).
	SEQ ID NO 2562 :	n represents t or deletion (Location 21).
5	SEQ ID NO 2574 :	n represents ct or deletion (Location 21).
	SEQ ID NO 2605 :	n represents a or deletion (Location 21).
	SEQ ID NO 2620 :	n represents t or deletion (Location 21).
	SEQ ID NO 2621 :	n represents t or deletion (Location 21).
	SEQ ID NO 2621 :	n represents 11 to 13 repeats of t (from Location 21).
10	SEQ ID NO 2627 :	n represents t or deletion (Location 21).
	SEQ ID NO 2629 :	n represents 16 to 18 repeats of t (from Location 21).
	SEQ ID NO 2631 :	n represents ctta or deletion (Location 21).
	SEQ ID NO 2632 :	n represents c or deletion (Location 21).
	SEQ ID NO 2634 :	n represents 10 to 12 repeats of a (from Location 21).
15	SEQ ID NO 2635 :	n represents gt or deletion (Location 21).
	SEQ ID NO 2636 :	n represents a or deletion (Location 21).
	SEQ ID NO 2641 :	n represents aatt or deletion (Location 21).
	SEQ ID NO 2643 :	n represents t or deletion (Location 21).
	SEQ ID NO 2649 :	n represents g or deletion (Location 21).
20	SEQ ID NO 2661 :	n represents at or deletion (Location 21).
	SEQ ID NO 2667 :	n represents 4 to 5 repeats of caaaa (from Location 21).
	SEQ ID NO 2676 :	n represents 9 to 10 repeats of a (from Location 21).
	SEQ ID NO 2681 :	n represents a or deletion (Location 21).
	SEQ ID NO 2687 :	n represents t or deletion (Location 21).
25	SEQ ID NO 2691 :	n represents t or deletion (Location 21).
	SEQ ID NO 2692 :	n represents g or deletion (Location 21).
	SEQ ID NO 2700 :	n represents t or deletion (Location 21).
	SEQ ID NO 2701 :	n represents t or deletion (Location 21).
	SEQ ID NO 2702 :	n represents a or deletion (Location 21).
30	SEQ ID NO 2712 :	n represents gaa or deletion (Location 21).
	SEQ ID NO 2713 :	n represents ag or deletion (Location 21).
	SEQ ID NO 2729 :	n represents 9 to 11 repeats of t (from Location 21).
	SEQ ID NO 2730 :	n represents a or deletion (Location 21).
	SEQ ID NO 2731 :	n represents t or deletion (Location 21).
35	SEQ ID NO 2813 :	n represents tat or deletion (Location 21).

- SEQ ID NO 2814 : n represents 14 to 17 repeats of ac (from Location 21).
- SEQ ID NO 2815 : n represents 16 to 27 repeats of a (from Location 21).
- SEQ ID NO 2816 : n represents t or deletion (Location 21).
- SEQ ID NO 2817 : n represents 8 to 10 repeats of a (from Location 21).
- 5 SEQ ID NO 2818 : n represents 9 to 11 repeats of gt (from Location 21).
- SEQ ID NO 2819 : n represents aa or deletion (Location 21).
- SEQ ID NO 2820 : n represents t or deletion (Location 21).
- SEQ ID NO 2821 : n represents 8 to 12 repeats of ac (from Location 21).
- SEQ ID NO 2822 : n represents a or deletion (Location 21).
- 10 SEQ ID NO 2842 : n represents agg or deletion (Location 21).
- SEQ ID NO 2844 : n represents 11 to 15 repeats of a (from Location 21).
- SEQ ID NO 2845 : n represents 11 to 14 repeats of a (from Location 21).
- SEQ ID NO 2848 : n represents gt or deletion (Location 21).
- SEQ ID NO 2864 : n represents ta or deletion (Location 21).
- 15 SEQ ID NO 2947 : n represents 16 to 19 repeats of a (from Location 21).
- SEQ ID NO 2948 : n represents aa or deletion (Location 21).
- SEQ ID NO 2950 : n represents t or deletion (Location 21).
- SEQ ID NO 2951 : n represents 10 to 12 repeats of t (from Location 21).
- SEQ ID NO 2952 : n represents aa or deletion (Location 21).
- 20 SEQ ID NO 2953 : n represents ttgacagtccaatat, ttgaca, gtccaatat or deletion
(Location 21).
- SEQ ID NO 2954 : n represents cta or deletion (Location 21).
- SEQ ID NO 2955 : n represents a or deletion (Location 21).
- SEQ ID NO 2957 : n represents 9 to 11 repeats of t (From Location 21).
- 25 SEQ ID NO 2958 : n represents c or deletion (Location 21).
- SEQ ID NO 2960 : n represents gagatgtgtggctcacat or deletion (Location 21).
- SEQ ID NO 2962 : n represents cc or deletion (Location 21).
- SEQ ID NO 2963 : n represents act or deletion (Location 21).
- SEQ ID NO 3045 : n represents a or deletion (Location 21).
- 30 SEQ ID NO 3055 : n represents 8 to 11 repeats of t (from Location 21).
- SEQ ID NO 3056 : n represents 10 to 13 repeats of t (from Location 21).
- SEQ ID NO 3112 : n represents g or deletion (Location 21).
- SEQ ID NO 3113 : n represents c or deletion (Location 21).
- SEQ ID NO 3194 : n represents t or deletion (Location 21).
- 35 SEQ ID NO 3195 : n represents 12 to 15 repeats of t (from Location 21).

- SEQ ID NO 3249 : n represents a or deletion (Location 21).
 SEQ ID NO 3250 : n represents at or deletion (Location 21).
 SEQ ID NO 3365 : n represents 16 repeats of cctgc or 16 repeats of cctgt (from Location 21).
- 5 SEQ ID NO 3366 : n represents t or deletion (Location 21).
 SEQ ID NO 3368 : n represents c or deletion (Location 21).
 SEQ ID NO 3379 : n represents acac or deletion (Location 21).
 SEQ ID NO 3388 : n represents gatttgggtatccag or deletion (Location 21).
 SEQ ID NO 3390 : n represents ag or deletion (Location 21).
- 10 SEQ ID NO 3391 : n represents ta or deletion (Location 21).
 SEQ ID NO 3397 : n represents t or deletion (Location 21).
 SEQ ID NO 3399 : n represents 12 to 14 repeats of gt from Location 21).
 SEQ ID NO 3411 : n represents cagaggct or deletion (Location 21).
 SEQ ID NO 3412 : n represents ct or deletion (Location 21).
- 15 SEQ ID NO 3413 : n represents ag or deletion (Location 21).
 SEQ ID NO 3425 : n represents gtaaa or deletion (Location 21).
 SEQ ID NO 3426 : n represents aaaaa or deletion (Location 21).
 SEQ ID NO 3427 : n represents a or deletion (Location 21).
 SEQ ID NO 3468 : n represents tc or deletion (Location 21).
- 20 SEQ ID NO 3470 : n represents t or deletion (Location 21).
 SEQ ID NO 3471 : n represents t or deletion (Location 21).
 SEQ ID NO 3472 : n represents gaagaaactgtgacagttt or deletion (Location 21).
 SEQ ID NO 3473 : n represents cct or deletion (Location 21).
 SEQ ID NO 3474 : n represents ttic or deletion (Location 21).
- 25 SEQ ID NO 3475 : n represents ttcttttaaattg or deletion (Location 21).
 SEQ ID NO 3477 : n represents ttcaggccttt or deletion (Location 21).
 SEQ ID NO 3479 : n represents ggcctg or deletion (Location 21).
 SEQ ID NO 3481 : n represents a or deletion (Location 21).
 SEQ ID NO 3510 : n represents 9 to 11 repeats of c (from Location 21).
- 30 SEQ ID NO 3511 : n represents 15 to 21 repeats of a (from Location 21).
 SEQ ID NO 3512 : n represents ggggtggcggtggg or deletion (Location 21).
 SEQ ID NO 3513 : n represents t or deletion (Location 21).
 SEQ ID NO 3514 : n represents a or deletion (Location 21).
 SEQ ID NO 3516 : n represents a or deletion (Location 21).
- 35 SEQ ID NO 3517 : n represents 10 to 12 repeats of t (from Location 21).

	SEQ ID NO 3518 : n represents tt or deletion (Location 21).
	SEQ ID NO 3520 : n represents tcctccttgaagctgacgt or deletion (Location 21).
	SEQ ID NO 3521 : n represents 12 to 18 repeats of ca (from Location 21).
	SEQ ID NO 3534 : n represents gtt or deletion (Location 21).
5	SEQ ID NO 3537 : n represents ga or deletion (Location 21).
	SEQ ID NO 3561 : n represents t or deletion (Location 21).
	SEQ ID NO 3580 : n represents t or deletion (Location 21).
	SEQ ID NO 3581 : n represents t or deletion (Location 21).
	SEQ ID NO 3582 : n represents t or deletion (Location 21).
10	SEQ ID NO 3605 : n represents at or deletion (Location 21).
	SEQ ID NO 3606 : n represents a or deletion (Location 21).
	SEQ ID NO 3607 : n represents c or deletion (Location 21).
	SEQ ID NO 3637 : n represents c or deletion (Location 21).
	SEQ ID NO 3645 : n represents t or deletion (Location 21).
15	SEQ ID NO 3646 : n represents ttc or deletion (Location 21).
	SEQ ID NO 3657 : n represents ctt or deletion (Location 21).
	SEQ ID NO 3689 : n represents 8 to 9 repeats of a (from Location 21).
	SEQ ID NO 3693 : n represents 10 to 12 repeats of t (from Location 21).
	SEQ ID NO 3699 : n represents 22 to 25 repeats of t (from Location 21).
20	SEQ ID NO 3710 : n represents t or deletion (Location 21).
	SEQ ID NO 3713 : n represents a or deletion (Location 21).
	SEQ ID NO 3714 : n represents a or deletion (Location 21).
	SEQ ID NO 3716 : n represents c or deletion (Location 21).
	SEQ ID NO 3717 : n represents 10 to 12 repeats of t (from Location 21).
25	SEQ ID NO 3718 : n represents a or deletion (Location 21).
	SEQ ID NO 3719 : n represents 9 to 11 repeats of t (from Location 21).
	SEQ ID NO 3722 : n represents a or deletion (Location 21).
	SEQ ID NO 3725 : n represents t or deletion (Location 21).
	SEQ ID NO 3729 : n represents a or deletion (Location 21).
30	SEQ ID NO 3741 : n represents a or deletion (Location 21).
	SEQ ID NO 3745 : n represents a or deletion (Location 21).
	SEQ ID NO 3754 : n represents 9 to 10 repeats of t (from Location 21).
	SEQ ID NO 3755 : n represents aag or deletion (Location 21).
	SEQ ID NO 3757 : n represents t or deletion (Location 21).
35	SEQ ID NO 3758 : n represents t or deletion (Location 21).

	SEQ ID NO 3760 :	n represents t or deletion (Location 21).
	SEQ ID NO 3761 :	n represents t or deletion (Location 21).
	SEQ ID NO 3763 :	n represents t or deletion (Location 21).
	SEQ ID NO 3765 :	n represents a or deletion (Location 21).
5	SEQ ID NO 3767 :	n represents a or deletion (Location 21).
	SEQ ID NO 3774 :	n represents 7 to 8 repeats of gt (from Location 21).
	SEQ ID NO 3786 :	n represents cct or deletion (Location 21).
	SEQ ID NO 3788 :	n represents tc or deletion (Location 21).
	SEQ ID NO 3804 :	n represents ca or deletion (Location 21).
10	SEQ ID NO 3826 :	n represents g or deletion (Location 21).
	SEQ ID NO 3849 :	n represents t or deletion (Location 21).
	SEQ ID NO 3878 :	n represents gccag or deletion (Location 21).
	SEQ ID NO 3918 :	n represents a or deletion (Location 21).
	SEQ ID NO 3921 :	n represents g or deletion (Location 21).
15	SEQ ID NO 3922 :	n represents t or deletion (Location 21).
	SEQ ID NO 3927 :	n represents aaa or deletion (Location 21).
	SEQ ID NO 3928 :	n represents a or deletion (Location 21).
	SEQ ID NO 3939 :	n represents c or deletion (Location 21).
	SEQ ID NO 3969 :	n represents 17 to 19 repeats of a (from Location 21).
20	SEQ ID NO 3972 :	n represents 16 to 18 repeats of a (from Location 21).
	SEQ ID NO 3973 :	n represents 4 to 6 repeats of ga (from Location 21).
	SEQ ID NO 3986 :	n represents a or deletion (Location 21).
	SEQ ID NO 4015 :	n represents 2 to 3 repeats of tc (from Location 21).
	SEQ ID NO 4021 :	n represents 6 to 7 repeats of a (from Location 21).
25	SEQ ID NO 4023 :	n represents 13 to 15 repeats of a (from Location 21).
	SEQ ID NO 4025 :	n represents 9 to 10 repeats of t (from Location 21).
	SEQ ID NO 4027 :	n represents 11 to 14 repeats of a (from Location 21).
	SEQ ID NO 4029 :	n represents 14 to 17 repeats of t (from Location 21).
	SEQ ID NO 4030 :	n represents 8 to 9 repeats of a (from Location 21).
30	SEQ ID NO 4037 :	n represents g or deletion (Location 21).
	SEQ ID NO 4057 :	n represents 14 to 17 repeats of t (from Location 21).
	SEQ ID NO 4061 :	n represents 7 to 9 repeats of g (from Location 21).
	SEQ ID NO 4066 :	n represents 9 to 10 repeats of a (from Location 21).
	SEQ ID NO 4074 :	n represents 9 to 10 repeats of a (from Location 21).
35	SEQ ID NO 4076 :	n represents 6 to 7 repeats of g (from Location 21).

- SEQ ID NO 4083 : n represents g or deletion (Location 21).
 SEQ ID NO 4098 : n represents 8 to 9 repeats of a (from Location 21).
 SEQ ID NO 4101 : n represents 4 to 6 repeats of c (from Location 21).
 SEQ ID NO 4123 : n represents ggCGaaggCGgCGgc or deletion (Location 21).
 5 SEQ ID NO 4125 : n represents ata or deletion (Location 21).
 SEQ ID NO 4128 : n represents 11 to 12 repeats of t (from Location 21).
 SEQ ID NO 4129 : n represents 12 to 14 repeats of t (from Location 21).
 SEQ ID NO 4133 : n represents 9 to 10 repeats of t (from Location 21).
 SEQ ID NO 4135 : n represents 6 to 7 repeats of ta (from Location 21).
 10 SEQ ID NO 4137 : n represents tgTataCGTataCaTataCGTataCaTataCaTataCGTata or
 deletion (Location 21).
 SEQ ID NO 4143 : n represents attt or deletion (Location 21).
 SEQ ID NO 4150 : n represents cct or deletion (Location 21).
 SEQ ID NO 4159 : n represents tggt or deletion (Location 21).
 15 SEQ ID NO 4160 : n represents a or deletion (Location 21).
 SEQ ID NO 4171 : n represents 9 to 10 repeats of t (from Location 21).
 SEQ ID NO 4178 : n represents a or deletion (Location 21).
 SEQ ID NO 4206 : n represents a or deletion (Location 21).
 SEQ ID NO 4255 : n represents a or deletion (Location 21).
 20 SEQ ID NO 4289 : n represents gtg or deletion (Location 21).
 SEQ ID NO 4291 : n represents gg or Tggtggggtgga (Location 21).
 SEQ ID NO 4307 : n represents ct or deletion (Location 21).

[Brief Description of Drawings]

- 25 Figure 1 shows TaqMan probes.
 Figure 2 shows an outline of the TaqMan PCR method.
 Figure 3 shows probes labeled with fluorescent dyes.
 Figure 4 shows an outline of the INVADER assay.
 Figure 5 shows a FRET probe.
 30 Figure 6 shows an outline of the INVADER assay.
 Figure 7 shows a probe in which the allele does not match the probe.
 Figure 8 shows one embodiment of allele identification using a ligation reaction.
 Figure 9A shows a structure of ATP-binding cassette subfamily A member 1
 (ABCA1) gene and the SNP location therein.
 35 Accession No.: AF275948.1 and AL359846.11

Figure 9B shows a structure of ATP-binding cassette subfamily A member 1 (ABCA1) gene and the SNP location therein. (continuation of Figure 9A)

Accession No.: AF275948.1 and AL359846.11

Figure 10 shows a structure of ATP-binding cassette subfamily A member 4 (ABCA4) gene and the SNP location therein.

Accession No.: NT_019258.1

Figure 11 shows a structure of ATP-binding cassette subfamily A member 7 (ABCA7) gene and the SNP location therein.

Accession No.: NT_025194.1

Figure 12 shows a structure of ATP-binding cassette subfamily A member 8 (ABCA8) gene and the SNP location therein.

Accession No.: AC005922.1 and AC015844.5

Figure 13 shows a structure of ATP-binding cassette subfamily B member 1 (ABCB1) gene and the SNP location therein.

Accession No.: AC002457.1 and AC005068.1

Figure 14 shows a structure of ATP-binding cassette subfamily B member 4 (ABCB4) gene and the SNP location therein.

Accession No.: AC079591.1, AC079303.3 and AC005045.2

Figure 15 shows a structure of ATP-binding cassette subfamily B member 7 (ABCB7) gene and the SNP location therein.

Accession No.: AL360179.3 and AC002417.1

Figure 16 shows a structure of ATP-binding cassette subfamily B member 8 (ABCB8) gene and the SNP location therein.

Accession No.: AC010973.4

Figure 17 shows a structure of ATP-binding cassette subfamily B member 9 (ABCB9) gene and the SNP location therein.

Accession No.: AC026362.9 and AC073857.10

Figure 18 shows a structure of ATP-binding cassette subfamily B member 10 (ABCB10) gene and the SNP location therein.

Accession No.: AL121990.9

Figure 19 shows a structure of ATP-binding cassette subfamily B member 11 (ABCB11) gene and the SNP location therein.

Accession No.: AC008177.3 and AC069137.3

Figure 20 shows a structure of ATP-binding cassette subfamily C member 1 (ABCC1) gene and the SNP location therein.

Accession No.: AC026452.5 and AC025778.4

Figure 21 shows a structure of ATP-binding cassette subfamily C member 2 (ABCC2) gene and the SNP location therein.

Accession No.: AL392107.4

5 Figure 22 shows a structure of ATP-binding cassette subfamily C member 3 (ABCC3) gene and the SNP location therein.

Accession No.: AC004590.1 and AC005921.3

Figure 23A shows a structure of ATP-binding cassette subfamily C member 4 (ABCC4) gene and the SNP location therein.

10 Accession No.: AL356257.11, AL157818.12 and AL139381.12

Figure 23B shows a structure of ATP-binding cassette subfamily C member 4 (ABCC4) gene and the SNP location therein. (continuation of Figure 158A)

Accession No.: AL356257.11, AL157818.12, and AL139381.12

15 Figure 24 shows a structure of ATP-binding cassette subfamily C member 5 (ABCC5) gene and the SNP location therein.

Accession No.: AC068644.5

Figure 25 shows a structure of ATP-binding cassette subfamily C member 7 (ABCC7) gene and the SNP location therein.

Accession No.: AC000111.1 and AC000061.1

20 Figure 26 shows a structure of ATP-binding cassette subfamily C member 8 (ABCC8) gene and the SNP location therein.

Accession No.: AC000406.1

Figure 27 shows a structure of ATP-binding cassette subfamily C member 9 (ABCC9) gene and the SNP location therein.

25 Accession No.: AC084806.9 and AC008250.23

Figure 28 shows a structure of ATP-binding cassette subfamily D member 1 (ABCD1) gene and the SNP location therein.

Accession No.: U52111.2

30 Figure 29 shows a structure of ATP-binding cassette subfamily D member 3 (ABCD3) gene and the SNP location therein.

Accession No.: NT_019284.3

Figure 30 shows a structure of ATP-binding cassette subfamily D member 4 (ABCD4) gene and the SNP location therein.

Accession No.: AC005519.3

35 Figure 31 shows a structure of ATP-binding cassette subfamily G member 1

(ABCG1) gene and the SNP location therein.

Accession No.: AP001746.1

Figure 32 shows a structure of ATP-binding cassette subfamily G member 2 (ABCG2) gene and the SNP location therein.

5 Accession No.: NT_022959.2

Figure 33 shows a structure of ATP-binding cassette subfamily G member 4 (ABCG4) gene and the SNP location therein.

Accession No.: AP001315.3

Figure 34 shows a structure of ATP-binding cassette subfamily G member 5 (ABCG5) gene and the SNP location therein.

Accession No.: AC084265.2 and AC011242.8

Figure 35 shows a structure of ATP-binding cassette subfamily G member 8 (ABCG8) gene and the SNP location therein.

Accession No.: AC084265.2

Figure 36 shows a structure of ATP-binding cassette subfamily E member 1 (ABCE1) gene and the SNP location therein.

Accession No.: NT_006296.2

Figure 37 shows a structure of ATP-binding cassette subfamily F member 1 (ABCF1) gene and the SNP location therein.

20 Accession No.: NT_007592.3

Figure 38 shows a structure of organic anion transporter 1 (OAT1) gene and the SNP location therein.

Accession No.: AP001858.3, AJ249369.1, and AP000438.4

Figure 39 shows a structure of organic anion transporter 2 (OAT2) gene and the SNP location therein.

Accession No.: AC26532.3

Figure 40 shows a structure of organic anion transporter 3 (OAT3) gene and the SNP location therein.

Accession No.: AP001858.3

Figure 41 shows a structure of organic anion transporter polypeptide 1 (OATP1) gene and the SNP location therein.

Accession No.: AC022224.22

Figure 42 shows a structure of organic anion transporter polypeptide 2 (OATP2) gene and the SNP location therein.

35 Accession No.: NT_024399.2

Figure 43 shows a structure of organic anion transporter polypeptide 8 (OATP8) gene and the SNP location therein.

Accession No.: NT_024399.2

5 Figure 44 shows a structure of transporter 1 ATP-binding cassette subfamily B (TAP1) gene and the SNP location therein.

Accession No.: X66401.1

Figure 45 shows a structure of transporter 2 ATP-binding cassette subfamily B (TAP2) gene and the SNP location therein.

Accession No.: X66401.1

10 Figure 46 shows a structure of SLC22A4 solute carrier family 22 (organic cation transporter) member 4 (OCTN1) gene and the SNP location therein.

Accession No.: AC008599.6

Figure 47 shows a structure of SLC22A5 solute carrier family 22 (organic cation transporter) member 5 (OCTN2) gene and the SNP location therein.

15 Accession No.: AC023861.3

Figure 48 shows a structure of SLC22A1 solute carrier family 22 (organic cation transporter) member 1 (OCT1) gene and the SNP location therein.

Accession No.: AL35625.5

20 Figure 49 shows a structure of SLC22A2 solute carrier family 22 (organic cation transporter) member 2 (OCT2) gene and the SNP location therein.

Accession No.: AL162582.18

Figure 50 shows a structure of SLC10A2 solute carrier family 10 (sodium/bile acid cotransporter family) member 2 (NTCP) gene and the SNP location therein.

Accession No.: AL157789.6

25 Figure 51 shows a structure of SLC15A1 solute carrier family 15 (oligopeptide transporter) member 1 (PEPT1) gene and the SNP location therein.

Accession No.: AL353574.8 and AL391670.6

Figure 52 shows a structure of microsomal epoxide hydrolase 1 (EPHX1) gene and the SNP location therein.

30 Accession No.: AC058782.8

Figure 53 shows a structure of cytoplasmic epoxide hydrolase (EPHX2) gene and the SNP location therein.

Accession No.: AC010856.3

35 Figure 54 shows a structure of catechol-O-methyl transferase (COMT) gene and the SNP location therein.

Accession No.: AC000080.2

Figure 55 shows a structure of guanidinoacetate N-methyl transferase (GAMT) gene and the SNP location therein.

Accession No.: NT_000879.1

5 Figure 56 shows a structure of phenyl ethanolamine N-methyl transferase (PNMT) gene and the SNP location therein.

Accession No.: AC040933.3

Figure 57 shows a structure of histamine N-methyl transferase (HNMT) gene and the SNP location therein.

10 Accession No.: AC019304.3

Figure 58 shows a structure of nicotinamide N-methyl transferase (NNMT) gene and the SNP location therein.

Accession No.: AC019290.3

15 Figure 59 shows a structure of phosphatidylethanolamine N-methyl transferase (PEMT) gene and the SNP location therein.

Accession No.: AC020558.3

Figure 60 shows a structure of aldehyde dehydrogenase 1 family member A1 (ALDH1A1) gene and the SNP location therein.

Accession No.: AC009284.2 and AL162416.3

20 Figure 61 shows a structure of aldehyde dehydrogenase 1 family member A2 (ALDH1A2) gene and the SNP location therein.

Accession No.: AC025431.7 and AC012653.8

Figure 62 shows a structure of aldehyde dehydrogenase 1 family member A3 (ALDH1A3) gene and the SNP location therein.

25 Accession No.: AC015712.7

Figure 63 shows a structure of aldehyde dehydrogenase 1 family member B1 (ALDH1B1) gene and the SNP location therein.

Accession No.: AL135785.9

30 Figure 64A shows a structure of formyl tetrahydrofolate dehydrogenase (ALDH1L1) gene and the SNP location therein.

Accession No.: AC079848.6

Figure 64B shows a structure of formyl tetrahydrofolate dehydrogenase (ALDH1L1) gene and the SNP location therein. (continuation of Figure 199A)

Accession No.: AC079848.6

35 Figure 65 shows a structure of aldehyde dehydrogenase 2 (ALDH2) gene and the

SNP location therein.

Accession No.: AC002996.1 and AC003029.2

Figure 66 shows a structure of aldehyde dehydrogenase 3 family member A1 (ALDH3A1) gene and the SNP location therein.

5 Accession No.: AC005722.1

Figure 67 shows a structure of aldehyde dehydrogenase 3 family member A2 (ALDH3A2) gene and the SNP location therein.

Accession No.: AC005722.1

10 Figure 68 shows a structure of aldehyde dehydrogenase 3 family member B1 (ALDH3B1) gene and the SNP location therein.

Accession No.: AC004923.2

Figure 69 shows a structure of aldehyde dehydrogenase 3 family member B2 (ALDH3B2) gene and the SNP location therein.

Accession No.: AC021987.3

15 Figure 70 shows a structure of aldehyde dehydrogenase 5 family member A1 (ALDH5A1) gene and the SNP location therein.

Accession No.: AL031230.1

Figure 71 shows a structure of aldehyde dehydrogenase 6 family member A1 (ALDH6A1) gene and the SNP location therein.

20 Accession No.: AC005484.2

Figure 72 shows a structure of aldehyde dehydrogenase 8 family member A1 (ALDH8A1) gene and the SNP location therein.

Accession No.: AL445190.9 and AL021939.1

25 Figure 73 shows a structure of aldehyde dehydrogenase 9 family member A1 (ALDH9A1) gene and the SNP location therein.

Accession No.: AL451074.4

Figure 74 shows a structure of alcohol dehydrogenase 1 (ADH1) gene and the SNP location therein.

Accession No.: AP002027.1

30 Figure 75 shows a structure of alcohol dehydrogenase 2 (ADH2) gene and the SNP location therein.

Accession No.: AP002027.1

Figure 76 shows a structure of alcohol dehydrogenase 3 (ADH3) gene and the SNP location therein.

35 Accession No.: AP002027.1

Figure 77 shows a structure of alcohol dehydrogenase 4 (ADH4) gene and the SNP location therein.

Accession No.: AP002026.1

Figure 78 shows a structure of alcohol dehydrogenase 5 (ADH5) gene and the SNP location therein.

Accession No.: AC019131.4

Figure 79 shows a structure of alcohol dehydrogenase 6 (ADH6) gene and the SNP location therein.

Accession No.: AP002026.1

Figure 80 shows a structure of alcohol dehydrogenase 7 (ADH7) gene and the SNP location therein.

Accession No.: AC027065.3

Figure 81 shows a structure of short-chain alcohol dehydrogenase family gene (HEP27) and the SNP location therein.

Accession No.: AL135999.3

Figure 82 shows a structure of UDP glycosyltransferase 1 family polypeptide A1 (UGT1A1) and the SNP location therein.

Accession No.: AC006985.2

Figure 83 shows a structure of UDP glycosyltransferase 2 family polypeptide A1 (UGT2A1) and the SNP location therein.

Accession No.: AC011254.3

Figure 84 shows a structure of UDP glycosyltransferase 2 family polypeptide B15 (UGT2B15) and the SNP location therein.

Accession No.: AC019173.4

Figure 85 shows a structure of UDP glycosyltransferase 8 (UGT8) and the SNP location therein.

Accession No.: U31353.1

Figure 86 shows a structure of glutathione S transferase A1 (GSTA1) gene and the SNP location therein.

Accession No.: AC021133.4

Figure 87 shows a structure of glutathione S transferase A4 (GSTA4) gene and the SNP location therein.

Accession No.: AC025085.4

Figure 88 shows a structure of glutathione S transferase M1 (GSTM1) gene and the SNP location therein.

Accession No.: AC000032.7

Figure 89 shows a structure of glutathione S transferase M2 (GSTM2) gene and the SNP location therein.

Accession No.: AC000031.5

5 Figure 90 shows a structure of glutathione S transferase Z1 (GSTZ1) gene and the SNP location therein.

Accession No.: AC007954.7

Figure 91 shows a structure of glutathione S transferase Pi (GSTPi) gene and the SNP location therein.

10 Accession No.: X08058.1 and M24485.1

Figure 92 shows a structure of glutathione S transferase T1 (GSTT1) gene and the SNP location therein.

Accession No.: AF240786.1 and AP000351.3

15 Figure 93 shows a structure of microsomal glutathione S transferase 1 (MGST1) gene and the SNP location therein.

Accession No.: AC007528.5

Figure 94 shows a structure of microsomal glutathione S transferase 1-like 1 (MGST1L1) gene and the SNP location therein.

Accession No.: AC007936.2

20 Figure 95 shows a structure of microsomal glutathione S transferase T2 (MGST2) gene and the SNP location therein.

Accession No.: AC019049.4

Figure 96 shows a structure of microsomal glutathione S transferase T3 (MGST3) gene and the SNP location therein.

25 Accession No.: AC064827.2

Figure 97 shows a structure of sulfotransferase 1A1 (SULT1A1/STP1) gene and the SNP location therein.

Accession No.: U52852.2

30 Figure 98 shows a structure of sulfotransferase 1A2 (SULT1A2/STP2) gene and the SNP location therein.

Accession No.: U33886.1, U34804.1 and AC020765.5

Figure 99 shows a structure of sulfotransferase 1A3 (SULT1A3/STM/HAST) gene and the SNP location therein

Accession No.: L34160.1 and AC012645.4

35 Figure 100 shows a structure of sulfotransferase 1C1 (SULT1C1) gene and the SNP

location therein.

Accession No.: AC019100.4

Figure 101 shows a structure of sulfotransferase 1C2 (SULT1C2) gene and the SNP location therein.

5 Accession No.: AF186263.1

Figure 102 shows a structure of sulfotransferase 2A1 (SULT2A1) gene and the SNP location therein.

Accession No.: AC024582.4, AC008745.5, NT_011190.1, and AC024582.4

10 Figure 103 shows a structure of sulfotransferase 2B1 (SULT2B1) gene and the SNP location therein.

Accession No.: AC040922.2 and AC008403.6

Figure 104 shows a structure of sulfotransferase-associated protein 3 (SULTX3) gene and the SNP location therein.

Accession No.: Z97055.1

15 Figure 105 shows a structure of tyrosyl protein sulfotransferase 1 (TPST1) gene and the SNP location therein.

Accession No.: AC026281.5

Figure 106 shows a structure of tyrosyl protein sulfotransferase 2 (TPST2) gene and the SNP location therein.

20 Accession No.: Z95115.1

Figure 107 shows a structure of cerebroside sulfotransferase (CST) gene and the SNP location therein.

Accession No.: AC005006.2

25 Figure 108 shows a structure of thyroid hormone sulfotransferase (ST1B2) gene and the SNP location therein.

Accession No.: AC027059.2

Figure 109 shows a structure of carbohydrate sulfotransferase 1 (CHST1) gene and the SNP location therein.

Accession No.: NT_008982.1

30 Figure 110 shows a structure of carbohydrate sulfotransferase 2 (CHST2) gene and the SNP location therein.

Accession No.: AC055737.10

Figure 111 shows a structure of carbohydrate sulfotransferase 3 (CHST3) gene and the SNP location therein.

35 Accession No.: AC073370.3

Figure 112 shows a structure of carbohydorate sulfotransferase 4 (CHST4) gene and the SNP location therein.

Accession No.: AC010547.5

5 Figure 113 shows a structure of carbohydorate sulfotransferase 5 (CHST5) gene and the SNP location therein.

Accession No.: AC025287.3

Figure 114 shows a structure of HNK-sulfotransferase (HNK-1ST) gene and the SNP location therein.

Accession No.: AC012493.4

10 Figure 115 shows a structure of estrogen sulfotransferase (STE) gene and the SNP location therein.

Accession No.: AC074273.1

Figure 116 shows a structure of NAD (P)H: quinone oxidoreductase 1 (NQO1) gene and the SNP location therein.

15 Accession No.: M81596.1

Figure 117 shows a structure of NRH: quinone oxidoreductase 2 (NQO2) gene and the SNP location therein.

Accession No.: AB050248.1

20 Figure 118 shows a structure of p53-inducible gene 3 (PIG3) in a quinone oxidoreductase homolog and the SNP location therein.

Accession No.: AC008073.3

Figure 119 shows a structure of NADH-dehydrogenase(ubiquinone)1 α -subcomplex 1 (NDUFA1) gene and the SNP location therein.

Accession No.: AC002477.1

25 Figure 120 shows a structure of NADH-dehydrogenase(ubiquinone)1 α -subcomplex 2 (NDUFA2) gene and the SNP location therein.

Accession No.: AB054976.1

Figure 121 shows a structure of NADH-dehydrogenase(ubiquinone)1 α -subcomplex 3 (NDUFA3) gene and the SNP location therein.

30 Accession No.: AC009968.6

Figure 122 shows a structure of NADH-dehydrogenase(ubiquinone)1 α -subcomplex 5 (NDUFA5) gene and the SNP location therein.

Accession No.: AC073323.5

35 Figure 123 shows a structure of NADH-dehydrogenase(ubiquinone)1 α -subcomplex 6 (NDUFA6) gene and the SNP location therein.

Accession No.: AL021878.1

Figure 124 shows a structure of NADH-dehydrogenase(ubiquinone)1 α -subcomplex 7 (NDUFA7) gene and the SNP location therein.

Accession No.: AC010323.6

Figure 125 shows a structure of NADH-dehydrogenase(ubiquinone)1 α -subcomplex 8 (NDUFA8) gene and the SNP location therein.

Accession No.: AL162423.10

Figure 126 shows a structure of NADH-dehydrogenase(ubiquinone)1 α -subcomplex 9 (NDUFA9) gene and the SNP location therein.

Accession No.: AC005832.1

Figure 127 shows a structure of NADH-dehydrogenase(ubiquinone)1 α -subcomplex 10 (NDUFA10) gene and the SNP location therein.

Accession No.: AC013469.8

Figure 128 shows a structure of NADH-dehydrogenase(ubiquinone)1 α / β -subcomplex 1 (NDUFAB1) gene and the SNP location therein.

Accession No.: AC008870.6

Figure 129 shows a structure of NADH-dehydrogenase(ubiquinone)1 β -subcomplex 3 (NDUFB3) gene and the SNP location therein.

Accession No.: AC007272.3

Figure 130 shows a structure of NADH-dehydrogenase(ubiquinone)1 β -subcomplex 5 (NDUFB5) gene and the SNP location therein.

Accession No.: AC068361.2

Figure 131 shows a structure of NADH-dehydrogenase(ubiquinone)1 β -subcomplex 7 (NDUFB7) gene and the SNP location therein.

Accession No.: AC010527.4

Figure 132 shows a structure of NADH-dehydrogenase(ubiquinone)Fe-S protein 1 (NDUFS1) gene and the SNP location therein.

Accession No.: AC007383.4

Figure 133 shows a structure of NADH-dehydrogenase(ubiquinone)Fe-S protein 3 (NDUFS3) gene and the SNP location therein.

Accession No.: AC067943.4

Figure 134 shows a structure of NADH-dehydrogenase(ubiquinone)Fe-S protein 4 (NDUFS4) gene and the SNP location therein.

Accession No.: AC024569.3

Figure 135 shows a structure of NADH-dehydrogenase(ubiquinone)Fe-S protein 5 (NDUFS5) gene and the SNP location therein.

Accession No.: AL139015.5

5 Figure 136 shows a structure of NADH-dehydrogenase(ubiquinone)Fe-S protein 6 (NDUFS6) gene and the SNP location therein.

Accession No.: AC026443.2

Figure 137 shows a structure of NADH-dehydrogenase(ubiquinone)Fe-S protein 8 (NDUFS8) gene and the SNP location therein.

Accession No.: AC034259.2

10 Figure 138 shows a structure of NADH-dehydrogenase(ubiquinone)flavoprotein 1 (NDUFV1) gene and the SNP location therein.

Accession No.: NT_009304.2

Figure 139 shows a structure of NADH-dehydrogenase(ubiquinone)flavoprotein 2 (NDUFV2) gene and the SNP location therein.

15 Accession No.: NT_011024.2

Figure 140 shows a structure of NADH-dehydrogenase(ubiquinone)flavoprotein 3 (NDUFV3) gene and the SNP location therein.

Accession No.: AP001748.1

20 Figure 141 shows a structure of gamma-glutamyl transferase 1 (GGT1) gene and the SNP location therein.

Accession No.: D87002.1

Figure 142 shows a structure of transglutaminase 1 (TGM1) gene and the SNP location therein.

Accession No.: M98447.1

25 Figure 143 shows a structure of cytochrome P450 subfamily 1 (aromatic compound-inducible) polypeptide 1 (CYP1A1) gene and the SNP location therein.

Accession No.: X04300.1 and AC020705.4

Figure 144 shows a structure of cytochrome P450 subfamily 1 (aromatic compound-inducible) polypeptide 2 (CYP1A2) gene and the SNP location therein.

30 Accession No.: AC020705.4

Figure 145 shows a structure of cytochrome P450 subfamily 1 (dioxin-inducible) polypeptide 1 (CYP1B1) gene and the SNP location therein.

Accession No.: AC009229.4

35 Figure 146 shows a structure of cytochrome P450 subfamily 3A (aromatic compound-inducible) polypeptide 4 (CYP3A4) gene and the SNP location therein.

Accession No.: AF280107.1

Figure 147 shows a structure of cytochrome P450 subfamily 3A (aromatic compound-inducible) polypeptide 5 (CYP3A5) gene and the SNP location therein.

Accession No.: AC005020.5

5 Figure 148 shows a structure of cytochrome P450 subfamily 3A polypeptide 7 (CYP3A7) gene and the SNP location therein.

Accession No.: AF280107.1

Figure 149 shows a structure of cytochrome P450 polypeptide 43 (CYP3A43) gene and the SNP location therein.

10 Accession No.: AC011904.3

Figure 150 shows a structure of cytochrome P450 subfamily IVB polypeptide 1 (CYP4B1) gene and the SNP location therein.

Accession No.: AL356793.10

15 Figure 151 shows a structure of cytochrome P450 subfamily IVF polypeptide 2 (CYP4F2) gene and the SNP location therein.

Accession No.: AC005336.1

Figure 152 shows a structure of cytochrome P450 subfamily IVF polypeptide 3 (CYP4F3) gene and the SNP location therein.

Accession No.: AD000685.1

20 Figure 153 shows a structure of cytochrome P450 subfamily IVF polypeptide 8 (CYP4F8) gene and the SNP location therein.

Accession No.: AC068845.3

Figure 154 shows a structure of cytochrome P450 subfamily XXVIIA polypeptide 1 (CYP27A1) gene and the SNP location therein.

25 Accession No.: AC009974.7

Figure 155 shows a structure of cytochrome P450 subfamily XXVIIIB polypeptide 1 (CYP27B1) gene and the SNP location therein.

Accession No.: AC025165.27

30 Figure 156 shows a structure of allylacetamide deacetylase (AADAC) gene and the SNP location therein.

Accession No.: AC068647.4

Figure 157 shows a structure of carboxyl esterase 1 (CES1) gene and the SNP location therein

Accession No.: AC007602.4

35 Figure 158 shows a structure of carboxyl esterase 2 (CES2) gene and the SNP

location therein

Accession No.: AC027131.4

Figure 159 shows a structure of granzyme A (GZMA) gene and the SNP location therein.

Accession No.: AC091977.1

Figure 160 shows a structure of granzyme B (GZMB) gene and the SNP location therein.

Accession No.: AL136018.3

Figure 161 shows a structure of esterase D/formylglutathione hydrolase (ESD) gene and the SNP location therein.

Accession No.: AL136958.9

Figure 162A shows a structure of carboxyl ester lipase (bile salt-stimulated lipase) (CEL) gene and the SNP location therein.

Accession No.: AL138750.8, AL162417.20 and AF072711.1

Figure 162B shows a structure of carboxyl ester lipase (bile salt-stimulated lipase) (CEL) gene and the SNP location therein. (continuation of Figure 297A)

Accession No.: AL138750. , AL162417.20 and AF072711.1

Figure 163 shows a structure of interleukin 17 (cytotoxic T lymphocyte-associated serine esterase 8) (IL17) gene and the SNP location therein.

Accession No.: AL355513.11

Figure 164 shows a structure of ubiquitin carboxyl terminal esterase L3 (ubiquitin thiol esterase) (UCHL3) gene and the SNP location therein.

Accession No.: AL137244.28

Figure 165 shows a structure of dolichyl-diphosphooligosaccharide-protein glycosyltransferase (DDOST) gene and the SNP location therein.

Accession No.: D89060

Figure 166 shows a structure of neuropathy target esterase (NTE) gene and the SNP location therein.

Accession No.: AC021153

Figure 167 shows a structure of L1 cell adhesion molecule (L1CAM) gene and the SNP location therein.

Accession No.: U52112

Figure 168 shows a structure of arylalkylamine N-acetyltransferase (AANAT) gene and the SNP location therein.

Accession No.: U40391

Figure 169 shows a structure of N-acetyltransferase homolog (ARD1) gene of *Saccharomyces cerevisiae* and the SNP location therein.

Accession No.: U52112

5 Figure 170 shows a structure of N-acetyltransferase (NAT1) gene and the SNP location therein.

Accession No.: X17059

Figure 171 shows a structure of N-acetyltransferase 2 (NAT2) gene and the SNP location therein.

Accession No.: D10870

10 Figure 172 shows a structure of ATP-binding cassette subfamily B member 2 (ABCB2) gene and the SNP location therein.

Accession No.: X66401

Figure 173 shows a structure of ATP-binding cassette subfamily B member 3 (ABCB3) gene and the SNP location therein.

15 Accession No.: X66401

Figure 174 shows a structure of glutathione S transferase M3 (GSTM3) gene and the SNP location therein.

Accession No.: AF043105.1

20 Figure 175 shows a structure of glutathione S transferase M4 (GSTM4) gene and the SNP location therein.

Accession No.: M96233.1

Figure 176 shows a structure of aldehyde dehydrogenase 7 (ALDH7) gene and the SNP location therein.

Accession No.: AC004923

25 Figure 177 shows a structure of high-mobility group protein 17-like 1 (HMG17L1) gene and the SNP location therein.

Accession No.: Z97055.1

Figure 178 shows a result of typing performed on two different groups of patients using the INVADER method.

30

[Abstract]

[Problem]

The present invention provides a method for detecting a genetic polymorphism(s).

[Means for solving the problems]

- 5 A method for detecting a genetic polymorphism(s), comprising creating oligonucleotide probes and/or oligonucleotide primers so that the probes and/or primers contain a polymorphic site(s) present in a gene encoding a drug metabolizing enzyme or so that the polymorphic site(s) is/are contained in the amplified fragment when at least one of said gene encoding the drug metabolizing enzyme is amplified; and detecting at least one genetic
- 10 polymorphism in a gene of a subject encoding the drug metabolizing enzyme using the resultant oligonucleotide probes and/or oligonucleotide primers.

[Representative drawing] none

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ABCA1	1	(5' flanking region -99)	acataacagagccgggaa G/C gggcggggagagggagag	1
ABCA1	2	(intron 1 159)	gggtttaaatgggagac G/T atgtctagtacagctctg	2
ABCA1	3	(intron 1 506)	gaattgctatactctccc G/C ggacaggagcgccacagtcc	3
ABCA1	4	(intron 1 5897)	gtacaaacccctttagctt I/G gcaaacctctcttaagacc	4
ABCA1	5	(intron 1 5929)	ttaagaccgatitaaatgc C/I tccctctcatgaagctctt	5
ABCA1	6	(intron 1 5962)	aagctctctggatccact I/C ttcccatcactaagttagaa	6
ABCA1	7	(intron 1 5985)	cccatcactaagttagaaat A/C agatccctctctcttactt	7
ABCA1	8	(intron 1 11416)	ttacatgccccttatagga G/A agaaagaagaatttgtct	8
ABCA1	9	(intron 1 11935)	tcctgtggagcaaatagag G/A gctgtcagacacttggtcc	9
ABCA1	10	(intron 1 12281)	gaatgttgatttgtaaaa I/A cttataacacagtgttttt	10
ABCA1	11	(intron 1 12924)	gtctgacaatcttatact I/C aggttgaacctccggggaag	11
ABCA1	12	(intron 1 13002)	gagctcaatcacagattct C/G tctagctcacaatgaattaa	12
ABCA1	13	(intron 1 17115)	ggagcaatgacttttggaag C/I ctctctcttccaccacagag	13
ABCA1	14	(intron 1 17848)	gagggtgactgtcacocct I/C gataggagccacacactaaa	14
ABCA1	15	(intron 1 21384)	gtgggtggggaggaattggag G/C aggaagcttgcttaagtgtg	15
ABCA1	16	(intron 1 23063)	ggaggacacctgtacaccca G/A cggagttagggggcggtgtg	16
ABCA1	17	(intron 1 23131)	agtgatcatatgtcagacc G/A tggagactgtttgtcggtt	17
ABCA1	18	(intron 2 2801)	aagaaaagtgtattattica A/G gttgtgatgtcttagattgt	18
ABCA1	19	(intron 2 2830)	tgtttagattgttagagttg C/G aaagatctggcttgcatctt	19
ABCA1	20	(intron 2 2856)	tctggttgcatctgttaca A/G ctgacagaactggggctcag	20
ABCA1	21	(intron 2 3187)	tgatagtgttgctgcagc A/G tacgacgttctatggcgag	21
ABCA1	22	(intron 2 3190)	tagctgtgctgcagcata C/I ggaacttcattggcgagttc	22
ABCA1	23	(intron 2 3194)	tgttgctgcagcatacga C/I gttcattggcgagttctctgt	23
ABCA1	24	(intron 2 3204)	agcatcaggagcttctatgc G/A cagttctctgtctctgagat	24
ABCA1	25	(intron 2 3401)	acataaagcctgtgtgtgc I/C gccaggaagactagaaacgc	25
ABCA1	26	(intron 2 13927)	gtcacacataccctggcact A/G tgciaaggctgggaatgcag	26
ABCA1	27	(intron 3 4163)	ccagccacattcatcttacc G/A tagtiacctctcttagagiat	27
ABCA1	28	(intron 3 4262)	tgtcaagagaggaactaagga I/C gccagggaactttctgttag	28
ABCA1	29	(intron 3 4306)	ccctctcatcacttctccaa C/I gctggtatcatgaaccccat	29
ABCA1	30	(intron 5 490)	gatggcatttgacttgtt G/A tctttaaaagtgaaatctt	30
ABCA1	31	(intron 5 583)	tatctggggagtgggcatit I/G ctgactgaggcattggctgc	31
ABCA1	32	(intron 5 1051)	ggctacaaaactgtctttc C/I ttgggcagtaaaagagggcaa	32
ABCA1	33	(intron 5 3051)	tagagaaacagtctaatct G/A ttttcttgaaatagtcgaa	33
ABCA1	34	(intron 5 3127)	aagtcaatgatttttttaggc A/G aaatggcctctcttctctt	34
ABCA1	35	(intron 5 5924)	ctttcttcacaaaattgcc C/I ccagagactttctgggaagg	35
ABCA1	36	(intron 5 6831)	ccagtcctcagoccttgcca I/C tgcitattgtgtgtctggaaa	36
ABCA1	37	(intron 5 12678)	gctcacocgtctgtctcacc G/C accctotggccatctctct	37
ABCA1	38	(intron 5 14214)	cagcttggtcccagaggcct G/A gacctgggtcccagaggctcc	38
ABCA1	39	(intron 5 14257)	gctggttcccggccttggtc C/I cagaggccctggatgtgtggc	39
ABCA1	40	(intron 5 18078)	ccataccacaccatgcacgtg C/I acagccaaaggggtgttgact	40

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ABCA1	41	(intron 5 18795)	ctgggtctctctggacctg G/A ccagctaaagggaatctcc	41
ABCA1	42	(intron 5 18948)	gattggtagtaactaagaac G/A catattccctatctctatagg	42
ABCA1	43	(intron 5 19053)	ctccccaacattaaaagtg I/C aaggatgottattcaaatg	43
ABCA1	44	(intron 5 19148)	ggcccaagaacacigcatitt C/A gcatgctccctaaatgaagc	44
ABCA1	45	(intron 5 19229)	atgctaacagtgtagagica C/I atgtaiggggaagcattcagg	45
ABCA1	46	(intron 5 19405)	cttgctcaattttattctgtc I/C atataactcaatattactga	46
ABCA1	47	(intron 5 19534)	catgtaccctcttagctcc G/A cggattaaactctctctctca	47
ABCA1	48	(coding region 474 (Leu 158 Leu))	gaacacctctctgggttctc G/A taccacaacctctctctccc	48
ABCA1	49	(intron 6 210)	gcacacctggctcattggcc A/C gctggttaaaataaaaattga	49
ABCA1	50	(intron 6 334)	acagttctgagggaataaac G/A tggttaaagggttattgatct	50
ABCA1	51	(intron 6 2288)	ctctttcaaaagcttgggt C/I cactggaccacgtatatgaagt	51
ABCA1	52	(intron 6 2322)	atgaagtagaatagtttagg I/C ccagaaggcaattaaagtaa	52
ABCA1	53	(intron 6 2820)	gtcctttgatacattctgag I/G ttacagtaaaagagaccctgatg	53
ABCA1	54	(intron 7 416)	catacataaagatgacattgt G/A ggcctgcacagttgggaaggc	54
ABCA1	55	(intron 7 471)	agaccacactatttagotta C/I ttagttaataacattgcaaaag	55
ABCA1	56	(intron 7 504)	ttgcaagaagaaaattccgac G/A aagttttttcaagcctaggaa	56
ABCA1	57	(intron 7 679)	gtctgggtaaatctctc G/C ctaccocaaacatcatcatt	57
ABCA1	58	(intron 7 1740)	acaaatgctcacoccttcag C/I tggaaatgattgaaatttgg	58
ABCA1	59	(intron 7 2122)	tgattaaaggctggctactaac A/G ggtgctttctgcatactcg	59
ABCA1	60	(intron 7 7753)	taggaattccaagctgtgaa I/C tttttactgaagctctttgg	60
ABCA1	61	(intron 7 8973)	atggaaattgtttatattg A/I ctacagattggccaattat	61
ABCA1	62	(intron 7 8976)	gaaattgtttatattgact A/G cagattggccaattatttag	62
ABCA1	63	(intron 7 11327)	ctacaactctatttccatt G/C agtccttataaaagaagtgg	63
ABCA1	64	(intron 7 11738)	ctgacgtttaaggagagacgg C/I gtaggtcccttggaggactg	64
ABCA1	65	(intron 7 12295)	agctgtaaattattgttct I/A tttttcttttagctttagct	65
ABCA1	66	(intron 8 387)	tagcaaggccaatcatttta C/G caacacacatgcttgctaac	66
ABCA1	67	(intron 8 697)	ggacactgtctgggtgctccc A/I gcataggaaagctgagccagg	67
ABCA1	68	(intron 8 3036)	ctttatggggaagaattt I/G tttttttgattggggagtgg	68
ABCA1	69	(intron 8 3176)	aaatggcctgggtctctgtc C/A cettctgtctgtatgctc	69
ABCA1	70	(intron 8 3364)	ggcagaaggcaagcttagg A/I cctagagagtgctggaccac	70
ABCA1	71	(intron 8 3373)	caaagcttagaacctagaga G/A tgcaggaccacgccaactcac	71
ABCA1	72	(intron 8 3561)	cagggaatttattaatgatt C/A tigtgaaatgtttggaaata	72
ABCA1	73	(intron 8 3654)	agtcccggaataacatttga I/C gtaagacagaacgctgctc	73
ABCA1	74	(intron 8 4715)	ggcagaggggtctcagaatc C/I gaatttccaacaatgtctcc	74
ABCA1	75	(coding region 936 (Pro 312 Pro))	cgtattctcgcggcatcc C/I gaggaggagggtgtaagat	75
ABCA1	76	(intron 9 2309)	ccctcaagagtcagtttaa A/G tttgtatcatgttagttgtc	76
ABCA1	77	(intron 9 2392)	atggaggaggtctgtcttca I/C gaaaacatttttccagatca	77
ABCA1	78	(intron 10 228)	tggagatgggagagactggc A/G cagggtctgtgtatgggt	78
ABCA1	79	(intron 10 319)	ttctgcggtccctggctccc C/I accigactccaggtgaacaa	79
ABCA1	80	(intron 11 377)	gaaagaagtgtggggagcaaa A/C gcatgatttatactagac	80

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ABCA1	81	(intron 11 521)	agtgctctagagacaattgg G/A ttcaaatgtggagcaggcgtg	81
ABCA1	82	(intron 11 2850)	ctctatacaatcattatgct G/C ccatigaaataataataca	82
ABCA1	83	(intron 11 2976)	ctccaaticggtagaaccag A/G gcttcattctctctgicgaa	83
ABCA1	84	(intron 11 3056)	gtttgcagctgcgtgttttc C/I ggcagcacatcgtgcaggc	84
ABCA1	85	(intron 12 340)	ggcaattattgtgaaactta I/C ctcaaatcgaattcgggtcc	85
ABCA1	86	(intron 12 381)	aattaaatttttgaatttt A/G tattaaataattatattagta	86
ABCA1	87	(intron 14 1728)	caggctcagaggcgttgccc C/I atcacocctggctcacgttg	87
ABCA1	88	(coding region 2040 (11e 680 11e))	atgggcttgacacacagcat C/A cctctgttttagctgtttcat	88
ABCA1	89	(intron 15 1382)	cttttagacagaaaaagtac G/A tgggtattatctctccacag	89
ABCA1	90	(intron 15 1453)	tataaaggagaaaccagtt G/A aaattaccatttgaagaac	90
ABCA1	91	(intron 15 1567)	ttctgcgtatgtttgggtaa G/A tcaattatctctttaggat	91
ABCA1	92	(intron 15 1617)	cagtgcctcatcagaaga I/A gaacagcattacgcctctgc	92
ABCA1	93	(intron 16 95)	agttgagacagagatgat I/A gtottttccaatgggacatg	93
ABCA1	94	(intron 16 452)	tgggttttctgttagtaat G/A ttttcigaactaagcacaac	94
ABCA1	95	(intron 16 657)	ctgttcctcagctcgtggt I/C cataggcatcagcagcccca	95
ABCA1	96	(intron 18 1730)	tgaagttaacgcagctgc C/G ctgtgccttacacitccact	96
ABCA1	97	(intron 19 426)	aggacottacagtggttagt A/G tcaggagggtcagggtcgtg	97
ABCA1	98	(intron 19 468)	aaagcacacgcgttagctc A/G gtggttcacagcacgattcc	98
ABCA1	99	(intron 20 876)	ccctccctcatcaagtgaa C/I acatgggctcagtgcagg	99
ABCA1	100	(intron 22 118)	catgggatactcttcigtta I/G cacagaagagataaaggcca	100
ABCA1	101	(intron 22 560)	aaagctttgccaacttaggg G/A tcatagccatcacagggtgaa	101
ABCA1	102	(intron 23 102)	acctctttggccatgttgaa A/G ccacctctccctgctctgt	102
ABCA1	103	(intron 23 287)	gcataaagaagaagacttgt C/I aagaggtaaagaccttggt	103
ABCA1	104	(intron 23 1063)	accttcacccctcaggaagc G/A aggcgttcacagggcacac	104
ABCA1	105	(intron 25 321)	ctcttaacttaagtacagt I/G gaggacagcggcatcagga	105
ABCA1	106	(intron 25 376)	gttagaattcgaacttg G/C gccagctcagacctactga	106
ABCA1	107	(intron 25 478)	catcacataggaaatgacaaa C/I gtttatggatggatagicta	107
ABCA1	108	(intron 25 579)	tcatttaattctcaaaaaa G/I atgaaaaaatgaacacitcag	108
ABCA1	109	(intron 27 153)	aatggtaaaagccacttgt C/I ttfgcagcatcgtgcagtgtg	109
ABCA1	110	(intron 28 1058)	actatcatgggagataatga C/I tatggttgcctatgatlgga	110
ABCA1	111	(intron 28 1317)	caggaccagctgtctcgtgt C/I acctggaatgtgagactat	111
ABCA1	112	(intron 30 372)	tatatgatttttagttttg I/C ttatcagctcttcgtctttt	112
ABCA1	113	(intron 30 506)	cccttttaaaaagtaagcagt A/G gataaaataaaticagigaag	113
ABCA1	114	(intron 30 1033)	cgtgattttcagtggtgcttt G/C atttccacatgaaggttgt	114
ABCA1	115	(coding region 4281 (Thr 1427 Thr))	tcctccctttgcagagaaac G/A ccttccagcagcagggagaga	115
ABCA1	116	(intron 33 626)	ggctcctgtttactgatttc C/I gtcttttctctctgctttt	116
ABCA1	117	(intron 33 719)	taatagccctcatgctagaa G/A ggagccggagcctgtgtata	117
ABCA1	118	(intron 33 726)	ccctcatgtagaaggagcc G/A gagcctgtgtataaggccag	118
ABCA1	119	(intron 33 889)	ctttctcctaactgtctcagot A/G tctaactgtgtgttaatca	119
ABCA1	120	(intron 33 1097)	ctgtgcacccactctctcagg G/C ttttaagtcaggctgttct	120

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ABCA1	121	(intron 35 234)	aacctatcaaacctcagtt t/c cctcatctgtgaaatggaga	121
ABCA1	122	(intron 37 411)	aactctgatacttttatcag c/i agcttatccatccatggcaa	122
ABCA1	123	(intron 37 1224)	caggcatagtgattccagag a/g tgaaggtaagtcocctgaa	123
ABCA1	124	(intron 37 1720)	aaattaaaaattactctgact g/i ggaatccaatcggticagtaag	124
ABCA1	125	(intron 40 251)	tgaaggtaaggaaaaatagig t/g tatiigtctggatccacacigg	125
ABCA1	126	(intron 40 252)	gaaggtaaggaaaaatagigt t/c atttggttgatccactggc	126
ABCA1	127	(intron 40 319)	agccttggaagaaatcaaac a/g taactttgagaatttaggtga	127
ABCA1	128	(intron 40 957)	cttgttactctctttttctctt g/c tcaatgggtgatagccatttg	128
ABCA1	129	(intron 41 146)	tgaatgggcatcccgacg c/i cctccctgcccatcctgga	129
ABCA1	130	(intron 42 239)	cattggttttatagcttac a/c tttatgtgttagttattaaa	130
ABCA1	131	(intron 42 321)	aataaatgggtgattttgag t/a ttgagtttcatagtcacaaa	131
ABCA1	132	(intron 42 322)	ataaatgggtgattttgagt t/c tgagtttcatagtcacaaa	132
ABCA1	133	(intron 42 533)	agatgaaaaattatgtatg a/a ataataaatgataggttct	133
ABCA1	134	(intron 42 546)	tgtagatgataatgaatgat a/g cggttctaaaaaagacaggtt	134
ABCA1	135	(intron 43 739)	tacagccacacttaaaatgg t/a cccattatgaatacatatt	135
ABCA1	136	(intron 44 18)	taggtgagaaaaagaatggc t/c tgtattttgcgcgaagaact	136
ABCA1	137	(intron 44 264)	acaataataattgcttggtt t/c ttaagagataaatttagtga	137
ABCA1	138	(intron 44 279)	tgtttttaagagataaatt t/c agtgatttttggttaaatga	138
ABCA1	139	(intron 44 508)	ttacattgtctacataaat c/i ccccatgtacatgtaccta	139
ABCA1	140	(intron 44 1477)	gatctctctctctctctt a/i cattttgcaagtagcaatgt	140
ABCA1	141	(intron 44 1665)	tggtgttaagaactgatttg g/a tiggatatgctgagggcc	141
ABCA1	142	(intron 44 1956)	gtgtgtcacactcaaat t/g totggsccttctcatttgg	142
ABCA1	143	(intron 45 68)	aataataccttatggcttt t/c ccacacgattgacttcagg	143
ABCA1	144	(intron 46 608)	ttactactactcaatagag g/c ttccagacaaaaagttgttt	144
ABCA1	145	(intron 47 336)	ttcacaattgtaaacacac t/c acaatgaacagcatcacc	145
ABCA1	146	(3' untranslated region 7479)	aacaaaaatgggtgtct c/i aggcacgggaaacttggttc	146
ABCA1	147	(3' untranslated region 8226)	aggagccactgtacaata c/i tgggcagccttttttttt	147
ABCA1	148	(3' untranslated region 8697)	ttccagaatttgaataataa c/i gctaaagggtgaagacttca	148
ABCA1	149	(3' untranslated region 9097)	aactattttgaagaaacac a/g acattttaatacagattgaa	149
ABCA1	150	(5' flanking region (-1033) ~ (-1032))	tgacttaaatatttagaat (A) ggtgtgtaggcctgcatcc	150
ABCA1	150	(5' flanking region (-1033) ~ (-1032))	tgacttaaatatttagaat ggtgtgtaggcctgcatcc	151
ABCA1	151	(intron 5 6368)	ttctgatggggttggtctg c/Δ tgagaatcatgactgggtgg	152
ABCA1	152	(intron 5 9709)	cattttctgtctgaacccc t/Δ caccattcagcgagctgt	153
ABCA1	153	(intron 5 13816)	tccttaactctctcttttt t/Δ catttgcctctccaccac	154
ABCA1	154	(intron 10 270~271)	cttttcaggaggagggccaaa (G) cgtcattgtctgtgtct	155
ABCA1	154	(intron 10 270~271)	cttttcaggaggagggccaaa cgtcattgtctgtgtct	156
ABCA1	155	(intron 20 611~612)	tttagccactctctccccc (C) gccacctctctattgagc	157
ABCA1	155	(intron 20 611~612)	tttagccactctctccccc gccacctctctattgagc	158
ABCA1	156	(intron 32 391~392)	gagtgcttgggtactctct (T) gatgggggaactccatgataa	159
ABCA1	156	(intron 32 391~392)	gagtgcttgggtactctct gatgggggaactccatgataa	160

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ABCA1	157	(intron 37 847)	gctgatatgtgaatgctc C/ Δ gtttcaaaagcaaaagcaaa	161
ABCA4	1	(5' flanking region -1005)	tgcataoaaagcaaaact A/C tctctctctcttggagct	162
ABCA4	2	(5' flanking region -819)	gtatagatttttcaagag A/I acacattctgagatttggagg	163
ABCA4	3	(5' flanking region -680)	agcacaccocattgacagg C/A tgaatgacagtaaataggcc	164
ABCA4	4	(intron 1 208)	tgccttccaggaagatgt G/A tttctgtctctcagccaca	165
ABCA4	5	(intron 1 234)	ctgtctcagccacatgaaa A/G ttttttgctacogtgcctg	166
ABCA4	6	(intron 1 510)	agtcacagatcaagtcacag I/C ttacctggcacacattttt	167
ABCA4	7	(intron 1 1527)	gcittaacaaccagcataaaa G/A agagcagcatgggacacgt	168
ABCA4	8	(intron 1 2077)	caggactgtagctgctggc T/C aaatgagccattctctgt	169
ABCA4	9	(intron 1 2174)	ccctcctaatctggccttc G/C ctggcatgggtgggagctc	170
ABCA4	10	(intron 1 2246)	gtccocaggagatggagcc A/G ctggcctgagggccttggc	171
ABCA4	11	(intron 1 2364)	ttctgtctggcacgcctcc G/A atggctcccccacotgtacc	172
ABCA4	12	(intron 1 4243)	ctcctgggtatgcctgta C/G gcagtttaagctcaaggaca	173
ABCA4	13	(intron 1 4287)	atgcgcctcggggaggggga A/C gctgacatgattttggaag	174
ABCA4	14	(intron 1 4309)	ctgagcatgatttgggaag C/I ggcagaagaggctatttga	175
ABCA4	15	(intron 1 4416)	tgcagcaaccccccgcgc C/I ccgcaaaaacaacacact	176
ABCA4	16	(intron 1 4996)	tttacccttggacagggcag G/A ccaagctggc t/c gatccctc	177
ABCA4	17	(intron 1 5007)	aacaggcag g/a ccaagctggc I/C ggtccctccctgatacaca	178
ABCA4	18	(intron 1 5080)	gtgtggctggtttcttag C/G aagcacatggttccaaagt	179
ABCA4	19	(intron 1 5152)	gggagatgaagtaagtaga G/A ggcagccctacagggttga	180
ABCA4	20	(intron 1 7110)	ccactggatctgcttttga A/G tcaagagctcttaagctcca	181
ABCA4	21	(intron 1 7290)	gattttgttgctttgcaa T/A ggatcacagtcatttattca	182
ABCA4	22	(intron 1 7483)	cttgagcctcttctcctaac I/C gcagatggagtg c/t tacaga	183
ABCA4	23	(intron 1 7497)	cttaac t/c gcagatggagtg C/I tacagagaaatcttactac	184
ABCA4	24	(intron 2 1067)	tcaagcagcagcagcaactg C/A gtggagcttcttgaactaa	185
ABCA4	25	(intron 2 1243)	caccagcagcagggactggc A/I cacatgagatgctcctgctt	186
ABCA4	26	(intron 3 26)	tgttgagatccctacactgc A/G gggagaggaagtggcacccc	187
ABCA4	27	(intron 3 101)	agcatggagcactgagtggt C/I ttgtggtttgtctgagcccc	188
ABCA4	28	(intron 3 330)	tgtctgggtggagtgaaatca I/C ttagggagaaaaactcagtt	189
ABCA4	29	(intron 3 470)	tgaagtcagggtttacaaggt C/G aagtttacttcttggagaa	190
ABCA4	30	(intron 3 634)	tgaataccaatgacccctct I/C ccaagaaaaatggccacata	191
ABCA4	31	(intron 3 1016)	cccttggggagctcagtagt A/G ttcttcagagagaagccttg	192
ABCA4	32	(intron 3 1554)	gaagattgggttctcatgtt I/C gcaicacattatagtgaa	193
ABCA4	33	(intron 3 1686)	ctagacattctcacagagoc A/G agggcagcaaggggggctc	194
ABCA4	34	(intron 3 1823)	ttcacctctctccatggagcc A/G gttccctctgctcctcaatg	195
ABCA4	35	(intron 3 1938)	caaatctctgggaacaaatc G/A ggttgacccagc t/g ttattct	196
ABCA4	36	(intron 3 1951)	acaaatc g/a ggttgacccagc I/G ttattctccctgtcccatca	197
ABCA4	37	(intron 3 2063)	ggctgtcagagcctaccctgc G/I tgaatgggtggaagg g/a cagg	198
ABCA4	38	(intron 3 2079)	ctgc t/g tgaatgggtggaagg G/A caggctcagagaattgggt	199
ABCA4	39	(intron 3 2186)	agacacacagatgggac C/I gagaggcagcagcccttgc	200

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ABCA4	40	(intron 3 2214)	ggacagaccctgccaaaact G/A ggagactgaatagatgcctc	201
ABCA4	41	(intron 4 3182)	ccccagagccacagcagcc C/G tctctctgggtgggtttgt	202
ABCA4	42	(intron 4 3515)	agtataataaaagcaggagc C/T atagcccccaactctcaaga	203
ABCA4	43	(intron 4 3952)	agagaagccactgtgcact G/C tctgtcgaacticaagacc	204
ABCA4	44	(intron 4 4637)	aatcacttgcgcccaaggica C/T cttaacigttaggtgtctt	205
ABCA4	45	(intron 4 5319)	accttaggggtcccgag A/G cccaagaacagaacctcc	206
ABCA4	46	(intron 6 2266)	ccacctgcagacctcagac G/A ggtctgggggttgctttc	207
ABCA4	47	(intron 6 2857)	ccagagagaaagctctgcc G/A tag t/c oggctcagtttaacca	208
ABCA4	48	(intron 6 2861)	aggagaaagctcigcc g/a tag I/C oggctcagtttaaccaagga	209
ABCA4	49	(intron 6 3078)	gcaggcattaaaatgggact I/G tgcctttatgtctctgggc	210
ABCA4	50	(intron 6 3375)	ttaaatgccaaatgagtct C/G attaacaagaagaaggagaa	211
ABCA4	51	(intron 6 3412)	ggaaatctcagtaaacac C/T gtagggcatctaccactt	212
ABCA4	52	(intron 6 4635)	ctttcgggtggatagtcta C/I gtaagtgctgggaagcc	213
ABCA4	53	(intron 6 -264)	aaacagcaattagaatcaact I/C tgaatatagtagtagtatta	214
ABCA4	54	(intron 7 828)	gatgtgggaaagttagagaa G/C agccaatgtactaatgctc	215
ABCA4	55	(intron 7 1019)	agcttcttgcactctaga I/C agcaagctcaatcatgttg	216
ABCA4	56	(intron 8 374)	gtaaacggcgtgtgggatg C/A ttttaacaacacaatctgt	217
ABCA4	57	(intron 8 874)	tgatgactgtgtatgttg G/A ggtacagcttatttaatttag	218
ABCA4	58	(intron 9 605)	tctgtctctgtctgtatct C/I tctctgttttaggccaact	219
ABCA4	59	(coding region 1268 (Arg 423 His or His 423 His))	aaottttgaagaactggaac G/A c/t gtagaaagtgtcacaag	220
ABCA4	60	(coding region 1269 (Arg 423 Arg or His 423 His))	acttttgaagaactggaac g/a C/I gtagaaagtgtcacaagc	221
ABCA4	61	(intron 11 5687)	atcagttaattgactttaga C/G tcagatatataaatattgt	222
ABCA4	62	(intron 11 7136)	gaactcccaacttaccttag I/C ggagctgtagtcacatagaa	223
ABCA4	63	(intron 11 7180)	agctcacaatgottctct C/A ggctgtaaaggttgaatttt	224
ABCA4	64	(intron 11 7701)	gttagacgcaggcaattacct G/I gggctttgccccagtgga	225
ABCA4	65	(intron 11 8073)	ggatgtttgccacatcca I/C tggcatttctcaaaaggaaac	226
ABCA4	66	(intron 11 8586)	cagctgcctgcgtggagag G/A gctcaaacctcttcgccag	227
ABCA4	67	(intron 11 11234)	ccaaataatttggttttc G/A ttttaggaattaaatttcag	228
ABCA4	68	(intron 11 11641)	aagaacaacaattattga C/G aacttttggtgtgtgacctg	229
ABCA4	69	(intron 11 11808)	tgtatttcttaagaataa C/I caattccatttcttttaac	230
ABCA4	70	(intron 11 11923)	aagatcattattaatatctc A/G tcagctgtgtgtcacttaag	231
ABCA4	71	(intron 12 305)	tcacctgtgtctgggaggt G/A tegttagctatocaaagcc	232
ABCA4	72	(intron 13 1461)	ttgggttcagtgtagct C/A tagctgtactcagatccc	233
ABCA4	73	(intron 14 1268)	ggagcttagccctgttctct I/C atctaggtttccctgttct	234
ABCA4	74	(intron 17 23)	gagtccttaaaacacaaat C/G ttaatgttgaatacaactc	235
ABCA4	75	(intron 17 715)	gggactcccttagctgaa G/A tacttcccatctgtttgtt	236
ABCA4	76	(intron 18 1282)	ggagatgaagaacctaaagc C/I gcttccagaattcatgagg	237
ABCA4	77	(intron 20 -195)	acagatttccattgtatg C/A atgaactatagaagccatcc	238
ABCA4	78	(intron 23 755)	ctggctccgcgtgggttct C/I tatgtccatccacggggagg	239
ABCA4	79	(intron 26 702)	tatcaataacaactcagagc I/G cagtctcctggccctttga	240

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ABCA4	80	(intron 27 156)	ctgtcttccaaacccttat C/I ttgattcttggtaacatgaa	241
ABCA4	81	(intron 27 385)	tttaagaacagtgagtcac G/A tgacttgctctttgaaatgc	242
ABCA4	82	(intron 28 299)	gacatgccatcagaccactg C/I gagtttcaggcagcctaac	243
ABCA4	83	(intron 29 168)	ctcttccacacttggtg G/G gggacattcactacacctcta	244
ABCA4	84	(intron 29 497)	gctgtcaataaggacacaaa C/I agactaatctcaaatctctc	245
ABCA4	85	(intron 29 567)	agctgtaggaataaaaaagg G/A agacaaaac g/a atccacaagc	246
ABCA4	86	(intron 29 577)	aataaaaagg g/a agacaaaac G/A atccacaagctagagatggt	247
ABCA4	87	(intron 30 -2494)	aatcacagctcctgctgc A/G tcatagggatcccaaaagaa	248
ABCA4	88	(intron 30 -2169)	aatgtacacgccaagtcct A/G gaaaaggccaagccagttcc	249
ABCA4	89	(intron 31 535)	ctaactgtgaattatcatct I/G tgatacctgocctttgagat	250
ABCA4	90	(intron 35 209)	tctcccaacatttatgtg C/A aagtaagtttacatttggtt	251
ABCA4	91	(intron 37 525)	taaatitgaatgagtaattc A/G tcatctcggcctcagtttc	252
ABCA4	92	(intron 37 766)	tgttgacaggtcggagaacc I/G cctatgaattgtacagggct	253
ABCA4	93	(intron 37 856)	aaaaccccatgaagtggtca A/G ggcagggcatcatattctcca	254
ABCA4	94	(intron 38 62)	tagtagagtagtggttggtc G/A agcagagccaggggcaagca	255
ABCA4	95	(intron 38 761)	tccttggcgaagttaattctt G/A atgaagagaciggggttct	256
ABCA4	96	(intron 38 1315)	cagagtcagactctggaag G/I c/a ggggggataagaacacagc	257
ABCA4	97	(intron 38 1316)	agagtcagactctggaag g/t C/A ggggggataagaacacagc	258
ABCA4	98	(intron 38 1561)	gtattttcatgtaaatatc C/A g/a atcacagctgtctatggaa	259
ABCA4	99	(intron 38 1562)	tattttcatgtaaatatc c/a G/A atcacagctgtctatggaaa	260
ABCA4	100	(intron 38 2874)	ctagacaaaaggg a/c agctcc C/I gccacatagaacattgcagg	261
ABCA4	101	(intron 40 1904)	ggaactatcacgcccacca A/C tctgaccccttttctcat	262
ABCA4	102	(coding region 5814 (Leu 1938 Leu))	ggaaataaaactgcacattt A/G aggtcacatgaactaaccaa	263
ABCA4	103	(intron 41 122)	atttggttccagtttatg I/G aggtcatcatccctggtt	264
ABCA4	104	(intron 41 411)	cccttccctcccttgcct C/A accctgtcagttctcagt	265
ABCA4	105	(intron 41 443)	gttcacagtcgggttcttc G/A tatctgcagattatcc a/g g	266
ABCA4	106	(coding region 5844 (Pro 1948 Pro))	c g/a tatctgcagattatcc A/G ggcacctccagccacagct	267
ABCA4	107	(intron 43 328)	ttttagcctattcctataa A/G aatgcacctgtctc c/g cat	268
ABCA4	108	(intron 43 345)	taa a/g aatgcacctgtctc C/G cattacctcctccacat	269
ABCA4	109	(intron 43 370)	acctccctccacattttt A/G caaaa c/t gtttcaggagattt	270
ABCA4	110	(intron 43 376)	ctccacacatttt a/g caaaa C/I gtttcaggagatttactgag	271
ABCA4	111	(intron43 670)	tttaacacagactggtcccta I/C ggcagacagagagagatga	272
ABCA4	112	(intron43 822)	gttaggtgtctgtacatct G/A tccagcatcgttgatcagg	273
ABCA4	113	(intron 43 915)	ggcagagacagtctcagca C/I gcttcactggcicagacagg	274
ABCA4	114	(intron 43 1242)	actgagctggagcgttagaaa G/I aaactataggcttaagacac	275
ABCA4	115	(intron 43 1671)	tagagaagttaacttccatc G/A ggcacatgcattcttcta	276
ABCA4	116	(intron 43 2036)	ttgaaggatactcagtaatt G/A cttttttcttcagttattt	277
ABCA4	117	(intron 45 176)	gtgtttgtttcacacagctc C/I ggagaaaaacaaagta c/t ggc	278
ABCA4	118	(intron 45 193)	ctc c/t ggagaaaaacaaagta C/I ggcacagccttgacttggga	279
ABCA4	119	(intron 47 238)	cccaagtcctcgttatggggc A/G tctgatacagatgcattgcag	280

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ABCA4	120	(intron 47 269)	atgcatcagagcctggctg G/A gatggaggaggctgtctacc	281
ABCA4	121	(intron 47 326)	accatttatctcaacagatc C/G gggacctgiggctatttac	282
ABCA4	122	(intron 47 715)	aagtcactaagcttggttgg G/A gagggaacagacataaac c/t c	283
ABCA4	123	(intron 47 734)	t g/a ggaggaaacagacataaac C/I caccitattatgctgaggt	284
ABCA4	124	(intron 47 931)	ggacactcgtatagatatcta T/C agaatagcagcatgtctcagg	285
ABCA4	125	(intron 47 1260)	acactctctggtgaccatc A/C ctoatccaagagagggtaac	286
ABCA4	126	(intron 48 1663)	tcctgcctctctcttaoctc I/C aggtgtttgtaaatitgtct	287
ABCA4	127	(intron 49 127)	agagagcccccacccacacca C/I ggccctacccaagtccocac	288
ABCA4	128	(5' flanking region (-1441)~(-1400))	gtaaatctcagttgaatcag (TCA)14-16 atttttcagctctggttctctg	289
ABCA4	129	(intron 1 4712 4720)	gagggcggggagactataggg (A)8-10 cagcctaattcaaggatgag	290
ABCA4	130	(intron 1 7295~7304)	ttgttgctttgcaa t/a ggaat CACAGICAI/Δ ttattcattcattcacc	291
ABCA4	131	(intron 2 951~952)	ccgtgcacatcagactctctt II/Δ accctcccccaggagcccca	292
ABCA4	132	(intron 3 2642~2653)	ccgtgggtgacagagcgagat (A)10-12 tagcatgagatattattact	293
ABCA4	133	(intron 4 5202)	cacaaagcatctgacacccc C/Δ atccagccctggcttaacttt	294
ABCA4	134	(intron 6 3029~3044)	cactaaacacaaaatttac (A)16-18 cctgaaagaaattgcaggca	295
ABCA4	135	(intron 6 5138~5139)	ttcatgacacatcagatgtt (G) cttttatggatttacaaga	296
ABCA4	135	(intron 6 5138~5139)	ttcatgacacatcagatgtt cttttatggatttacaaga	297
ABCA4	136	(intron 6 5985)	tttctcttctcaaacccccc C/Δ agactaggagaaaggtctgtc	298
ABCA4	137	(intron 6 6094)	gggacgcagacagaaaaagacc I/Δ agttctgttgagccaaaaga	299
ABCA4	138	(intron 6 -161)	tattttttcaattaaataaa A/Δ gagttttttgtttctaaaag	300
ABCA4	139	(intron 7 809~810)	gggcccagatgacacactga (TG) tctggaaaagttagagaa g/c a	301
ABCA4	139	(intron 7 809~810)	gggcccagatgacacactga tctggaaaagttagagaa g/c a	302
ABCA4	140	(intron 8 472~484)	atcttccccaccttttacta (T)10-13 ggtctctatggggtaaaagg	303
ABCA4	141	(intron 9 48~71)	gtacccctggacctccagaa (GT)11-13 gagagagatgigccttcttg	304
ABCA4	142	(intron 9 554)	ataggggcagaaaaagacaca A/Δ ccaaaagtctctctcactt	305
ABCA4	143	(intron 10 11)	catgatcagagtaaggggggg G/Δ tiggagagatggggaggggag	306
ABCA4	144	(intron 11 4242)	ggagagaaaatgatgttagt G/Δ cctctgtataataggcccccag	307
ABCA4	145	(intron 11 13743~13753)	tgtcttttttgggtaattgg (T)9-11 cctcttcagagagaagaaaa	308
ABCA4	146	(intron 13 636~637)	cggggtggagggttggggagg (G) ctcatttgtcattatagatg	309
ABCA4	146	(intron 13 636~637)	cggggtggagggttggggagg ctcatttgtcattatagatg	310
ABCA4	147	(intron 18 569~570)	tgtctgcctcatctctctc II/Δ aaactagtctctgtattctc	311
ABCA4	148	(intron 20 (-304)~(-297))	tataacctgacttttttttc (A)7-9 ggattgcttttttaaacata	312
ABCA4	149	(intron 22 1236~1246)	ctgaattagttcccttggg (T)9-11 agttaactcctgtttttg	313
ABCA4	150	(intron 26 4626~4635)	gataatcaatcgtlaaagg (A)9-10 tggcattagagatccagacc	314
ABCA4	151	(intron 33 115~116)	taaaacctgtgtttgttt GT/Δ ttacatggttttttagggccc	315
ABCA4	152	(intron 36 1078)	taagcagctatcacttaaca A/Δ tacaacacagagattatca	316
ABCA4	153	(intron 37 290~291)	ccttgaccacagcctggggg (T) cagccattcccca a/g cccctc	317
ABCA4	153	(intron 37 290~291)	ccttgaccacagcctggggg cagccattcccca a/g cccctc	318
ABCA4	154	(intron 38 896)	ataaaaagaggggggaaaaa A/Δ gaaggcagctcgtgcagggg	319
ABCA4	155	(intron 38 1209~1210)	gtagcccccctgagactgact GT/Δ ttccagatottgttagggtt	320

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ABCA4	156	(intron 38 1322)	agacitggaaag g/t c/a ggggg G/ Δ ataagaacacagcccgagca	321
ABCA4	157	(intron 38 3107)	ggcccccacotctgaagag A/ Δ ggggggtgggggttggccc	322
ABCA4	158	(intron 40 152)	tttttccaataatacaagt A/ Δ gaggatcgggttaaaatagg	323
ABCA4	159	(intron 43 330)	tgtagcctattcctataa a/g a A/ Δ tgcacattgttc c/g catta	324
ABCA4	160	(intron 43 1354)	tttaattggccagccatgc C/ Δ ttgtgtggcctttgttcattg	325
ABCA4	161	(intron 47 1305'1308)	cactctctgaaggagaag AAG/ Δ caccatggcccaagcccta	326
ABCA7	1	(5' flanking region -1596)	agaatttgcccccctccc C/I t c/t ctgcactctctgcagaag	327
ABCA7	2	(5' flanking region -1594)	aatttgcccccctccc c/t t C/I ctgcactctctgcagaagcc	328
ABCA7	3	(5' flanking region -1180)	ggcagtgatgacgggcag G/A tgcaccaatagcagcgtgc	329
ABCA7	4	(5' flanking region -460)	agagctgggtcgtgctcc A/G gctgggcaactgctgtctc	330
ABCA7	5	(5' untranslated region -9)	ctctgtcccgtcccctgccc A/G gtctccactggcctcttgg	331
ABCA7	6	(intron 5 91)	cccgggcccaaggccctccc G/A ttccaggatccaggctgtc	332
ABCA7	7	(coding region 563 (Glu 188 Gly))	cagctttggaggccgcig A/G ggacciggccagggaggtac	333
ABCA7	8	(intron 8 103)	gcgggagggtcacgaaact A/G ttggaagaataggaggttag	334
ABCA7	9	(intron 8 166)	tgcggaggatcaggagcaca C/I gcaggagcaggcagagggg	335
ABCA7	10	(coding region 955 (Thr 319 Ala))	acgggaacttcagagagctc A/G cctgtctgaggatgtccgg	336
ABCA7	11	(intron 9 421)	ttttttttttttttttt I/A taagatggagctcactc	337
ABCA7	12	(intron 9 463)	gtgcccaggciggagctga G/A tgg c/t gagatctgggtcact	338
ABCA7	13	(intron 9 467)	ccaggctggactga g/a tgg C/I gagatctgggtcactgaa	339
ABCA7	14	(intron 9 488)	gagatctgggtcactgcaa C/I ctccgctccttggtattcaag	340
ABCA7	15	(coding region 1184 (His 395 Arg))	cgcacacgcctgattggggc A/G cctggggcagcctggggcc	341
ABCA7	16	(intron 10 10)	gagtgacggagggtgaggcc I/C gtccacctgggggtctgtt	342
ABCA7	17	(coding region 1388 (Arg 463 His))	cctgggcccggccacatgc G/A catcaaatccgatggaca	343
ABCA7	18	(intron 12 115)	cagctgcgaactttgcacc I/G ttacaccactccacgtgacc	344
ABCA7	19	(coding region 1824 (Ala 608 Ala))	cccttcctgtcagcgcgc A/G ctgtggttctgtgtctcaa	345
ABCA7	20	(intron 13 55)	ggtagcgtggagggtgacag A/G caggggcgcccccacgtggg	346
ABCA7	21	(intron 13 78)	ggggcgcccccacagtgggtg C/A gcgcccagggccaatccag	347
ABCA7	22	(coding region 1851 (Gly 617 Gly))	cgttgctctcagcgtggg A/G gacatcctcccctacagcca	348
ABCA7	23	(coding region 2153 (Asn 718 Thr))	cgaaggcgcgagtggaaca A/C cgtgggcaacccggcctacgg	349
ABCA7	24	(intron 15 34)	ggcggggctccggccgggt C/G gcacctgctttggggaggcc	350
ABCA7	25	(intron 16 8)	ctggaccacaagggtgaggc A/C ctacgaggcttaatagctgg	351
ABCA7	26	(intron 16 161)	tcocgcagctttatagcc C/I cggccagcagggtcccgat	352
ABCA7	27	(coding region 2385 (Leu 795 Leu))	cacccactctcagtgct G/A gtagagagagcaacggccggg	353
ABCA7	28	(coding region 2421 (Val 807 Val))	cccgctcagtcagtcgt C/A tccgttcgcagcctggagaa	354
ABCA7	29	(intron 20 166)	cgaacagtaagagtgggg A/G tagacagaggttcccttgga	355
ABCA7	30	(coding region 3027 (Ala 1009 Ala))	ctgctggagagaccgtgtggc C/I gtgtgagcaggtggcgcctt	356
ABCA7	31	(intron 22 1386)	gggTggggcgtTgagccggg C/I tccctgaagcacccctttgt	357
ABCA7	32	(coding region 3417 (Leu 1139 Leu))	gggactccggacacagcct C/G gaggaggtgtgagccctgggg	358
ABCA7	33	(intron 23 147)	ggagctgtgggtgcagat G/A tcccttgggaaggcctgggg	359
ABCA7	34	(coding region 3528 (Leu 1176 Leu))	gctggcctagacgttaacct A/G cggctcaagatgcggccaca	360

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ABCA7	35	(coding region 4046 (Arg 1349 Glu))	ccagcctgcagctagacc G/A gccgggagccggcgctgc	361
ABCA7	36	(intron 30 81)	ccccctggagctctccgg C/A cccccggccctcagctccc	362
ABCA7	37	(intron 32 1)	caaggagcagctctgagg G/C tgcactgtgagtcctccac	363
ABCA7	38	(intron 33 54)	ccactcttgccactgccct G/A tcggccctttaggcagg	364
ABCA7	39	(intron 34 245)	cagtaacttggggagcgag G/A caggaggactgtctggcc	365
ABCA7	40	(coding region 5057 (Gln 1686 Arg))	ggtgagccgagatctgaac A/G ggtctcttattcttccccc	366
ABCA7	41	(intron 38 65)	ggccactcactttctgaa A/G gacctgcactctccaggta	367
ABCA7	42	(intron 40 154)	ctctactccacacagcgga C/G caggccctgagacacccctg	368
ABCA7	43	(intron 40 277)	ctgagcccccgggccccca T/C cccagcgtggccgggaac	369
ABCA7	44	(coding region 5592 (Ala 1864 Ala))	gtggccggggaacccagtc T/C ggcacctcagcatgggata	370
ABCA7	45	(intron 41 286)	ctcttgactctgcctctg T/C ggcctggccacttgcctct	371
ABCA7	46	(intron 41 389)	tggccttccagtttgcag C/I cgtttcacttgctcttccat	372
ABCA7	47	(intron 41 991)	cacactatggccctgcccc C/I ac c/t cat c/g cc a/g gctccacca	373
ABCA7	48	(intron 41 994)	actatggccctgcccc c/t ac C/I cat c/g cc a/g gctccaccacac	374
ABCA7	49	(intron 41 998)	tggcctgcccc c/t ac c/t cat C/G cc a/g gctccaccacacacatg	375
ABCA7	50	(intron 41 1001)	ccctgcccc c/t ac c/t cat c/g cc A/G gctccaccacacacatggcc	376
ABCA7	51	(intron 41 1051)	actcatgctggctccacca C/I accatggcccccccatatc	377
ABCA7	52	(intron 41 1131)	tggcctggccatggccatt A/G tggccctgctccacactca	378
ABCA7	53	(coding region 5985 (Leu 1995 Leu))	gaagcctctgctcgccct G/A gccatcatggtgaatggcg	379
ABCA7	54	(intron 44 201)	ggcgagagaccaggagcgt G/C agccggggctcttgggtgga	380
ABCA7	55	(intron 44 233)	ctgggtgagattagaaaca C/I aatcaggtgtggttggagt	381
ABCA7	56	(intron 44 313)	agttaggggaggccctggtt A/G gtggcgggggccataggaaa	382
ABCA7	57	(coding region 6133 (Ala 2045 Ser))	tggcgccggagcttccctggg G/I cggagctgcggaggcaccat	383
ABCA7	58	(coding region 6159 (Gly 2053 Gly))	ctgcgcgagggcaccatggagg C/I cgcctgcgttccagctgcc	384
ABCA7	59	(intron 45 27)	acggcgccggggctgggctg G/C gggagcaggctgggggcca	385
ABCA7	60	(3' flanking region 108)	caggctgaggtgtcacatac G/A gsccaagtggcgattcatag	386
ABCA7	61	(3' flanking region 376)	cttacaggagagccgggtgccc C/I ggagcacaggccaggggccgg	387
ABCA7	62	(3' flanking region 687)	cagcaggagagacttggagg G/A g/a gggagagagttccactgc	388
ABCA7	63	(3' flanking region 688)	agcaggagagacttggagg g/a G/A gggagagagttccactgcg	389
ABCA7	64	(3' flanking region 1169)	cttcgacctgaaccacttca C/I ggggctgcaggcggtgat	390
ABCA7	65	(intron 9 398~422)	cgtaactaaccagctcctgc (I) 22-26 aagagatggagctcactct	391
ABCA7	66	(intron 12 175~184)	gggactctgaggctctggt (G) 8-10 actctgagggtctggggcc	392
ABCA7	67	(intron 30 81~87)	ccccctggagactctccgg (C) 6-7 ggccctcagctccccctccc	393
ABCA7	68	(intron 34 349~361)	agaaagagaaagagagaaag (A) 12-14 cagaaatgtgttgggtga	394
ABCA8	1	(intron 1 204)	ctggtaattaatattagata A/G ataaaacattgaggttagaa	395
ABCA8	2	(intron 1 266)	aacattatgtgttttaaac A/G taactgagtgtagaataag	396
ABCA8	3	(intron 1 733)	ttgccatatgataataaag T/A attcatgtttttagctagcct	397
ABCA8	4	(intron 1 861)	agactggagtttgaatgcta C/I ctgaagactgtatgattcc	398
ABCA8	5	(intron 1 907)	gaggagatcatctcttggc C/I aatgtctattaaactgcga	399
ABCA8	6	(intron 1 1262)	cagaaacttttggcctctct G/A taggctagctcactgtgaaa	400

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ABCA8	7	(intron 1 1537)	agctctttaaagatacca I/C gctgaatttttgcacctta	401
ABCA8	8	(intron 1 7622)	tcgttaacagaatgataat I/C tagccatcttattcc c/t a	402
ABCA8	9	(intron 1 7639)	t t/c tagccatcttattcc C/I agaaacaacaggctcataag	403
ABCA8	10	(intron 1 7720)	tcgatgtttacaactgcc C/I tggagaacagaaaaagagaa	404
ABCA8	11	(intron 1 9397)	cataatataacataatgc G/A cacacacacatatacaca	405
ABCA8	12	(intron 1 9519)	agtagttcatgttggacaaa I/C atgcttgagaatgcagaaa	406
ABCA8	13	(intron 1 12973)	ttgataacaggcacaggcca I/C cacaaaataaatgatgaaca	407
ABCA8	14	(intron 1 13100)	catggagattaggctacg I/C tttttgtttgttcaggat	408
ABCA8	15	(intron 1 13128)	ttgttgcaggatatttctt I/C ttcttaagaacttcataata	409
ABCA8	16	(intron 2 420)	caattagtttcttcaaaa A/G gtgaaaaagtggaaattgta	410
ABCA8	17	(intron 2 505)	catataaaaaattgtgatta A/I actttgttatattttaaaaa	411
ABCA8	18	(intron 2 819)	gcaatgcccttggaaatact C/I ttaaaaacacatigacttica	412
ABCA8	19	(intron 3 915)	ttgtttcgatagatcagta G/A ggtgacttagttiaacaatgat	413
ABCA8	20	(intron 3 1539)	aaagggaatctgtgtgat C/I gccctgtcattcattcatag	414
ABCA8	21	(intron 3 2341)	ttccttttttgcacttc C/I gtocaaattccactcaagct	415
ABCA8	22	(intron 3 2882)	tattctatattctgactct A/G ttatattctataataataa	416
ABCA8	23	(intron 3 3314)	atttaaatatctctctct A/G tattaccatttcaaatita	417
ABCA8	24	(intron 4 89)	gaggtagtagtgcacaaata G/A agcatcactatctgtcataa	418
ABCA8	25	(intron 4 3264)	ttccattggccttattgoc C/I gtttatatccagtggttaga	419
ABCA8	26	(intron 4 3403)	aaagacacacacaaaattctt C/G atcagcagaaaaacacagga	420
ABCA8	27	(intron 5 389)	gcttaactgaatatataaatt G/C agaaaaagccatgccaaagcaa	421
ABCA8	28	(intron 5 479)	tggagtggttgagtaactca A/G aatgcttggactoc g/a aggttc	422
ABCA8	29	(intron 5 494)	actca a/g aatgcctggactoc G/A aggtccacagcaggtcaatga	423
ABCA8	30	(coding region 792 (Ala 264 Ala))	atgggtttcgggattcacc G/A ttctgttgagtcacaaagcag	424
ABCA8	31	(intron 6 200)	ctctcccaagtagctgggact G/A cagggtccg a/g ccaccatgcc	425
ABCA8	32	(intron 6 210)	agctgggact g/a cagggtccg A/G ccaccatgctggataattt	426
ABCA8	33	(intron 6 1751)	gtgagttattattgtgtgg C/I ttgacagctgtttgtttt	427
ABCA8	34	(intron 6 1808)	atttcattatagttttcaaa G/I aatatigtataaaacaaaagaa	428
ABCA8	35	(intron 6 2412)	tattcctaattctaaagaat I/C ctgcccaaaacttttacctt	429
ABCA8	36	(intron 6 2506)	tggatgaataagtgaaigaa G/A agttatctttaga a/g tccattt	430
ABCA8	37	(intron 6 2519)	gaatgaa g/a agttatctttaga A/G tccatttcaggcttctctt	431
ABCA8	38	(intron 7 28)	agtgaaataaatacttctcc A/G tccacctatagcctaaaaat	432
ABCA8	39	(coding region 991 (Gly 331 Ser))	taagaatacttttctcacc G/A gctgtgtgtgttctctctc	433
ABCA8	40	(intron 8 74)	tggatccatcagggtgtaat C/I atttaaaaactcagcatgtt	434
ABCA8	41	(intron 9 1417)	acacatactiaaataattt I/C ctctgttctacttttgtttt	435
ABCA8	42	(intron 9 2504)	agaggaataattatgtttgg G/A aatgaaataaagcagaaata	436
ABCA8	43	(intron 10 2013)	tggccaaagatctttccaac C/I tgtgccagtggttccacagga	437
ABCA8	44	(intron 10 2378)	ctgaagaaaattgtcacttt G/A aagtatcttttctttttt	438
ABCA8	45	(intron 11 -697)	aaaaaaaaaaaaagagag A/G gagaaagaaaataatttga	439
ABCA8	46	(intron 11 -528)	tataaaagttagaaaaaaat G/I a/g tatgttttagaataagat	440

Table 1

Designation of Gene	No.	Location	Sequence	SEO ID No
ABCA8	47	(intron 11 -526)	taaaagttagaaaaaat g/t a A/G taigttttagaaaatagatgt	441
ABCA8	48	(intron 11 -342)	ctcaaggaggttttagccat G/A taataacttactattaatct	442
ABCA8	49	(coding region 1632 (Asn 544 Asn))	ggttcagtcaccattctataa C/I aataagcttttcagaaatggc	443
ABCA8	50	(intron 14 252)	cttatcgcaaaataagigaa G/A tigtgtttcttaagagatcaa	444
ABCA8	51	(intron 15 130)	tttgttttttagacggagt A/C tegtatcatctcgctcactg	445
ABCA8	52	(intron 16 534)	acatatacattcattcaaat A/G cacatttttatggtagaaca	446
ABCA8	53	(intron 16 588)	gaatcatcaggaaagtgtta C/I gaaattctgattagtactt	447
ABCA8	54	(intron 16 645)	atttaagaaaaattttaga C/I gttttagggtggaatgaagaa	448
ABCA8	55	(intron 17 431)	tgtcagggtttttctttttt I/A ttcitttaigttagaaaattgg	449
ABCA8	56	(intron 17 1390)	gctgtaaacctcgtttttgtg C/A ttagggtaccoccatgattcta	450
ABCA8	57	(intron 17 2452)	caagttataccttagtagaac G/A cggaaga g/c tctaatacatgag	451
ABCA8	58	(intron 17 2460)	acctatagtagaac g/a cggaaga G/C totaatcatgagat g/c cttag	452
ABCA8	59	(intron 17 2475)	gaaga g/c tctaatacatgagat G/C cttagcagagagccaatctcta	453
ABCA8	60	(intron 18 152)	gaagaagcacaggagagagg C/I agaattcttgacatccaaagg	454
ABCA8	61	(intron 19 7477)	aaaactattttgaaagaca C/I ttggaaactaaaaaaatottt	455
ABCA8	62	(intron 21 196)	ttgtttaaagtataaataaaa I/C g/c acaaaaacatttttcaaaag	456
ABCA8	63	(intron 21 197)	tgtttaaagtataaataaaa t/c G/C acaaaaacatttttcaaaaga	457
ABCA8	64	(intron 21 287)	actgtgtgtgggtggggggga G/I gggggagggtatagcattggg	458
ABCA8	65	(intron 21 403)	ccctgcacaatgtgcacatgt A/G ccctaaacactaaagtataa	459
ABCA8	66	(intron 21 1207)	ccaagcc g/a gagtgcagtgcc A/G ggaatcatatgcactgtaac	460
ABCA8	67	(intron 24 692)	ctcctagatatagacaaaaa A/C caagggtgcacaatggccatg	461
ABCA8	68	(intron 25 212)	ccgtgatttaatatgggaag G/A aagggttaagggttagtggga	462
ABCA8	69	(intron 26 67)	aataattttcagttctgtac A/G caotgtgaaacttcttttat	463
ABCA8	70	(intron 27 515)	gtgtctccaaaaccacatca G/I ttctatotttttgtctattaca	464
ABCA8	71	(intron 27 661)	ccctggattatatacagaotta G/A aatggagaggaanaagtoaat	465
ABCA8	72	(intron 30 1967)	caaaaattagatacaagggg G/C tgaattgactttaattgta	466
ABCA8	73	(intron 31 112)	ctctaaatgtcgaoccaggt C/G acactgggttagatttaacaac	467
ABCA8	74	(intron 33 401)	cttctcactaggttgtgaga C/I gctgtgtgttaaaattttatgt	468
ABCA8	75	(intron 35 484)	taacagcatcatcctg a/t tgt A/G ttatttttcatagacagaaa	469
ABCA8	76	(intron 36 258)	tttgcgtatgtgttggtaaa A/G cctaagtcacaaactcagtta	470
ABCA8	77	(intron 36 375)	atatatttttactgtcttag C/G ctgtatatttaagaaaactgac	471
ABCA8	78	(3' flanking region 674)	ggcgttgacatagaaagccc G/A gaagcttcttgatgtgotta	472
ABCA8	79	(intron 1 56'57)	ttttgtccttttgtgtgagt I/I/Δ gtttcagagggtttttgtcttt	473
ABCA8	80	(intron 1 1180'1191)	taagttataataataaaacg (A) 9-11 gaaattccctctgtacagag	474
ABCA8	81	(intron 1 987'9885)	ctctcggcaaatagtagtagc (A) 8-12 tcaactgagtacaaaagct	475
ABCA8	82	(intron 1 12588)	gtactagagtgcactcctt I/Δ gcaacaggacggcccaaaagg	476
ABCA8	83	(intron 6 78)	tcaatgcactttttttttt I/Δ gaaatggagctctogctctgt	477
ABCA8	84	(intron 9 265)	gtatatggatttttttttt I/Δ agacctctttagaaagotagt	478
ABCA8	85	(intron 9 2666)	atttttttaaaaggtatcca A/Δ tagtcaattctcaattttctc	479
ABCA8	86	(intron 11 -447)	ggatattctgggtttttttt I/Δ ctacaacactcaagtttttttg	480

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ABCB8	87	(intron 15 8407)	gtggaataatttttgactta / / Δ gcatttggtcaataaaaatt	481
ABCB8	88	(intron 15 9458~9470)	tatgtogagtaacatatgtc (I)11-15 ctgaatgccagcttgagtt	482
ABCB8	89	(intron 16 54~56)	tgaataatagtcacatcat CAI/Δ aattattatcatiaaacta	483
ABCB8	90	(intron 17 433)	tcaggttttttttttt t/a t / / Δ ctttatgttagaaatggac	484
ABCB8	91	(intron 24 1462)	actccatctcaaaaaaaa A/Δ gagagaaaaaattctgcat	485
ABCB8	92	(intron 33 155)	caatacttgcaaaaaaaa A/Δ gatctttccctgatgatatt	486
ABCB8	93	(intron 34 184)	atactgaatggttttttt / / Δ ctcttttctcatatgacctc	487
ABCB8	94	(3' flanking region 1240)	atcttggaccacaaaaaaa A/Δ ctttatcigtgttggcggtg	488
ABCB1	1	5' flanking - 196	gotttggagccatagtcagt / / C actcaaaattttatttatct	489
ABCB1	2	5' flanking - 16	tactctttacctgtgaagag / / C agaacatgaagaatactact	490
ABCB1	3	intron 1 + 71660	cttgcctggaggaagggtgct A/C gaaatatataccaaatccaag	491
ABCB1	4	intron 1 + 80091	gaaataatattcaagttctg A/C aataatatacgtaccctatag	492
ABCB1	5	intron 1 + 103126	gatagaatcagaattcctc / / C ggtctcaagaaaggtcat	493
ABCB1	6	intron 1 + 103148	tgctcaagaaaaaggctcatg C/I gataaatttaagttctgctag	494
ABCB1	7	intron 1 + 108428	aataattttatcatctctg A/G tcaacatttcaacaaactca	495
ABCB1	8	intron 1 + 112042	cataagttgaaatgccccca A/G tgattcagctgtagcggtt	496
ABCB1	9	intron 2 + 491	gcctcttggtctgacgggg G/Δ actagaggttagctcacct	497
ABCB1	10	intron 4 + 36	attaactattcaaaatactt C/I ggaatttgcactctctta	498
ABCB1	11	intron 5 + 1596	ttagctctcttactgcttca / / C agtggagaatcaaatactt	499
ABCB1	12	intron 8 + 1789	aaacactctgaattataaac C/I gctctcgggaaccacagctca	500
ABCB1	13	intron 14 + 24	agttgctcttgcctttggc / / C ttttagagggtgcaaaaaata	501
ABCB1	14	intron 14 + 81	tgcaggaagttaggaacta C/I tataaatcggagaagaaggaa	502
ABCB1	15	intron 15 + 38	caaccaacotgatttataa A/G cataagaacattctactact	503
ABCB1	16	intron 17 + 73	gtttggtggctagggctac A/G gtaggagtgaggacaacagaga	504
ABCB1	17	intron 18 + 564	caacagtaaggttacatct G/A aaaggaaatgctctcgttta	505
ABCB1	18	intron 18 + 2062	ttcccttgaggaaatggttat C/I ctctggttctcttgagctcca	506
ABCB1	19	intron 18 + 2293	ccacatcaggttttcccccag A/G caacttgggacagtttgaaa	507
ABCB1	20	intron 20 + 557	aaacccctaaccattgacac G/A tgtgaatgttttctctgggga	508
ABCB1	21	intron 21 + 24	cggtccctcttctactcigt G/A ttgtcttaattggccattt	509
ABCB1	22	intron 21 + 2725	ctgacctgtttttggctgac A/G ggttttagtttctctccctca	510
ABCB1	23	intron 21 + 4725	ttcttggtattaaaagatcca A/G agagataggaaatgttaatt	511
ABCB1	24	intron 22 + 8507	tgcacttaggaaaaaaaacaa / / C atggaaaatgtgtaaaatata	512
ABCB1	25	intron 22 + 8537	tgtaaaataatacttttttt / / A aaaaaaaggacacacatttat	513
ABCB1	26	intron 22 + 8565	aggacacattttattcagcat / / C atgacagactattacattt	514
ABCB1	27	intron 22 + 8952	caacttggtttctggtttg G/A caagtactggcctgtacca	515
ABCB1	28	intron 22 + 9520	caccaacaaatatctttttc A/G cagttgggtgggcatctggt	516
ABCB1	29	intron 22 + 9836	agactctgaacttagacatga C/I ggcaggggaaagagagactt	517
ABCB1	30	intron 24 + 377	taaaatacagaatgtgttga C/A taagtctgcaagcctttgg	518
ABCB1	31	intron 24 + 1493	ggggaggtgtccaggcaca A/Δ catgagagctggacttgat	519
ABCB1	32	intron 24 + 1495	ggaggtatccaggcacgaac A/I tggagagctggacttgatac	520

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ABCB1	33	intron 25 + 342	tgagccttgatctctctggg C/I tcaagcgtcctcctgcctc	521
ABCB1	34	intron 26 + 134	cttggataaagctgagagc C/G taaatatggtctocaaagtg	522
ABCB1	35	intron 26 + 1272	gtccttcaattttgtgtga A/G citaaaaacaggactotaaa	523
ABCB1	36	intron 26 + 1394	tattaagtggtgttaaaag A/G ttigtgtataatgaattga	524
ABCB1	37	intron 26 + (1987-1988)	aaggcctggagagagaaag (AAG) gaggtatttgcctccagac	525
ABCB1	37	intron 26 + (1987-1988)	aaggcctggagagagaaag gaggtatttgcctccagac	526
ABCB1	38	intron 27 + 59	gcagcctctctgctctatag G/I tigtattataaaggcgtggt	527
ABCB1	39	intron 27 + 80	ttgatttataaaggcgtggt I/C tccagaaagtgaaagaaat	528
ABCB4	1	exon 3 + 3	aacacccittattttatagat C/I caatgactgagtcagaat	529
ABCB4	2	intron 3 + 45	cagcatctctacttatacca I/C gctcgtcttaaggcttctct	530
ABCB4	3	intron 3 + 498	actcaaataggtggttaggag C/I agagacaattcaatcacagac	531
ABCB4	4	intron 3 + 515	gagcagagacaattcaatac A/G gacagaagcttagaigaga	532
ABCB4	5	intron 6 + 1030	tagttttgccatgtagaatt G/C aaaaagtgatagatggtgt	533
ABCB4	6	intron 6 + 1437	gttaagcctgtctcaatcaa G/A ttagtattatcttctgtcta	534
ABCB4	7	intron 6 + 2449	ttgacttagogacactgtta G/A catacttatcttctctgtgt	535
ABCB4	8	intron 7 + 451	cttctgtgcaccigtgtgt A/C taagtttgcttatttagt	536
ABCB4	9	intron 7 + 530	agttagacagcgtggtgat C/G acacggacagagctaactg	537
ABCB4	10	intron 7 - 152	aacagaaatcatgaattaaag I/C tgttaatgatttgaagcct	538
ABCB4	11	exon 8 + 40	aggataaatgttttatgtcg C/I ctgggtacacatcatggccat	539
ABCB4	12	intron 8 + 130	ctggttgactccagatatca I/C agaaggagtgttaaatctct	540
ABCB4	13	intron 8 + 248	aatacacaggaagcttctaa A/G taaagtaaggaaagtcactct	541
ABCB4	14	intron 8 + 531	ctaaagagtgatgatttca A/G tacgtcccttgggaactcacc	542
ABCB4	15	intron 8 + 4240	ctgaggttcacagcttctct I/A tagagatgtttacttagtct	543
ABCB4	16	intron 8 + 4343	tgtagaagaaaaaaaggtt C/I atattacaagagggtctgac	544
ABCB4	17	intron 8 + 4677	ccaagatatcttcaataact G/C tccatagtcctagggtgccc	545
ABCB4	18	intron 9 + 113	tttaccagatttcaactatt A/G ttatcatttttgcctccaaa	546
ABCB4	19	intron 9 + 982	tgtcctatacagtttttgtt I/A taagtttagtaaatgtatta	547
ABCB4	20	intron 11 + 241	gcactttggaggcccaaggt A/G cataaatcaacttgaggctcag	548
ABCB4	21	intron 11 + 457	tcaagcttgggtgacagagt A/G agacttcaatcicaaaaaaa	549
ABCB4	22	intron 11 + 1337	tactcttggaggacctatca C/G cagggtgggtcagatatagc	550
ABCB4	23	exon 12 + 3	tgttcttcttctgtccagat A/I ctctggcatttagtgacaa	551
ABCB4	24	intron 12 + 1288	cagaccacataaccctcag I/C tggacctcaggatgtcagtg	552
ABCB4	25	intron 13 + 206	ttgggataaagaaatagcat G/A tggtagaccatttgtgaaa	553
ABCB4	26	intron 13 + 988	cagtcgggttggagcttgc I/C acccttcttcaacttctca	554
ABCB4	27	intron 13 + (1413-1414)	tttatcttcaacttgaattt (I) ctacgttaagttatgtaat	555
ABCB4	27	intron 13 + (1413-1414)	tttatcttcaacttgaattt ctoagtttaagttatgtaat	556
ABCB4	28	intron 13 + 1931	cttgcgaatgttgcctctcc A/G caaaaaaaaggaaggaat	557
ABCB4	29	intron 22 + 767	acagtggtgcgtatcataga A/Δ cctgtagcaatccaccagca	558
ABCB4	30	intron 23 + 784	agtatcttctaaacttctgc I/C atgcaggaataattattta	559
ABCB4	31	intron 25 + 158	gaaatatttactgtattaa I/C gctcagaacttaataaag	560

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ABCB4	32	intron 25 + 2920	ctgagcttccctatacatct t/a ttccattcctcggatgctgt	561
ABCB4	33	intron 29 + 411	cttctcttaccttgaaattc A/C ggcctcgaactttgacttt	562
ABCB4	34	3' flanking + 458	agaaatgaattgcctctac T/C gagctaaactctgaaagcaca	563
ABCB7	1	intron 1 + 220	agaggcagagggttctggg C/A agaggacacctggagcgcg	564
ABCB7	2	intron 1 + 480	agttaacctccttgcigaca G/A gogtcttctttagataggcca	565
ABCB7	3	intron 1 + (512-513)	gataggccaaacgcgtact A/T Δ ctttccaaacatagacgcg	566
ABCB7	4	intron 1 + 1690	agttcccaataaggcagat G/A aagttaaagataaaatttcta	567
ABCB7	5	intron 1 + 5309	aattaataatatttattgct G/A tattttgtcagtttatct	568
ABCB7	6	intron 1 - 11274	tgtttcttttcaagccagcc A/G gctttaaaaaaagttagct	569
ABCB7	7	intron 1 - 11085	caggttttcagggtcactgt A/G gacctgaagaataatgagag	570
ABCB7	8	intron 1 - 10037	atttactttctcaactct T/C ttattacattatctcatcat	571
ABCB7	9	intron 1 - 21	ccactctgaactccccc G/A cttttttcttctgicagcag	572
ABCB7	10	intron 3 + (135-136)	ttctctaataaaaaaa (A) catatttaattgacacatagtt	573
ABCB7	11	intron 3 + (135-136)	ttctctaataaaaaaa catatttaattgacacatagtt	574
ABCB7	12	intron 3 + 333	aaacaatttgggtgtgtgc G/A tgtgttcaagggttaattgtt	575
ABCB7	13	intron 12 + 524	taaccaacttgcctcagta C/T gaacacagtgccgaaccca	576
ABCB7	14	intron 13 + 1543	atcctgtgaggtgggaagc G/A tatggtatgacataataaa	577
ABCB7	15	intron 13 + 2400	tgttacatttaccgtcatt C/G tcattttccacactgctat	578
ABCB7	16	intron 15 + 2201	cctcttctcaacttagcaa G/C agtctggagatttacttacc	579
ABCB8	1	5' flanking - 2272	ggcttagcctaaaggctga T/C gttggggccagtacccttga	580
ABCB8	2	5' flanking - 2070	agctatgaacaaagacct G/A tcccttagaggtagcaaaa	581
ABCB8	3	intron 1 + 25	aaacggaaaaaaccttactag A/C gggggcatttgacgcccg	582
ABCB8	4	exon 2 + 308	tgtgtgtcttggggtagcc G/A tctgtgtgaggtttcccca	583
ABCB8	5	intron 2 + 334	ccccacttaaaacatttgt C/G cctctgtctcccaattcca	584
ABCB8	6	intron 4 + 12	cctgtcctcgttacttccagc C/T gcagggtgcagagttgggt	585
ABCB8	7	intron 5 + 547	agttcatagcattctcgtc G/A gccccctcaggcctgctgt	586
ABCB8	8	exon 7 + 57	ggcaatgtcggactgtgcg A/T gcttgcctatggagcaacg	587
ABCB8	9	intron 9 + 1231	tttcgcagctgcattggaca C/T cctcgcgtgcccgtttctg	588
ABCB8	10	intron 9 + 2164	cctcttgaggtctcttctag C/T gctgcctatgtggagattct	589
ABCB8	11	intron 9 + 2645	ttctgtcctgttgcctcccc C/ Δ ggtgcctttagcaagtgt	590
ABCB8	12	intron 9 + 2646	tcctgtcctgttgcctcccc G/A gctgcctttagcaagtgt	591
ABCB8	13	intron 9 + 3229	caggcccgaggaggagtc G/A tgggtcagctgggtcctct	592
ABCB8	14	intron 12 + (113-114)	tcctccactgcacaaaggg (GG) ccttcttctcgggacaatc	593
ABCB8	15	intron 12 + (113-114)	tcctccactgcacaaaggg ccttcttctcgggacaatc	594
ABCB8	16	intron 13 + 128	tgctctcgggagacctggc C/T gcttcacatgtctcagct	595
ABCB8	17	intron 13 + 305	atccagggtctagagagct A/G tagtggagggtctgagctgc	596
ABCB8	18	intron 14 + 135	acagttgttcagggaagac C/G agaaccacagccaaagggga	597
ABCB8	19	intron 14 + 159	accacagccaaagggagac A/T gtcgttctgttgggacacagg	598
ABCB8	20	intron 15 + 747	gttgagccttgggtctgt A/G agggggacagagggaatcat	599
ABCB8	20	3' flanking + 333	cctatccccctgctcacc G/A ggacccacagttccccatctt	600

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ABC88	21	3' flanking + 1168	ccctctttcagggtgtgat G/A cagtgcattgatggagcagc	601
ABC88	22	3' flanking + (1719-1721)	tagaccgcaggacccggcc G/C/Δ ttactaacctgcctcggcc	602
ABC89	1	intron 1 + 69	agggtgccaggccagcag G/C gttagggcgctcggccac	603
ABC89	2	intron 1 + 8873	tggccccagcacatggggc T/C ggaactaccctcaaggcttc	604
ABC89	3	intron 1 + 8940	acagctcagctcccgagg G/A tgcacacggcacaagctgg	605
ABC89	4	intron 1 + 11410	agatcaaggatccagagg T/C tggatgtgacctcogtgc	606
ABC89	5	intron 1 + 12863	gggaagccagatccacaa G/A gctcgtgacttcacttcca	607
ABC89	6	intron 1 + 19731	gcaagtgtcaagatcgagc G/A agggagggccctgacgaggg	608
ABC89	7	intron 1 + 29649	cagaatccagatcccgtaa T/C gtgttaagaagcctgcaca	609
ABC89	8	intron 1 + 31793	ggccagggggagggttac C/I ggccagacoggtggggcaaaa	610
ABC89	9	intron 1 + 37537	agagtcacagggttgggtg C/A cccgggaaggtagcatcta	611
ABC89	10	intron 1 + 38293	taccagccctgtgtttcag G/A gaccatgtgacctgtcaact	612
ABC89	11	intron 1 + 44661	ccgagagtgctggttcac A/G gcaggattgcgtcctgcag	613
ABC89	12	intron 1 + 49576	aaagtggcccgctggcttgc C/I cccctgaagccctaaagcaac	614
ABC89	13	intron 1 + 64669	ccacagacagccgggttagc C/A cacttcgcagctcaacacac	615
ABC89	14	exon 2 + 448	ctgggtttggccctgttc G/A tctgacgtacatttcactc	616
ABC89	15	intron 7 + 3364	ggtaccaggagtcgggtatc A/G gtggacacaggaacgcgtgctc	617
ABC89	16	intron 11 + 113	ggcccccaggagctctocca G/I actatcagcctcctggctg	618
ABC89	17	exon 12 + 370	ccagggcctcagcactgaa A/G gacgacctgccatgtcccat	619
ABC810	1	5' flanking - 424	tcgcgtcggcgctccgcc C/I ggtcgcggcggtgagaag	620
ABC810	2	exon 1 + 491	acaaggcggttgcgccc G/I cagcgccggactcccgagg	621
ABC810	3	intron 1 + 37	ccacttcctcccgccggcc T/G ctctctccacacgcgggg	622
ABC810	4	intron 1 + 217	actcgtttgcagatttaca C/I tigtttcttctgtgacacac	623
ABC810	5	intron 1 + 405	ggtttataactttttttt T/Δ aaccataaacacattatttg	624
ABC810	6	exon 3 + 185	agggccggggcccgagcttc C/I gtaggcatcagtaigtggt	625
ABC810	7	intron 6 + 1269	caatttcacactgctgctt C/G cacgaatgggttgggaaac	626
ABC810	8	intron 9 + 632	ccccactccacttgggttag G/A gcagggtggatgggtgggt	627
ABC810	9	intron 10 + 2373	tactcaggcactcagaca G/C cctcaccatcagaggctca	628
ABC810	10	intron 11 + 108	tccttttcctgtttttgtt T/G tttttttttcttggagttg	629
ABC810	11	intron 11 + 2379	cattggttttttagttatc T/A gtgtgtgcatacatcatca	630
ABC811	1	5' flanking - (2596-2595)	tggtgttagagctttctct (TT) gagacatttttgcctaaggtt	631
ABC811	1	5' flanking - (2596-2595)	tggtgttagagctttctct gagacatttttgcctaaggtt	632
ABC811	2	5' flanking - 1746	agctgaagttaataaacac G/A atcaactcagtaactacact	633
ABC811	3	5' flanking - (326-314)	aggggaagtttaaaaggta (T)9-12 gcttgttaatttttaagt	634
ABC811	4	5' flanking - 135	agaggtttcccaagcacac T/C ctgtgtttgggtttatgct	635
ABC811	5	intron 1 + 511	aaatatagatcaaaaaaaa A/Δ tgagctgtggatgcattgtt	636
ABC811	6	intron 1 + 581	aatttcagtttttagttcac C/I caagccagttggagtcacat	637
ABC811	7	intron 1 + (1938-1951)	aagacagtttttaagggtttt (A)10-13 gaaagaaaaaaactgtag	638
ABC811	8	intron 1 + 4517	ggtttccacatcctcatct G/A ataaaaaaaattttggcca	639
ABC811	9	intron 1 + 5651	aaagagaataggttagtgga T/C tagtattcctgtgtttaatg	640

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ABCB11	10	intron 1 + (12200-12201)	aaagatggtctctagcccc C//Δ gtttgatttggggcaattac	641
ABCB11	11	intron 1 + 13023	gtttgctacttattgattaaa G/A aagaagaagagataataat	642
ABCB11	12	intron 2 + 739	cttgcatctattctgacctta C/I actgggaaaaacagtatg	643
ABCB11	13	intron 2 + (921-922)	tatttggatttcaaaaagt (CAGATCTTCTTCAGCTAATTTAGAAATG) tgcgtgccatttgatattca	644
ABCB11	14	intron 2 + (921-922)	tatttggatttcaaaaagt	645
ABCB11	15	intron 3 + 644	agccacacgtttcttattgc G/A tgggaagtttaaaaaatggg	646
ABCB11	16	intron 3 + 2231	agtgaacccagagattgagct A/G tactgaatctctagaagag	647
ABCB11	17	intron 3 + 2406	aaagggtggtctttaaattc I/C taatgttttctcattcaggtt	648
ABCB11	18	exon 4 + 10	tttctcatcagggttacaaga I/C gagaagaaggtgatggcgt	649
ABCB11	19	intron 4 + 434	acaatttatagttattctca A/G tggccacacagtttatcta	650
ABCB11	20	intron 4 + 518	gtatagtagtagtctaaaaac G/I aaagtcagctctctgaaataa	651
ABCB11	21	exon 5 + 120	ggcacaatgacagaatttt I/C attgactacgagttgagtt	652
ABCB11	22	intron 5 + 320	gggaggtgacccatgaattt I/C acttgagtatcatctccaag	653
ABCB11	23	intron 5 + 16076	agaagaggttaacagtaagcc I/G cctgatttacagcacacatc	654
ABCB11	24	intron 6 + 303	atttgcaggttgttttagtag G/C gggcagttgagtagcttgaa	655
ABCB11	25	intron 7 + 1141	aaaggattcagcaggcatga A/G gaaagaagaagctttgcaaga	656
ABCB11	26	intron 8 + 2463	ccatttggttaataagcaatga A/C ctatgacatgggtctaaactta	657
ABCB11	27	intron 8 + 2677	tcaatgatgttacagtgaga A/C tctaataatgttattaaacc	658
ABCB11	28	intron 8 + 2699	ctaataatgttattaaacca I/A gccacatgttaaatgaatct	659
ABCB11	29	exon 9 + 24	gttccaagtttacggacta I/C gaggcgaagccctatgocaa	660
ABCB11	30	intron 9 + 108	cacttgggtgtggcctcc A/G gaggaagtacttgttcaaga	661
ABCB11	31	intron 10 + 2475	taatcatccaaccacgga C/A ttatttcatiaagaacatg	662
ABCB11	32	intron 10 + 2478	ttatcccaaccacggactt I/A atttcattgaagaacatgata	663
ABCB11	33	intron 10 + 2711	ttacagatttggaagaaagcca C/I tgaagtattgcaggtccaga	664
ABCB11	34	intron 10 + 3539	agtacgtgtaattagtatca C/G tigtgcacagagaaaaaatg	665
ABCB11	35	intron 10 + 3623	tgcagaaggtgtgtcttcttca I/C gaccttctgagtttcagaa	666
ABCB11	36	intron 10 + 3661	gaattcaattataaaaaataa A/I cacataatggagcgtgacat	667
ABCB11	37	intron 10 + 5100	gggccaactctttggcttggc A/G atagactgtggccaatgaaa	668
ABCB11	38	intron 10 + 5292	gctatttggtaggaacatct G/A gccatgacaggttagccttc	669
ABCB11	39	intron 10 + 5912	gagtaaatattcagtaaaaaa A/Δ taaagtggtattttaaatca	670
ABCB11	40	intron 12 + 116	tgtttccagtaattaggaat G/A gaggtgtcttctctctgaaag	671
ABCB11	41	intron 12 + 326	gataaatgacaaggcaatta G/C aacaatcagggaagcacaggt	672
ABCB11	42	intron 12 + 335	caaggcaattacaacaatca A/G gaagcacaggtttotcccaa	673
ABCB11	43	intron 12 + 2572	cccatcctctggccaatgttt C/I cttttactggttttgaagg	674
ABCB11	44	exon 13 + 23	tctaaatgaactcaacatgg I/C cattaaaccagggggaaatga	675
ABCB11	45	intron 13 + 70	atggcagatattgatcaaa C/I agaaaggttagcatacatt	676
ABCB11	46	intron 13 + (1578-1579)	ttattggcctctatttttc (C) tggccattggctcaagtatga	677
ABCB11	47	intron 13 + (1578-1579)	ttattggcctctatttttc tggccattggctcaagtatga	678
ABCB11	48	intron 14 + 32	catacatctctgggagaac C/I aagaggtcatagaggaaaa	679
ABCB11	49	intron 14 + 80	cacaattatacacatttctt C/I tegtatgattcccaagtcac	680

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ABCB11	48	intron 14 + 439	tatttgtaaaaacaattc A/G ttgtatatctccattctaag	681
ABCB11	49	intron 14 + (1262-1263)	cagccttgattatattt (T) gctggtgtctaacaggag	682
ABCB11	49	intron 14 + (1262-1263)	cagccttgattatattt gctggtgtctaacaggag	683
ABCB11	50	intron 14 + 1283	gctggtgtctaacaggag A/C aaagagacacggatttgctc	684
ABCB11	51	intron 14 + 1339	tgagatagatttaggacc G/A tgaccaattttattttggt	685
ABCB11	52	intron 14 + 1359	tgaccaattttattttggt I/C tgaaaaattttatttgaagt	686
ABCB11	53	intron 14 + 1480	tattgattagacaataaacc G/A tctgggaagggaattttct	687
ABCB11	54	intron 15 + 370	cttttctaagtctgcaca G/A cotatttaagaatatccca	688
ABCB11	55	intron 16 + (550-559)	aaagtttagtgttttatca (T) 9-12 gctactctgaaggacttct	689
ABCB11	56	intron 17 + 188	tttctctcccaattcatgg I/G ttttgggttagcttcicac	690
ABCB11	57	intron 17 + 194	tcaccaattcatggttttt I/G gttagcttctcatcttcctg	691
ABCB11	58	intron 17 + (197-198)	caattcatgggttttgggt (T) agcttctcatctctctgggg	692
ABCB11	58	intron 17 + (197-198)	caattcatgggttttgggt agcttctcatctctctgggg	693
ABCB11	59	intron 17 + (289-296)	gggaactcttttaaaaaa G/A(A) 4 tctggttttagtctctct	694
ABCB11	60	intron 17 + 1070	ttagacttggttttctctat C/I tttctcttgagacaagtt	695
ABCB11	61	intron 17 + 1651	tgtaaaatctcatcttgta I/C atgctgacgattttctctg	696
ABCB11	62	intron 17 + 2226	ccttaagtctctctctatca I/A gcaactgttctctccagct	697
ABCB11	63	intron 17 + 2979	ctctctctctctctcagc I/Δ ctactatttcaactgttggt	698
ABCB11	64	intron 17 + 3288	aatcccaatctctacotia I/G caatctcatoccatgaatctt	699
ABCB11	65	intron 17 + 3289	atcccaatctctacottag C/I catctcatoccatgaatctt	700
ABCB11	66	intron 18 + 97	aatatgagttttctaggtat A/G tatctagcaggttttcaagt	701
ABCB11	67	intron 18 + 98	atatgagttttctaggtata I/C atctagcaggttttcaagt	702
ABCB11	68	intron 18 + 892	ctctgaaagtttagtataca C/I ctatttgttttgaatacaa	703
ABCB11	69	intron 18 + 2681	atgtatgagatcaagtcagg A/G tcaaatatttagacaccata	704
ABCB11	70	intron 18 + 3780	ggacatctctgtggggcaat C/G gtccagaaaaatgttggtat	705
ABCB11	71	intron 18 + 5741	ctcaccgataaatacaac C/I gtagcaaaaggttttctttt	706
ABCB11	72	intron 18 + (5882-5883)	tgcgtattccctcagttcag (C) tttttattcaagccacagca	707
ABCB11	72	intron 18 + (5882-5883)	tgcgtattccctcagttcag tttttattcaagccacagca	708
ABCB11	73	intron 19 + 10022	tggttaagttaaaaaaaa A/Δ gagattcaactataattgct	709
ABCB11	74	intron 21 + 322	caagattcaatctgcccc C/Δ aggggtgtgtgaacaggcc	710
ABCB11	75	intron 22 + 257	ctgttcaattctctctcgca I/C agtattcatttccacattcc	711
ABCB11	76	intron 22 + 552	taattaatatcttctctgt G/C gggtaaataggagatggta	712
ABCB11	77	intron 22 + 569	tgggggtaaataggagat G/A gtagcataaacacttctcaa	713
ABCB11	78	3' flanking + 243	aaacacacagaatgacata G/A aactaaaggccgcaggaaatc	714
ABCC1	1	5' flanking - 1661	catcacccttggggagccc A/G ggccaataaaaaaatcacag	715
ABCC1	2	intron 2 + 635	gatgtccctcactgaacct I/C ggctcggggcagacttgggg	716
ABCC1	3	intron 2 + 4769	ggcgaggagtggactcagg G/Δ ttctgtgtccaaatgggttc	717
ABCC1	4	intron 2 + 10069	tatggaggttttctcttct I/C tctgtgagttttctctctga	718
ABCC1	5	intron 2 + (11965-11984)	taaaagccaatcaaatcaac (T) 18-20 aaacaagccacgatttggc	719
ABCC1	6	intron 4 + 4302	cacctgtaatccacgaacct I/G gggaggccaaggcaagtggga	720

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ABCC1	7	intron 4 + 4394	gtcttactaaaatacaaa A/C attagctaggcatggggg	721
ABCC1	8	intron 4 + 4524	ccactggctccagccggg I/C gacaagagaaactctgtc	722
ABCC1	9	intron 6 + 9045	aggctcttaactaccctgc G/A ctccaagaatcagtgccgg	723
ABCC1	10	intron 7 + (3059-3071)	agctttttgatgcacct (A)11-13 gccattttctcgtcatgacc	724
ABCC1	11	intron 8 + (886-889)	ttctatgtacagtaagaaa GAAA/Δ agcagctgccaattaaacaa	725
ABCC1	12	intron 11 + 198	tgaatttcagggtgattt C/A tcttgggtcagtgccgttt	726
ABCC1	13	intron 11 + 784	tgaggattccagagat C/G aagcaatgtgtcagtactc	727
ABCC1	14	intron 12 + 122	agccttgcctccagttgga C/G tcacttggggagoccttaaca	728
ABCC1	15	intron 12 + (3138-3148)	accocatctctatigaagaag (A)10-12 tcaataaaaaaacatttac	729
ABCC1	16	intron 12 + 3227	tggtgatttgagtgagg C/I tgatccagggctggccocag	730
ABCC1	17	intron 13 + 2060	tgctcattacaactatcct I/C ctggcaggttggcaaat	731
ABCC1	18	intron 13 + (2061-2062)	ctcattacaactatctctc (C) ttggcaggttggcaaat	732
ABCC1	18	intron 13 + (2061-2062)	ctcattacaactatctctc ttggcaggttggcaaat	733
ABCC1	19	intron 13 + 11776	ggcacttggggaggcccaaa G/A cggctccaggccctgtca	734
ABCC1	20	intron 14 + 179	aaagaagaagaaacacatttg A/I ctcttgacagagaacitcgc	735
ABCC1	21	intron 16 + 219	ctagcacagagggttccctg G/I gattgaattacagcagcc	736
ABCC1	22	intron 16 + 310	ggaagttctacttccagtg C/I gggtgatccaggagactctg	737
ABCC1	23	intron 16 + 890	ctctccagagaaaacaatct G/I tagaagccctgattgaaaa	738
ABCC1	24	intron 17 + 1171	aaccocaggctcaagaagc G/A tgggaataatgcatactcc	739
ABCC1	25	intron 17 + 1332	cacctcttagtctcgtgc A/G acigcacatttgtctctgg	740
ABCC1	26	exon 18 + 53	gattcagaatgattctctcc G/A agaaaacatctttttgagat	741
ABCC1	27	intron 19 + (3373-3379)	ccaagctaggcagttctaca CA/Δ tgtgcactcaactggccggg	742
ABCC1	28	intron 20 + 2730	cggtgaggtctgtctctcta C/I ccttccgtccaggtagacaa	743
ABCC1	29	intron 20 + 2789	cttggccocagataggctcc G/C caccccgcctttcttccc	744
ABCC1	30	intron 20 + 2919	gatgcaaatgcgcgccacca C/I cctggcacctcgtgcgttca	745
ABCC1	31	intron 20 + 3024	cttaccatacaactggggcac C/I cccctctctcaccacccacc	746
ABCC1	32	intron 20 + 9718	gtggctggctcagtgacga A/C caggagaagtgaagctgag	747
ABCC1	33	intron 20 + 9733	gacgaacaggagaagtgaag G/C ctgaggcttataggagggtg	748
ABCC1	34	intron 20 + (9895-9896)	gcgtgtccagtgctcacac A1/Δ ggtgtgagacagggctgca	749
ABCC1	35	intron 20 + 9952	ggatcattcttctctctc G/A gtgaltggctatttgtgtt	750
ABCC1	36	intron 20 + 11120	gcggagtgggggcagtagtc A/G tcatcactcaactgatttatg	751
ABCC1	37	intron 20 + 11147	tcactgagttatttgaacc G/A ggaagagatatgatctgtg	752
ABCC1	38	intron 20 + (11629-11631)	tattttgaatactactt C1/Δ tcaatgcttgggaatcacgg	753
ABCC1	39	intron 20 + 11864	gagctccagataccacctgc C/I ccacaaccagacagcctgtt	754
ABCC1	40	intron 21 + 3860	tggagagtgcactgtgtggg G/Δ tgttggcatatattcatat	755
ABCC1	41	intron 22 + 878	ttaaagatogttattttgg G/A caagtgttaataattctoca	756
ABCC1	42	intron 22 + (4445-4446)	gttggggctggggctgggggt (GGGGC1) gggtgggtgatgtgtaag	757
ABCC1	42	intron 22 + (4445-4446)	gttggggctggggctgggggt gggtgggtgatgtgtaag	758
ABCC1	43	intron 23 + 62	gttgaggctttgtctaatta I/C agaatggatccttagagtc	759
ABCC1	44	intron 24 + 3171	aacctgaggctcaacatat C/I tcaaacaccgtgcacagct	760

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ABCC1	45	intron 24 + (3349-3368)	ctctgaaattggtgcacg (1)19-22 cctgcatttaccacaaatg	761
ABCC1	46	intron 24 + 3369	tttttttttttttttttttt I/C cctgcatttaccacaaatg	762
ABCC1	47	intron 24 + 3584	caagagttttttttttt A/G caacaaaggaaatgatttta	763
ABCC1	48	exon 25 + 60	gagtcggtcagcgctccc G/A gctatccatttcaacga	764
ABCC1	49	intron 27 + 4539	tcctttttactcactcag G/A tggagaaacaaatcacattta	765
ABCC1	50	intron 30 + (1708-1714)	gaccacacatctctctgg (1)6-7 ctccgggtcaagtgtcgggc	766
ABCC1	51	exon 32 + 652	tggagaaatcattttctcc C/I ctggcagtgctccaggcc	767
ABCC1	52	3' flanking + 158	ctgatgctctccaggacac G/A aaaaagaccatctttgaat	768
ABCC1	53	3' flanking + (187-199)	ccatctttgaatacaatga (1)11-13 aagtactgtccggggagaa	769
ABCC1	54	3' flanking + 2227	cattagaataggtagtatca G/A ccagccggcagtggtggcgc	770
ABCC2	1	exon1+77	catattaatagaagagtcctt C/I gttccagacgcagtcacagga	771
ABCC2	2	intron1+413	gataagttctagaaactggca A/C ctaatgatatggactagaag	772
ABCC2	3	intron2+192	atcaaaaggctttgatatt I/G gcataagaatggtagctctt	773
ABCC2	4	intron2+1020	agtgctgcgattacaagcct G/C agccaactgcacagccctcg	774
ABCC2	5	intron2+3639	gtcatatcccccaccccaat C/A gacccaatagggtacaatgaa	775
ABCC2	6	intron2+3930	aaactcggcaggagaatttc A/G ctggagctgcagtcaggaact	776
ABCC2	7	intron2+3989	agttatgaaccgatttttc C/I gggactgggtgttctagctct	777
ABCC2	8	intron2+4078	agtttccagatgtgttccc I/C aggcatttcctgggtgagga	778
ABCC2	9	intron2+4171	cttattctttggcagcttgg C/I ttctaccacctcttagctt	779
ABCC2	10	intron2+4257	gggtattggaaagtcttgc G/A gctcgtggaggctgcgggtgt	780
ABCC2	11	intron2+4436	ggactagtggaagaattaga C/G ctttcctgaataaataagatc	781
ABCC2	12	intron2+5227	taccataattttatgtgtcct A/G tatgacatgaatttcattgg	782
ABCC2	13	intron2+5373	gttaaggatataigaaactca A/G gfgtgtctataggataaatt	783
ABCC2	14	intron2+5538	ttatagggttaagcacatg G/I tcatatgttttaaaagccttt	784
ABCC2	15	intron3+772	ggatagaaggcaagattttt A/I aaaaaatttaattgcttaact	785
ABCC2	16	intron3+1145	acatcctcttcccctcagtc C/I tgggttagggcagctattct	786
ABCC2	17	intron7+1658	ggactcttaccagcttagtt G/I cctggttttctaaatctaaaa	787
ABCC2	18	exon10+40	tggccagaaggagtagacac G/A ttggagaacacagtgaacctg	788
ABCC2	19	intron11+1672	aactttttaagtcttaagac I/A ggaaggcctgtgtcctaggc	789
ABCC2	20	intron12+148	cccttcacggcccccagtc A/G cttttcctcctttgtaccat	790
ABCC2	21	intron13+180	catgagttttctgagcccca G/C ttatctaatataaaatga	791
ABCC2	22	intron13+1497	gtcagaggtcccccagtc I/C atagccagttcctctttaga	792
ABCC2	23	intron15+169	atgagctgaagaacaaagggt I/C taagccccctccctgataa	793
ABCC2	24	intron15+949	ttccagggtgacacatttagt A/G cctaatttgggaaatgttaa	794
ABCC2	25	intron15+984	tgtaattctagtcacatccc A/C ttagtgaagaaggagggttc	795
ABCC2	26	intron16+4059	catcctgatgcacagttatt C/I aaatttaagctccatttgtt	796
ABCC2	27	intron19+10899	atgtatggagtattttatgga G/A taaagtattccatgcigtat	797
ABCC2	28	exon22+51	caagcaataggattgttttc G/A atatttctcatcatccttgc	798
ABCC2	29	intron23+56	tatactgaggaatcttttga C/I agggaggaattattatgtcc	799
ABCC2	30	intron23+432	tggcagtagagcagggtgag G/A aggattattcgcagaggaa	800

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ABCC2	31	intron23+734	tggccaactactactactag G/A cactggggcactcaatgaat	801
ABCC2	32	intron23+801	atgggcagaccaccaactcac I/G gatttttagtattatgag	802
ABCC2	33	intron26+154	ctggccactcttttaacca I/C ggaagtatttccttactcttc	803
ABCC2	34	intron27+124	gggtccctaagtttctctt C/G cttactactcaagggaactaa	804
ABCC2	35	exon28+52	cagattggccagcaagg A/C agatccagtttaacaactac	805
ABCC2	36	exon28+84	acaactacaaggcgga C/I cgacctgagcggatctggt	806
ABCC2	37	exon28+129	agaggatcacttgtagat C/I gtagatagagagagtagg	807
ABCC2	38	intron29+154	ttccctaggatggacagtc A/G ttccagaaactttgaaatgt	808
ABCC2	39	intron30+91	gtgttaggtgatgcctggca I/C agaattttatccaggctctg	809
ABCC2	40	intron31+170	gcacaaattttacatcacgc A/G aatgaaaacgacaaggta	810
ABCC2	41	3' flanking+371	gtgaattttattataagct C/I gttctcttaaaactttatc	811
ABCC3	1	5' flanking - 1064	tccttctgagccccaacaag C/I ggtgctgagttggcgtctgg	812
ABCC3	2	5' flanking - (827-820)	ctggggttcacctgtctctt (C)7-8 aacctgatacaggctgaagc	813
ABCC3	3	intron 1 + 1226	tatttgtacatatatgcct I/G tgtgtgtgtacgcacacag	814
ABCC3	4	intron 1 + (1389-1399)	aaacttggggcaatggaggt (A)10-12 cgttaaaaaggcataattgg	815
ABCC3	5	intron 1 + 2070	ggcgaacttctcttgatgct C/I gtagctatatacacacctcct	816
ABCC3	6	intron 1 + 4477	gcctgtagtccacagacagg G/A aatggtcttgaacacttg	817
ABCC3	7	intron 1 + 6189	agtgaccaatgaagtgcga I/C gaggggacctctgccacgtg	818
ABCC3	8	intron 2 + 268	ttgtatttttagtagagatg G/A ggtttgccattttggcagg	819
ABCC3	9	intron 2 + 376	tgtgccagccagcattctg G/C tttaatgaggccctctccc	820
ABCC3	10	intron 2 + 446	ctcacctgacctgtctgggg C/I catgggaatctgaacaactga	821
ABCC3	11	intron 8 + 2323	gagcttggtgtgagagcgt C/G atogataggcgtgcagcag	822
ABCC3	12	intron 12 + 85	ctcattggactctacctga C/ Δ acaacctccacgctcag	823
ABCC3	13	intron 19 + 1581	ttctgttgccctttcaatc C/I cctcattttattttcatgc	824
ABCC3	14	exon 22 + 180	aacacttccctgaggctggg C/I gctatgctgcttttagaat	825
ABCC3	15	intron 30 + 1979	cctctgtctgttccatcct C/G tctacctcaccctccact	826
ABCC3	16	intron 30 + 2340	atgcaccagccagccctgaa A/C gaatgagtaagattggagg	827
ABCC3	17	3' flanking + (555-558)	ttttcttgagcaagccaaca AAGA/ Δ gtttcttttgcaggcag	828
ABCC3	18	3' flanking + 1455	aacccctatgattagaact G/A tagtgcgttttaggaagcca	829
ABCC3	19	3' flanking + (1650-1659)	aattcacagttaacaaagct (A)9-11 tcttgttataaattacaca	830
ABCC4	1	5' flanking - 644	atcaatcgggtcactct C/I gagttaccggcttttctga	831
ABCC4	2	exon 1 + 67	ggagggagcccgccggccac C/I gccgcctgacgcggcacc	832
ABCC4	3	intron 1 + (864-865)	ctttgaccagctcttctcc C/ Δ gtttcaatacttcttctc	833
ABCC4	4	intron 1 + 21255	ggatggaaatagtgagcaca A/G accttggcattttaaggaccg	834
ABCC4	5	intron 1 + 21503	ctgttttaccacttgggg I/C cagcaaatcagcccccttta	835
ABCC4	6	intron 1 + 21900	tgatgctcaagcaatacaaa C/G tagaaaaatataggaggctgg	836
ABCC4	7	intron 1 + 22005	aagggggagtcatactccag C/I gtcatttttagtttgctt	837
ABCC4	8	intron 1 + (22256-22264)	tttgtgtgtatttgctgc (T)8-9 cctggaaggaagtgtattggc	838
ABCC4	9	intron 1 + 27784	ccagggaactggtgtgcacac C/G ctgagctctgtagtggtcct	839
ABCC4	10	intron 1 + 27821	ggctaaagactcaaaccttg A/I ggggaaggcccgaggaaagaa	840

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ABCC4	11	intron 1 + 27837	ctgagggaaggccagga A/G agaaaggagccatggccta	841
ABCC4	12	intron 1 + 27880	gggtgtatttggacocca C/T gccatccaggccgacagag	842
ABCC4	13	intron 1 + 40310	accaagcaggaggagtga A/I tigtgcagactgggatatt	843
ABCC4	14	intron 1 + 40372	ttcttgaataaaaggatgc G/A agtcaatgtatgtgaagt	844
ABCC4	15	intron 1 + 40413	ttcttcaaatccaattcct G/A actgatttcttgccttcca	845
ABCC4	16	intron 1 + 40958	gaagtttacogaaaaacaaa A/G caagaaactcccagtaaaa	846
ABCC4	17	intron 1 + 50060	tgtgctatggggaacatga G/A gctcatagaaactgaagact	847
ABCC4	18	intron 2 + 181	gcctgggggaaactcctgtt G/I cctgtccctccgtagaggct	848
ABCC4	19	intron 2 + 254	gaggtctgtccctcctaggig G/A aagttgttggttggaggag	849
ABCC4	20	intron 2 + 290	aggaggtgtctggtcttacc T/C gfgtactatgagggtcttca	850
ABCC4	21	intron 2 + 543	ttacgaagctttttctcat T/C gtaggttctgggataaagaa	851
ABCC4	22	intron 3 + 557	ggccttgacactgggtggc G/A gttgtgccccagaggctgga	852
ABCC4	23	intron 3 + 718	gtgtcttctctgtgtcg G/A agtggattctgttggaaag	853
ABCC4	24	intron 3 + 801	acattccatgaaaaatcaaa G/A acagccagaaggccaataac	854
ABCC4	25	intron 3 + 1022	aggggtggatgtgtgtgtg T/C tacaaaagggtggctttaa	855
ABCC4	26	intron 3 + 1471	tgttgggtgtccagcgat A/G gttttccacatggccccga	856
ABCC4	27	intron 3 + 1490	tagtgttccacatggcccc G/A atcagtttcagtgtggaaaga	857
ABCC4	28	intron 3 + (1833-1834)	ggcgicgacccacttgggg (G) tggggctctaaocccaga	858
ABCC4	28	intron 3 + (1833-1834)	ggcctgcacccacttgggg tggggctctaaocccaga	859
ABCC4	29	intron 3 + 1870	cabatggtagctggactaca G/A tgagatttgggttaagctttt	860
ABCC4	30	intron 3 + 1927	gaagttagagcttagaagc G/A tgaatttctctagagacttg	861
ABCC4	31	intron 3 + 1970	gacaggccacactcgtgtc A/I agggcatgtgtaactttac	862
ABCC4	32	intron 3 + 2039	gattcaggggagctttaata T/C gggtaacagtgtgtggagagc	863
ABCC4	33	intron 3 + (2067-2068)	ttggttagagactggctcttt (C/T) tagcgggtgggttatlgggc	864
ABCC4	33	intron 3 + (2067-2068)	ttggttagagactggctcttt tagcgggtgggttatlgggc	865
ABCC4	34	intron 3 + 3563	cattgacigtatggctctggc G/A gatgtcaagttccctgttt	866
ABCC4	35	intron 3 + 3696	tgtttggcaaggatgaagc C/G ccagatgagtcactagtatg	867
ABCC4	36	intron 3 + 4093	aagtaactcttggattttt T/C ttttcttctctcttagcag	868
ABCC4	37	intron 3 + 4097	aatccttggattttttttt T/Δ ottttctcttagcagtgaa	869
ABCC4	38	intron 3 + 9724	aaaaaccagactactcacc A/G atgagccatttcttgact	870
ABCC4	39	intron 3 + 9988	aaggcaaaagagcactgagc G/A tctggcigtatgoccagggtg	871
ABCC4	40	intron 3 + 10952	gttaaaattgcattccctac A/G tctgttcagaaaggttaagcc	872
ABCC4	41	intron 3 + 11125	gccaaatttctgtgtgtt A/G attttgactccacactacc	873
ABCC4	42	intron 3 + 11244	ccaagagcctggaaactccc C/Δ aagtctgttcttttcccca	874
ABCC4	43	intron 3 + 11916	gtcttgccaaaaaataaaaa A/Δ tttagctctacatgagtg	875
ABCC4	44	intron 3 + 12047	actatactcagcatgggig A/G cagagcaagaataatctgaa	876
ABCC4	45	exon 4 + 205	tgaggttacagtagtagcatg T/G gccatatgatttatcggaag	877
ABCC4	46	intron 4 + (412-414)	ttatggaaatttttggttt G/T/Δ cattaaacotttcaattaca	878
ABCC4	47	intron 4 - (9757-9756)	tgacatctgcatttttttt (T) cctgctgcacaaatctcttc	879
ABCC4	47	intron 4 - (9757-9756)	tgacatctgcatttttttt cctgctgcacaaatctcttc	880

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ABCC4	48	intron 4 - 6373	atgttttttcttagatga C/G agttttcttgaatctcaaa	881
ABCC4	49	intron 4 - 6267	acttcacacattccacagtat I/C gttcttaalggaatcgggat	882
ABCC4	50	intron 4 - 6096	agatccttattcttcagg I/G gtacaaatttcaaggctttt	883
ABCC4	51	intron 4 - 6057	tigtatgttagattgatt C/I cttcccaagagttgttaatt	884
ABCC4	52	intron 4 - 5295	agttgtctggcttacagtag A/G tgccttactaaatggtagctt	885
ABCC4	53	intron 4 - 803	agtttcacctgttttcagccc C/I gcttcacatgagcttcacctg	886
ABCC4	54	intron 4 - 736	attcacagcctccacatcc C/I ccttctccgtacttctgtcc	887
ABCC4	55	intron 4 - 728	gcctccacatcctctctc C/I gtacttctgtcctagtagg	888
ABCC4	56	intron 4 - 624	ccaccagtgctccctcagtt A/C gaactgtccaccagttctctg	889
ABCC4	57	intron 4 - 470	ttgatactccatatttgta C/I ttcccaattgaacacattgaa	890
ABCC4	58	intron 4 - 411	ggtagagagactaaggcccc G/A tgtgtttaataatgttgcaac	891
ABCC4	59	intron 4 - 323	tgttctctcagacagcctctc C/I gttctccotaatttgctc	892
ABCC4	60	intron 4 - 246	gtcctttgtacttggggc A/G tgtccaaattcattaaatga	893
ABCC4	61	intron 4 - 199	agatttttcttctctaac C/I ctctgtttgtcgtctctgaca	894
ABCC4	62	intron 5 + 73	cctttattttcttgagg C/I aggggtcactctctgttcaaa	895
ABCC4	63	intron 5 + 403	aaggatcacgcttgttgc G/A caggctggctcgaagattct	896
ABCC4	64	intron 5 + 937	ccagaatggcttccactgtg G/C tgggtcttggctttctgt	897
ABCC4	65	intron 6 + 150	ggctcagccaaggggcctc C/I gtccttatctgaaggcaaa	898
ABCC4	66	intron 6 + (380-381)	tgtgttagagctgttttcaac (A1) gtgtatatatgtgtgttatt	899
ABCC4	66	intron 6 + (380-381)	tgtgttagagctgttttcaac gtgtatatatgtgtgttatt	900
ABCC4	67	intron 7 + 894	tttgtgtgttggccagg A/I ggtctcaaacctcigggttc	901
ABCC4	68	intron 8 + 82	tattagatcactatgttc C/G agtgaatgacatttaactc	902
ABCC4	69	intron 8 + 100	tcagtgtaatgacatttaa C/I tctctcaatacccaaacgtg	903
ABCC4	70	intron 8 + 5212	tcagggaattgtggtccaat A/I tgcagctagggaagaatcc	904
ABCC4	71	intron 8 + 5444	gaacacttaatttccctca I/G gtacatagtttctggggga	905
ABCC4	72	intron 8 + 8969	tcacctctctgagtactag A/G gaaagtcacagtagccctc	906
ABCC4	73	intron 8 + 9106	ccagtctcaataggtttac I/C gtgtgcatagttttttatt	907
ABCC4	74	intron 8 + 9412	tgtttgtaagtgcaggatgg G/A ggacaactctctgccctgta	908
ABCC4	75	intron 9 + 116	tggcttgcttatttactgaa A/G ctatgttacaagaattctca	909
ABCC4	76	intron 9 + 1384	cacggcagggaagctgcaccc I/C ggggtggagatgatgtctg	910
ABCC4	77	intron 9 + 1459	agatttgggagacagaggcg A/G gggctctctcagggtact	911
ABCC4	78	intron 9 + 1632	agcagcactctctgccagcc C/A cactgcctccgtctctccct	912
ABCC4	79	intron 9 + 3630	gtaaatttttcaattttgaag G/A ttatcttgaatcttattcc	913
ABCC4	80	intron 9 + 3830	gggttccacccttcaggga C/I gccagattcattttgaagaa	914
ABCC4	81	intron 9 + 3940	gagcatttaccaaagtgt C/I gtgcagaagaatagccactt	915
ABCC4	82	intron 10 + 1504	gggcaaggctgcattgcagt G/A gcttattctgtctcagtg	916
ABCC4	83	intron 11 + 1817	ttttaggagttgagaaca G/C atggcaaattttctagttt	917
ABCC4	84	intron 11 + 3342	actggaattattctggcttg I/C aggtacagagattgcatgtg	918
ABCC4	85	intron 11 + 3377	catgtgtaatacaaacctgc I/C ggacagaatggcttcgagc	919
ABCC4	86	intron 11 + (3610-3625)	tcctggccaccctccccgc (A)15-17 gtcttagagaaaaaatagg	920

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ABCC4	87	intron 11 + 3737	ataagttcattcagcagctaaaa A/G tatatttgagataaaaaaat	921
ABCC4	88	intron 11 + 6953	agagttagacacaagaagaatg C/A caccitgatctgtaagaggg	922
ABCC4	89	intron 13 + 442	ctaigacaggttagaagtga G/C gtccitgggacccaacatagg	923
ABCC4	90	intron 13 + 459	tcagcttccttgggaccaaca I/C agggctttcttgggaaggct	924
ABCC4	91	intron 13 + 633	tgaacacitaaaacaccacag G/A catgtaggcctggcttgct	925
ABCC4	92	intron 13 + 645	accacacagcatgtagcct G/I gottgccttgaactagtt	926
ABCC4	93	intron 13 + 3306	aattgtctcaacagagttaga A/C aattggattgaacaatatgc	927
ABCC4	94	intron 14 + 252	taattttagaaccttttggttt A/G cctcttccatgaccttaattc	928
ABCC4	95	intron 15 + 124	tggatttcgtgttttcaggg C/I tctattccatgatattggta	929
ABCC4	96	intron 15 + 1552	tttggacttcgtcctgttcc C/I ccacagctttgtcaacagag	930
ABCC4	97	intron 16 + 157	cctacttggtttccatgtcc G/A ttacaaagaccitgcgaaaaa	931
ABCC4	98	intron 17 + 329	cccaaatgtgttctatttt I/C aaaaaaatgtatttatctaa	932
ABCC4	99	exon 18 + 56	atggaggaggaagaatgtaacc G/A agaagctagatcttaactgg	933
ABCC4	100	intron 19 + 7202	aattaaaaataatgttttt I/ Δ cacataacaatgggttatatg	934
ABCC4	101	intron 19 + 7445	ttttggcataatttttaact I/C actagaatgttctgtattcat	935
ABCC4	102	intron 19 + 9018	taogttagtgcctgaagaga A/G aaacgtaacattgttcttt	936
ABCC4	103	intron 19 + 11388	aagagttcagagattttggg A/G gttggaggaaaaaatagcat	937
ABCC4	104	intron 19 + 11646	cattatttttaatttttt I/ Δ cctctgttgggtgcagaat	938
ABCC4	105	intron 19 + 13517	gagaaacttacattattttt A/I aaaaatgctataactagtcc	939
ABCC4	106	intron 19 + 21033	tggagtgccctgggctagc G/A ctgaaccttcaggtttttcag	940
ABCC4	107	intron 19 + 21095	agacttttgaaagaagcaga A/I cigaaggtaagacigagtaa	941
ABCC4	108	intron 19 + 21634	gtgctatttcgagcacica C/I gcccacattgggcatgggct	942
ABCC4	109	intron 19 + 21715	tgttttgcacccccctaca C/I agcttgcctcatgtctctc	943
ABCC4	110	intron 19 + 23090	agcaacagacttggagactt G/A agctctotaaaagtctcatta	944
ABCC4	111	intron 19 + 24297	cgaatgtgtaagtgtggga A/G cctttttgagatagcagcac	945
ABCC4	112	intron 19 + 25947	gagtcataaatataatagc C/A aaaaactagaacacattttaa	946
ABCC4	113	intron 19 + 30193	acagatttgcagagctctac A/C aaagtgataatattctgca	947
ABCC4	114	intron 19 + 36938	aagccagtgcaatctcttgg C/G tatcttctgtggactacttt	948
ABCC4	115	intron 19 + 37322	gttccaatgaggctgaccc C/I gctcaccctgtgtaaccgcg	949
ABCC4	116	intron 19 + (38361-38362)	cggggttagcttccctagct (I) ggggagggtttctgagaaaa	950
ABCC4	116	intron 19 + (38361-38362)	cggggttagcttccctagct ggggagggtttctgagaaaa	951
ABCC4	117	intron 19 + 38746	taaaagacatctgtgtaatta I/C gtaaaataaagataaagtcaa	952
ABCC4	118	intron 19 + 42343	tgttaaggcagaatcacagcag C/I aacgattgagtgttcccgga	953
ABCC4	119	intron 19 + 44733	agcagctctggggaataaaaa A/ Δ tacagaggttatcatattgt	954
ABCC4	120	intron 20 + (405-419)	aagggaataactataggcac (I) 13-15 ggatagaaccagggttggtt	955
ABCC4	121	intron 20 + (637-648)	ctaagtccttaagctgtctt (A) 12-13 ccaacaatcctacagaata	956
ABCC4	122	intron 20 + 842	caagctggggcaactttttt I/ Δ tcccaagtgtttattttgga	957
ABCC4	123	intron 20 + 843	aagctggggcaactttttt I/C cccaagtggtttattttggaa	958
ABCC4	124	intron 20 + 1347	ggaccctgattttttttt I/ Δ cttttgcaaacattttttaa	959
ABCC4	125	intron 20 + (14553-14567)	tcctcacacaccctcatct (A) 13-15 tcagcagcttgactgagctt	960

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ABCC4	126	intron 20 + 15487	ggtttttccagtgatag C/I acatgtagaagcagctactg	961
ABCC4	127	intron 20 + 16161	gggttgagtoatgaagccga I/C agtgcgcttgcatcgca	962
ABCC4	128	intron 20 + 30891	agtcgccactgtttctatc C/I ttctcaagaagcaagcgttg	963
ABCC4	129	intron 20 + 31180	cttgacagtgctcattacat G/A tcatgtgtatgttatcat	964
ABCC4	130	intron 20 + 31283	ggttaagctcaaaaaaa A/ Δ ccctgttagacattttgact	965
ABCC4	131	intron 21 + 4204	ttgacctgcctgaaccc A/I gttggagataaaacagtgcc	966
ABCC4	132	intron 22 + 1026	gtgcctactccagctaaaa A/C tcttctgtagctcaactgag	967
ABCC4	133	intron 23 + 377	gcctgtgcatgaggttgag A/G aaaattctcagcaggagagt	968
ABCC4	134	intron 25 + 4122	cccttttgattaaattgca C/G/I tgggacaagaaccaccoccca	969
ABCC4	135	intron 25 + 6418	ttgcactgaggtaatgctg C/A agaaattaaagtggaggtat	970
ABCC4	136	intron 25 + (8765-8776)	tgcactcgtgattttttc (I) 5-11 aatcctgcgctggatctc	971
ABCC4	137	intron 26 + 67	tatgtttaattgtttttact G/C ttatigctttttttaattgg	972
ABCC4	138	intron 26 + (101-109)	taattggatgaaggattgt (I) 8-9 caaccaatagagcatgttt	973
ABCC4	139	intron 28 + 391	tagatatgactttttttt I/ Δ aaatctctatgttgagtag	974
ABCC4	140	intron 29 + 2569	atctcttttttotaacg C/I accactatctccacattaa	975
ABCC4	141	intron 29 + 7820	gaaaacaacctgtctctg C/I ttggaggcttcagcatattct	976
ABCC4	142	intron 30 + 6269	tagatgttctttggcattg A/G aaagatgggttatctgttt	977
ABCC4	143	intron 30 + 6320	gttaataagggttaattag C/I tctactttgttaattacatt	978
ABCC4	144	intron 30 + 6474	ctttgatctatggttttca A/G tccacagatgttcataactt	979
ABCC4	145	intron 30 + 6519	ttccactatgaattatattt C/I ctgccattttaacacacctt	980
ABCC4	146	intron 30 + 6574	aatggtttggctctaaatc C/I acaciggttcaaaactagac	981
ABCC4	147	intron 30 + 6680	agggtgtctcctgtatag A/G cgtggttaggttttaactctg	982
ABCC4	148	intron 30 - 704	acgtttatcagaaaacctgt A/C tctcttctagttcagctaga	983
ABCC4	149	intron 30 - 228	atctatgaatcagagtgatc A/G gaactaaatggatctacag	984
ABCC4	150	intron 30 - (14-5)	acattcttttaigtctacc (I) 9-10 ctagtatacttcaaaagaa	985
ABCC4	151	exon 31 + 146	agtcggttcogaaggcaattt G/I ccactagtttttggactatg	986
ABCC4	152	3' flanking + 173	atttttaaggagtaggaca A/G agttgtcacagggttttgg	987
ABCC4	153	3' flanking + (430-440)	tgtaccccttactcccatc (A) 10-11 tggatacatggttaaaggat	988
ABCC4	154	3' flanking + 556	aaagggtcttgatactgaa G/A gacacaaatgtgacctcca	989
ABCC4	155	3' flanking + 1144	cttccctgaatgtcatata I/C gtatatagacatgcacacgt	990
ABCC4	156	3' flanking + 1426	tttagtgactgaatgca A/I cagtatcataatgagggtt	991
ABCC5	1	intron 1 + 628	ttctgcccacacagacogcg G/C gtggctttgtgtttatcaca	992
ABCC5	2	intron 1 + 1834	tgagttccagtgacctctc C/I gtttcaaaactgtcacccgc	993
ABCC5	3	intron 1 + 3055	agaaagcttttaaaaaaa A/ Δ ccaacctttctattgtatc	994
ABCC5	4	intron 2 - 20280	gaatgactcgtactaagta I/C ttttgaagtgcagacacca	995
ABCC5	5	intron 2 - 20260	tttttgaagttcagacacc A/I tctagaatctgtctgaccgt	996
ABCC5	6	intron 2 - 19204	tgaataaaagcattcgcaca C/I ctacccactttcttctgggac	997
ABCC5	7	intron 2 - 19043	ttggctggcatttagctggc G/A ttacttcagctaacatgaag	998
ABCC5	8	intron 2 - 18824	ttgaacactttcaagatgc A/G tgcacagcacigaacagagt	999
ABCC5	9	intron 2 - 18807	tgcatacacagcacigaacc G/A agtggcttggtgcagataaa	1000

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ABCC5	10	Intron 2 - (18735-18734)	atagaagcttaactacaa (A) cagctactctacatagatga	1001
ABCC5	10	Intron 2 - (18735-18734)	atagaagcttaactacaa cagctactctacatagatga	1002
ABCC5	11	Intron 2 - 15903	taccaaagcctgctcatgga G/A gtgaaagcaagactgacat	1003
ABCC5	12	Intron 2 - 15901	ccaaagcctgctcatgagg C/I agaaagcaagactgacatgt	1004
ABCC5	13	Intron 2 - 15847	tggatgaacctcaaggcc G/A tctggccagctcccattta	1005
ABCC5	14	Intron 2 - 15605	aggagagccacgacactga C/I agctgtacctgacctgagag	1006
ABCC5	15	Intron 2 - 13571	cagattgtgcccagatacc G/A ctttatttgagggtgtgcc	1007
ABCC5	16	Intron 2 - 13402	taccctgctgttgcggcc G/I ccaggaaagggattggattgt	1008
ABCC5	17	Intron 2 - 13325	ccagaggccctgcgcagg G/C gaaaagcccttggttgcctt	1009
ABCC5	18	Intron 2 - 7293	ttgttaggataaaattgca C/I ttagtgcctgtcttaaacca	1010
ABCC5	19	Intron 5 + 374	ccgggctgtgagccagcac C/I gggaaacataccaagtgcctg	1011
ABCC5	20	Intron 5 + (2212-2213)	cgctcctgcagctctct C/I Δ tggtaatgctaactcigt	1012
ABCC5	21	Intron 5 + 3283	accagagagagctcgggt C/I tggaaatcagctagctacc	1013
ABCC5	22	Intron 5 + 3469	tggcttcttttctgtg C/I ttttcttttttttttttga	1014
ABCC5	23	Intron 7 + 443	caotttattaaagacgta C/I gattacataaacatttggccc	1015
ABCC5	24	Intron 7 + 458	cagtaagattacataacatt I/G ggccatcctagcaagcagg	1016
ABCC5	25	Intron 9 + 176	caaaaacaaacaaacaa A/G acaaaaaaaataccacat	1017
ABCC5	26	Intron 9 + 214	catatggagatgactgtg G/I tctctccttacttggacctg	1018
ABCC5	27	Intron 10 + 703	tgtggctggaattccttga I/C gtggccactgcataagattag	1019
ABCC5	28	Intron 10 + 3580	catgggctggagctgtgaa A/G accagttaggtacttggcatgt	1020
ABCC5	29	Intron 10 + 3655	atccttgaataactcttta G/A gggagagaaatgatgaaat	1021
ABCC5	30	Intron 10 + 3854	gaagtttagaatcatgacac I/C tggggaagataggtacagg	1022
ABCC5	31	Intron 10 + 5040	ctttgaagcatgagagttt C/I ttggcaagaagatgttctct	1023
ABCC5	32	Intron 10 + 5316	cagttaatgtcattaggtc C/I gotttaggtgtgtgagggg	1024
ABCC5	33	Intron 12 + 234	tgactgtgtcccagctgga G/A ccatttggctcactgccttc	1025
ABCC5	34	Intron 12 + 300	tggcacagggtatcccggt A/G ttgaaaatgtcagagataag	1026
ABCC5	35	Intron 12 + 318	gtattgaaaatgtcagagat A/G agagatgagcagacacccta	1027
ABCC5	36	Intron 12 + 1545	gtagcatccctaaccaca C/I aaatgtctactatcagtccc	1028
ABCC5	37	Intron 13 + 20	ggcaaggaatgttttgctt C/G gtcatgctttccatcttggc	1029
ABCC5	38	Intron 14 + 278	ttctatccagatattttta A/G actacaagtaagcgttgca	1030
ABCC5	39	Intron 16 + 1663	tgactggagacttttttt I/ Δ aaatattatagatcaattc	1031
ABCC5	40	Intron 16 + 1664	gactggagaactttttttt A/I aaatattatagatcaattca	1032
ABCC5	41	Intron 17 + 20	ggtaatggccttttttgaaa I/G ttttagatttgcatacaag	1033
ABCC5	42	Intron 18 + 232	ggcacactgagcgtatctg C/I tctcatccgttgtgtattag	1034
ABCC5	43	Intron 19 + 249	ggaccagtaggaacagagcc G/A tccctggccctgaccactc	1035
ABCC5	44	Intron 20 + 846	ttaccagagaagaaaaaggc G/A gtgggtggggagagaccca	1036
ABCC5	45	Intron 20 + 1154	tcttgagacgaaaaaaaaa A/ Δ tcagagcatccaggtttcta	1037
ABCC5	46	Intron 22 + (1424-1425)	gaggaatgcaggggaatat (AT) caactctggttttaacaggg	1038
ABCC5	46	Intron 22 + (1424-1425)	gaggaatgcaggggaatat caactctggttttaacaggg	1039
ABCC5	47	Intron 24 + 132	atcccacagaattctccagca A/G tctctcaaccgtgtctggaa	1040

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ABCC5	48	intron 24 - 874	gtctgagagagtaggatt A/G cagtcagtggtggtacaaag	1041
ABCC5	49	intron 24 - 630	tgatataaaattacocaa G/A cagttatatacacagcatttt	1042
ABCC5	50	intron 24 - 102	acagggtggcagctacotct G/C tgggtactatggtgtgco	1043
ABCC5	51	exon 25 + 120	taccgagaaaacctccctct C/T gicctaaagaagaatcctt	1044
ABCC5	52	intron 26 + 263	ctgggcccagggtctgctc C/T gtagcttcggacaagtatt	1045
ABCC5	53	intron 26 - 3257	ccagggtgaattgctgtgt I/C gttcacactttggagagata	1046
ABCC5	54	intron 27 + 873	gtttttccctcgtctctatc G/A ggaattcttcatttgaaga	1047
ABCC5	55	intron 29 + (2733-2734)	gtgtccaaagaagaagacacg (TGCCAAAGGAAGACACG) cttatgtttctcttctgtggcc	1048
ABCC5	55	intron 29 + (2733-2734)	gtgtccaaagaagaagacacg cttatgtttctcttctgtggcc	1049
ABCC5	56	intron 29 + 2959	acatgattttccacggctac A/G tagaagtccatccatagaat	1050
ABCC5	57	intron 29 + 4020	aataaaaaataaaggggga G/A gtcacagcagggtagtga	1051
ABCC5	58	exon 30 + 684	ccctctgccgcctcccccac G/A gcgcctccagggtggctgg	1052
ABCC5	59	exon 30 + 947	agctatccacagagagctcc C/T actgcctcagggttcctatgg	1053
ABCC5	60	exon 30 + (1145-1160)	tcacgcagtcgtcgacag (TC) 6-8 cctccaaagtctgcaacttt	1054
ABCC5	61	3' flanking + 4	attattttgattttgttaa A/C ctcttgtgtatcaacaat	1055
ABCC5	62	3' flanking + 2008	cccgacagctggcagacc C/Δ tgtttcaaaaggaggactcc	1056
ABCC5	63	3' flanking + 2052	cccgctaggacagccacc A/G ccaggcagtttaggaccgtgg	1057
ABCC7	1	5' flanking - 834	gctaaacactccaaagct I/G ccttaaaaatgcgcactggg	1058
ABCC7	2	5' flanking - 729	cctcttgcagattttttt I/Δ ctctttcagtaagtgctcta	1059
ABCC7	3	exon 1 + 125	tagcaggagccccagccccc G/C agagaccatgcagggtcgc	1060
ABCC7	4	intron 1 + 6200	ctatgtgagacgtiaaag G/A tagagggtggccaagaaggaa	1061
ABCC7	5	intron 1 + 7538	agttcttttcttagctagg C/A ctacagaggtgcaactacct	1062
ABCC7	6	intron 1 + 13519	gaacttaaatcttgagtc A/C acaatttggtctacatactg	1063
ABCC7	7	intron 1 + 14110	attacacagattttttttt I/Δ aattttggggaaagtogatt	1064
ABCC7	8	intron 1 + 14293	gccaggcagatttcctgactc C/Δ tataaccagagcattacag	1065
ABCC7	9	intron 1 + 14316	taaccagagcttatcagag C/G atttatgccccaaagagaa	1066
ABCC7	10	intron 1 + 14433	cagaataacaatgatggctc G/A gaaaaatatgggtatttctg	1067
ABCC7	11	intron 1 + 14824	acgttttgacagttgacaaa G/C ttctttctttaagctttaa	1068
ABCC7	12	intron 1 + 23401	aataattttgaaatacacta C/G ggtatcctgcatagtatgtt	1069
ABCC7	13	intron 3 + 879	gaaaaatttcagtticacata C/A ccccatgaaaaatacattta	1070
ABCC7	14	intron 3 + 922	acttatcttaacaagatga G/C tacacttaggcccagaatgt	1071
ABCC7	15	intron 3 + 933	caagatgagtacacttagg C/T ccagaatgttctctaaigtct	1072
ABCC7	16	intron 3 + 13704	tttttccaaaataaaaaaaa A/Δ tcagggtatctcgtaaatg	1073
ABCC7	17	intron 3 + 13758	tattaaagaacatgactgtt A/G aaacagattagggaataa	1074
ABCC7	18	intron 4 + 240	ctctgtttagttttttttt I/Δ ctctaatcatgtttatcatt	1075
ABCC7	19	intron 4 + 376	ttatgttcaagaagaagagt A/G taatatatgattgttaatga	1076
ABCC7	20	intron 4 + 586	tgtccagacagagagaccaaa I/C tgcgaggcatcatttaggt	1077
ABCC7	21	intron 4 + 1089	tttcaatctgaacattttac G/A taagtgaagactttgttga	1078
ABCC7	22	intron 4 + 1615	aaagttagggtgtattgtat C/I tgccttcttcttcaatggt	1079
ABCC7	23	intron 4 + 1946	aatacaacaacaacttgagct I/C tgcotatacttttcaagaat	1080

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ABCC7	24	intron 6 + 783	tatctaagttttgagagctaa A/G tagcacctttgttgaatccc	1081
ABCC7	25	intron 6 + (1104-1131)	gattgattgattgatt (GAT)6-7 tacagagatcagagagctgg	1082
ABCC7	26	intron 7 + (731-732)	gtagcaatgagacattttt (T) cttcagttgagctccatgtt	1083
ABCC7	26	intron 7 + (731-732)	gtagcaatgagacattttt cttcagttgagctccatgtt	1084
ABCC7	27	intron 7 + 1434	gaaagtgtgtgttaacctg I/C ataatctggcagaaatgtt	1085
ABCC7	28	intron 8 + 752	catgctctcttcagctccc A/G ttcttcattatatacacta	1086
ABCC7	29	intron 8 + 1109	tatggcaagacttcagtat G/A cgtgacttaattcttcott	1087
ABCC7	30	intron 8 + 1312	atgaagacattcattttttt I/ Δ ctccgtccaattgttgatta	1088
ABCC7	31	intron 9 + (6521-6522)	gtgtgtgtgtgtgtgtgt (GT) ttttttaacagggatttggg	1089
ABCC7	31	intron 9 + (6521-6522)	gtgtgtgtgtgtgtgtgt ttttttaacagggatttggg	1090
ABCC7	32	intron 10 + 2119	gaacactttatagttttttt I/G ggacaaaagatctagctaaa	1091
ABCC7	33	intron 11 + 3867	ttttcttcaagaatttaga A/ Δ gagggagaaaattgttttaa	1092
ABCC7	34	intron 11 + 11844	tgaatacaaatcatctaaaa A/ Δ gcittcagaaaccagacttt	1093
ABCC7	35	intron 11 + 12144	atattaacagagttacata I/C acttaacacttcatacat	1094
ABCC7	36	intron 11 + 20975	gtgtgtagtaaatgccag G/A gtaaatcacatagcatctaa	1095
ABCC7	37	intron 11 + 27057	atggaagagagtttttagta G/A agggaggaaggaggaggtg	1096
ABCC7	38	intron 11 + 27131	gagagagactttttttttt I/ Δ aaggcgaggtttactacot	1097
ABCC7	39	intron 13 + 152	gtattactcaaatctgctgc I/A gccctactggccaggaic	1098
ABCC7	40	intron 13 + 287	tttcagatcatctgccttg I/C gatataattactttaatta	1099
ABCC7	41	intron 15 + (85-86)	atcacatataatgcacac A/ Δ aaatatgtatataacacat	1100
ABCC7	42	intron 15 + 106	taaatagtatataacaca I/A gtatacatgtataagtatgc	1101
ABCC7	43	intron 15 + 3341	ggaggtataaatgttaaat A/C actgagaccocaaacttaca	1102
ABCC7	44	intron 15 + 5556	tgcatttgactaatagtaat A/T attttaggcagctttatga	1103
ABCC7	45	intron 15 + 5919	tgttagtctatgtggaac C/A gtgaggaataattttatat	1104
ABCC7	46	intron 17 + 2479	caaaaaggtatggaagtcag A/C ggagaaggagagaccctatgt	1105
ABCC7	47	intron 18 - 81	aagtatgcaaaaaaataaaa A/ Δ gaaataaatcacigacacac	1106
ABCC7	48	intron 19 + 751	cattaataaataacaaatc A/G tatctattcaagaagaatggca	1107
ABCC7	49	intron 19 + 820	tgacatttgtatagatta I/C tctaatttagctcttttcag	1108
ABCC7	50	intron 21 + 1532	ttacctttaactttttttt I/ Δ agtttgaatcagctctcttta	1109
ABCC7	51	intron 21 + 1607	atgcttttgagttgggtct C/T ataaatgtatagaaaatgtt	1110
ABCC7	52	intron 21 + 11260	atgtggaacaatcagacta I/C atgcttttactttctctat	1111
ABCC7	53	intron 22 + (130-131)	agatacaatataaacacac A/ Δ gttttattatataggagtoat	1112
ABCC7	54	intron 23 + 1837	ctgtcctaaagttttaaaaag A/ Δ aaaaaaagggaaggaa	1113
ABCC7	55	intron 24 + (7100-7112)	cttttaaacactcttagaca (T)12-14 agtttaacatgttacaaaac	1114
ABCC7	56	intron 25 + 237	actcttccccctgtcaaca C/T atgatgaagcttttaaatac	1115
ABCC7	57	exon 27 + 115	ggatgaagctcttcccccac C/T ggaactcaagcaagtgcag	1116
ABCC7	58	exon 27 + 334	ggatgaatgaagttttttt I/ Δ aaaaaaagaacatttggtaa	1117
ABCC8	1	5' flanking - 1099	aaggggctgaagggtctt I/C cttttgttccctgactg	1118
ABCC8	2	5' flanking - (424-422)	cacccaccaccaccaccac CAC/ Δ aaggtaacgtctgccccac	1119
ABCC8	3	intron 1 + 1212	agcctgggcaacatagtag A/G cccccccgcccctttctaca	1120

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ABCC8	4	intron 2 + 1003	aggagactgtgaatccacg C/A ctgcatgtttggctggatt	1121
ABCC8	5	intron 2 + 1253	catctactaaggaagaatc C/I agtaaccacgaagatgaga	1122
ABCC8	6	intron 2 + 1382	ccagacgtgacitctgcag I/C gctgctgctctctgtt	1123
ABCC8	7	intron 2 + 2371	tttcagagctgtctggaat I/A tagggggcagggtgggaggg	1124
ABCC8	8	intron 3 + 1957	ccctacccttagccagggg C/I cccacatgagtatgaatgg	1125
ABCC8	9	intron 3 + (2088-2089)	agagaaaccttattaacca (CCA) gggcgtggcgtaccagtctc	1126
ABCC8	9	intron 3 + (2088-2089)	agagaaaccttattaacca gggcgtggcgtaccagtctc	1127
ABCC8	10	intron 3 + 2204	taagcacacagttatcaccc G/A tggatggattgtcttttc	1128
ABCC8	11	intron 3 + 2286	ttatctcccttgaaggac A/G ctccacagagccagaattc	1129
ABCC8	12	intron 3 + 2312	cagagccagaaattctagaa C/G agggaaaaagtgaggaggagg	1130
ABCC8	13	intron 3 + 2356	ctgtgaactcagggacaga A/G ggaatgggtattggsgaaa	1131
ABCC8	14	intron 3 + 2359	tgaactcagggacagaagg A/C aatgggtattggsgagaatgg	1132
ABCC8	15	intron 3 + 2370	gacagaaggaaatgggtatt G/A ggaagaatggccagccctcca	1133
ABCC8	16	intron 3 + 2382	tgggtattggagaatggcc A/G gccctccaggggctgatgt	1134
ABCC8	17	intron 3 + 4910	gggacagccttcagctgtg G/A aattcctcagctcttagaga	1135
ABCC8	18	intron 3 + 4969	cattattccagctcagggc A/G tgagacagaagcccgatgc	1136
ABCC8	19	intron 3 + 5003	cgaatgcttctgcctccat C/G ctaatgtcctctgcagggga	1137
ABCC8	20	intron 3 + 5019	ccatcctaattgtcctctgc A/C gggacccaaggttgatggca	1138
ABCC8	21	intron 4 + 14	ggtgagggtaagcaggccac C/I tggggcagggtgggtggga	1139
ABCC8	22	intron 4 + 187	agacactgcctctggccac G/A tgtgctctacccagggtcc	1140
ABCC8	23	intron 4 + 204	cacgtgtgctctacccagg G/C tccagaggaggaggggggt	1141
ABCC8	24	intron 4 + 254	gttcgtgaggttgccgat G/A acttccgtagaagggaag	1142
ABCC8	25	intron 4 + 357	tgtattcattatcgtcacgt G/C gtaaatgaatgagttaagtgt	1143
ABCC8	26	intron 5 + 92	ggcattaggtcaaaatctctg G/A tgggacaaaaggsgaaaactg	1144
ABCC8	27	intron 6 + 4205	tcgtgaaaagtacatgggg G/A catgaagatcatiggcttga	1145
ABCC8	28	intron 6 + 5519	gattccagggaatgtttaa A/C aggacgggtcttctcctaac	1146
ABCC8	29	intron 6 + 5575	tctgaccagttaccagccag G/C ggggcaagtcttccatcccc	1147
ABCC8	30	intron 6 + 6587	gttgccatctgagatcttgc C/I ggaagtacacaaagagaccct	1148
ABCC8	31	intron 6 + 6747	ttccactggcctttctgct C/I agtaattgtctacattacagg	1149
ABCC8	32	intron 9 + 191	gaggaagctgctccgggtg A/G ggacaggaagcgggcattggc	1150
ABCC8	33	intron 10 + 1963	cccaggagtcacacctcct I/G tgtccagctagaccatgggtg	1151
ABCC8	34	intron 10 + 2724	cctgggacatgttttcttat A/G taacacagcatcaaaaagtgt	1152
ABCC8	35	intron 10 + 2938	ccgcgccagcactcctcac G/C tgtccaagtccactaggag	1153
ABCC8	36	intron 10 + 3094	tccgaggagtggttttttt I/ Δ ccttcgtttagtcagcagt	1154
ABCC8	37	intron 10 + 3368	tcctgtcatatggggcacc A/G tcagactcttggggcagcga	1155
ABCC8	38	intron 10 + 8897	ggatttgattaaaagcctca C/I gggcagagaaattogccatc	1156
ABCC8	39	intron 11 + 308	tgtgtattgtagaagtgatg G/A gaaatccagacaagaagct	1157
ABCC8	40	intron 11 + 1171	ggcctctcatttcccttcca G/A tgcgtgagcgtttccagttg	1158
ABCC8	41	exon 12 + 7	ggctctgtccacagacttcc G/A tggggcagctcagcttcttc	1159
ABCC8	42	intron 12 + 356	accaagaatgaggccatccc G/I tccccacgtggctgccccat	1160

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ABCC8	43	intron 12 + 934	tgggttcaaatggaatgg G/I gcaataactcagcaaaattat	1161
ABCC8	44	intron 12 + 1370	ggagaggagctggacagg C/G atgaaggcagagcctggtgg	1162
ABCC8	45	intron 15 + 412	ggaggaggaccaggatgg C/I gttcttgggaocacaagga	1163
ABCC8	46	intron 15 + 688	actcccccggccactcac A/G totgcacottccctccctg	1164
ABCC8	47	intron 16 + 4464	actcattccaagtattgat G/A agaagagaggtaggtactgg	1165
ABCC8	48	intron 16 + 4574	ttgaagatcttaagtgttt I/C tggttcacatttcgcaaa	1166
ABCC8	49	intron 16 + 5011	agctaaagcaaaacagcct C/I tgacctggcaagcattccca	1167
ABCC8	50	intron 16 + 7608	tgctcctactttcttttgac C/G cttataacttcctgaactcg	1168
ABCC8	51	intron 16 + 7730	ccagctcctactagtggtctgga G/A ggaaggacatgggttgggg	1169
ABCC8	52	intron 16 + 8369	ttgcaaaactgagttaggccc I/C ggagagcttacttgigtg	1170
ABCC8	53	intron 16 + 9708	tgaccttggccctacttat I/G ccagaccacatgattgggtc	1171
ABCC8	54	intron 17 + 651	tatagattaaatgaggctcig A/G gtccctcaaaaacctccctc	1172
ABCC8	55	intron 17 + 692	cccttacctctccaaaaa A/G cttgagataaccttagaggtg	1173
ABCC8	56	intron 17 + 1541	ctcaggatctctcaggag C/I atggttacctcccatgagag	1174
ABCC8	57	intron 18 + 580	actaagcagatttctacaa C/I tgcacotccccatccccctg	1175
ABCC8	58	intron 18 + 658	gaacaagccctgagaaatgc C/I ttccgcacccctactcccg	1176
ABCC8	59	intron 18 + 660	acaagccctgagaaatgcct I/C ccgcacccctactcccgcc	1177
ABCC8	60	intron 19 + 93	gcocttcacatgatcccca I/C acccagccatctcactcccc	1178
ABCC8	61	intron 19 + 123	tctcactccccagggtgctta I/C ctgcactccagctctccat	1179
ABCC8	62	intron 19 + 219	cataggggagaggccaggaa C/I ggagggaaggagagagccc	1180
ABCC8	63	intron 19 + 845	tagtatitaaactgcccaaa C/I gctgtgtaagtgcigacct	1181
ABCC8	64	intron 20 + 338	ttccctccacaagcttagac A/G aacaggattctcctgact	1182
ABCC8	65	exon 21 + 10	tttggtagcagggcataaac C/I tgcctgggtcaacgccag	1183
ABCC8	66	intron 21 + 192	caaggatagcacaatgacc C/Δ attgcaagcttcagatggag	1184
ABCC8	67	intron 23 + 17	gaaggtaggtatccagg A/G tggccaagcagccaccctg	1185
ABCC8	68	intron 23 + 67	gtctgttagaacctgaact C/I ataaagcttctcctgtcctt	1186
ABCC8	69	intron 26 + 268	gtgaggtctgcacatccaa G/C taaagattgttttctcctcc	1187
ABCC8	70	intron 26 + 308	cgataagtgggttaattg C/I ccatcccccaccatgattc	1188
ABCC8	71	intron 26 + 348	cagctccctgcccctccctc A/G ctctctcctccagccagc	1189
ABCC8	72	intron 26 + 807	gacagctgtgagtcaggcc G/A agccggcagctgagaaaggc	1190
ABCC8	73	intron 26 + 834	cagctgagaaaggccagct G/C gtcagatgggttgagaaac	1191
ABCC8	74	intron 28 + (118-121)	ctcccaaaaataaaaaaaa AAA/Δ cagaaatgaaggaaatagaa	1192
ABCC8	75	intron 28 + 1348	tgggtaagcggagagacagg G/A ttgaacgtttgatttgggt	1193
ABCC8	76	intron 29 + 1253	ctcttagggatcttgcttaa G/I taaagaagcagagacaaag	1194
ABCC8	77	intron 29 + 1589	cagatcccgagcttctgttaa A/G cagcctcagatcaggccaaa	1195
ABCC8	78	intron 29 + 2322	gcgcctcacactctctataac G/A cgcacatgccctgatgcaca	1196
ABCC8	79	intron 29 + 2348	atgccttgatgcacacacat I/C ttcaacagcacttactcta	1197
ABCC8	80	intron 29 + 2418	agacacgtcacctcccca C/I gtctccacctgggggtgtg	1198
ABCC8	81	intron 29 + 2494	tcagtcctccctcagacacatg C/A cctctctccacgcagacaca	1199
ABCC8	82	intron 29 + 2735	gcggcccaaggagatgatga C/I ggcagccagggttatcaga	1200

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ABCC8	83	intron 30 + 386	gctcctggggctccagcctt C/I gcagcccttggtgtgtctcg	1201
ABCC8	84	intron 33 + 93	ggcttcagctcaactcgtg G/I cctccagggccgagccctc	1202
ABCC8	85	intron 33 + 358	agggaactggggcagacag C/I gaggccaccccttgattgag	1203
ABCC8	86	intron 38 + 54	cccaggacaggacggcct G/C tiggcgcgtcatcagtgca	1204
ABCC8	87	intron 38 + 466	aggacattctggccacatgc C/Δ tcatcctcctcctccaagcc	1205
ABCC8	88	intron 38 + 529	tggcccccacccgggtgggt A/G ttcccaccatcctgaccgcg	1206
ABCC9	1	intron 3 + 38	tggtttctccttaagag C/A tatttgttttccccccaaa	1207
ABCC9	2	intron 3 + 305	gctggccttctgcttcag I/A agttgatatttaagaatcag	1208
ABCC9	3	intron 3 + 320	tgcagagttgtattttaag A/G atcagagctctgigaggag	1209
ABCC9	4	intron 3 + 631	ttctgtggaaatcagaggct G/C totaaaatttcoataattt	1210
ABCC9	5	intron 3 + 8644	tggacgcactcaacattttc A/G agttattactcctcaactc	1211
ABCC9	6	intron 4 + 757	aggatatacatgaacactga A/C tottagtaaaaactatcttt	1212
ABCC9	7	intron 4 + 1022	tactgtggaatttttcttgc A/C acagagatatgtattttica	1213
ABCC9	8	intron 5 - 1217	cagtgttagatgtgtttct A/G ttgccaatcatctacaatat	1214
ABCC9	9	intron 6 + (100-106)	tatgagttgtcaaataggg (I) 8-9 cagagaattgaatgctttct	1215
ABCC9	10	intron 6 + 1347	tcagtgatattcctactaaa A/Δ caaaatttggtaagtatgt	1216
ABCC9	11	intron 6 + 1618	cttttatttgcgtcttacc G/A ttttactaaggttggatata	1217
ABCC9	12	intron 6 + 1835	cttttaataatgcaaacig C/I acacctggctataaaaaga	1218
ABCC9	13	intron 7 + 407	ccatagaatttttcttttc I/G tttttotcaaaaaaattaaa	1219
ABCC9	14	intron 7 + 423	tttctttttotcaaaaaa C/I taaatgtttgtatttttt	1220
ABCC9	15	intron 8 + 743	ttctgtagaatgaagcttaag A/I gctagatctatttgaaaaa	1221
ABCC9	16	intron 8 + 850	tttttaacttattgtttgoc I/G ttctatttttttaatagaana	1222
ABCC9	17	intron 9 + 585	cgaatttgcgtcttttagag A/I aatctttgcaaaaataaaaa	1223
ABCC9	18	intron 9 + 1394	attttttotgttaagtat G/C agtgatagagctgacigcag	1224
ABCC9	19	intron 12 + 1167	atttgaagacttttaaat G/A agataattgtgcgggtct	1225
ABCC9	20	intron 12 + 1195	tgtgcgggtgtctatatctt A/G ctagaanaactagaatttat	1226
ABCC9	21	intron 12 + 2123	ataagtgctctccagtggt G/A attggacttagagcatttc	1227
ABCC9	22	intron 12 + (2653-2656)	caaacagaaataatgaaag TAAC/Δ tattatctaaaaataaaaa	1228
ABCC9	23	intron 13 + (3043-3044)	aacatactctcctctctct (C)C(II) aagtcocaaatatattagtat	1229
ABCC9	23	intron 13 + (3043-3044)	aacatactctcctctctct (C)I aagtcocaaatatattagtat	1230
ABCC9	23	intron 13 + (3043-3044)	aacatactctcctctctct aagtcocaaatatattagtat	1231
ABCC9	24	intron 14 + 85	ttctgtgaaaagtgcccaaa I/A tgtgcctttaaatgttttt	1232
ABCC9	25	intron 14 + 275	agtgccacatgtatttttc I/C ggtattcctatgtttatcaa	1233
ABCC9	26	intron 14 + 453	ctaatttcaaaccttgctat I/C tggactctcccagcattg	1234
ABCC9	27	intron 14 + 3709	atcccctagtgatgatact G/A agoitgccctccatcttctct	1235
ABCC9	28	intron 14 + 3813	ctgaatttatattagctga C/I ttccaagtctcagacatcta	1236
ABCC9	29	intron 14 + 4000	ttcttttactcaatgtagc A/Δ ccaaatcagaagggtacatt	1237
ABCC9	30	intron 16 + 1466	atccacatgrratttaataac A/C tigtgtagcttgtaacca	1238
ABCC9	31	intron 16 + 5357	attttggaagagaattata I/G aaccttccacacactgaattt	1239
ABCC9	32	intron 17 + 1368	aatcctggtgttttttttt I/Δ ctttttcaatttttcagtagg	1240

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ABCC9	33	intron 20 + 98	aagtaactcaagaagaatg G/A ttaacttggtaaatcgtaa	1241
ABCC9	34	intron 22 + 28	ctcatagtcagagagttc A/C gagcccaattcagaagagtt	1242
ABCC9	35	intron 22 + 194	tgaaactataaaattctaat G/ Δ ccattcttggatgaggtgca	1243
ABCC9	36	intron 22 + 1370	ccaggcaaaaaagaaga G/ Δ gtaaacitaaagattgggac	1244
ABCC9	37	intron 22 + 1487	agcaagccaggaagaagtc C/G attaagtgtattagaat	1245
ABCC9	38	intron 23 + (455-462)	atagccatgaagataagaa AATAGAA/ Δ tgccattgttaigtctcag	1246
ABCC9	39	intron 24 + (460-465)	aaacttctctctcctgc TTAAAA/TTTTAA gcaagccttgaaggagagtg	1247
ABCC9	40	intron 24 + 595	gcatgaaaaataatgaagaa A/G acaatttctgacattga	1248
ABCC9	41	intron 28 - 926	aaatattcagaatttgggg G/A ttagagcatttggcgtcat	1249
ABCC9	42	intron 29 + 2692	cttgaagtctttttttt I/ Δ aaagtaatgaaaatttctaa	1250
ABCC9	43	intron 29 + 5464	agacaacactgctttttgt G/A tgticacaattcaacgacag	1251
ABCC9	44	intron 29 - 1830	aaatggctgaaagaaaaa A/I tcaattgtgttaaatattt	1252
ABCC9	45	intron 31 + 102	tgctttgtcttccactta G/A tatccagaataactctctcat	1253
ABCC9	46	intron 33 + 877	aaatgaactatagtaaat A/G tagtttttttgggttcaga	1254
ABCC9	47	intron 36 + 1281	aaattacacttttttttt I/ Δ gcaggagaatttttgcaga	1255
ABCC9	48	3' flanking + 197	aatggagctcagcatgtgt I/G ticaaatatatacatgcaaa	1256
ABCD1	1	(5' flanking region -1772)	agtcaccaggctaggcaca G/A gcacctctctgctaactcg	1257
ABCD1	2	(5' untranslated region -59)	acaatctctcagccactg C/I ctoaatgtgtccccaggca	1258
ABCD1	3	(intron 1 906)	gggcacaaatggcatccatcc C/I cgaaggcctgtgtgtctc	1259
ABCD1	4	(intron 1 2924)	gagacctggccccccaat C/I gtaacctctggctctcggcc	1260
ABCD1	5	(intron 1 3056)	aagcctctgtgtgtgtgca C/I cccccaggtggagctggc	1261
ABCD1	6	(intron 2 2972)	agaagtctccctgtcttcc G/A tcaagttgtgtctgtctga	1262
ABCD1	7	(intron 2 3258)	ggcagaagaccctgcagcc G/A ctgcctccatgtgtgcat	1263
ABCD1	8	(intron 2 4612)	ggctctcacaggacattcc C/I accacttcagccacacocca	1264
ABCD1	9	(intron 5 2748)	aatggcctgcgtgtggcct C/I gggcattgggagcctcicaa	1265
ABCD1	10	(intron 6 212)	atctgtgtgggtgtgtgca C/I gggcggcgatgtgagcgtgt	1266
ABCD1	11	(intron 5 2835)	ggcgtcagcggctgtgtgcc C/ Δ tgcagttggaggaagcagtg	1267
ABCD3	1	(5' flanking region -2834)	acatcccttttctgctggc A/G gattgaactttttagtica	1268
ABCD3	2	(5' flanking region -2118)	tacagaatcacctttgtcaa G/A ccttaagccttttattgaag	1269
ABCD3	3	(5' untranslated region -40)	gtagccgcgcgcgcgcgc C/I gccgcgtccctcgcgcgt	1270
ABCD3	4	(intron 1 -6763)	atactttgccatttgagata I/C cagtttggagttgatagctg	1271
ABCD3	5	(intron 2 731)	ctttggaactatactagttt C/I cttaggcattgtgottagaa	1272
ABCD3	6	(intron 2 3551)	accacagtggtctttttt A/G tatttaaaaaaattatggg	1273
ABCD3	7	(intron 2 5936)	cagaactcacttctctattc A/G gtttttagataaacattgttt	1274
ABCD3	8	(intron 2 6083)	tggctctttaattttatgat A/G tgtttgttatagtatctta	1275
ABCD3	9	(intron 3 614)	tccttcttctggaagtatt A/I tttcatttttatttatgga	1276
ABCD3	10	(intron 3 651)	gtgaatctaggtgtagtc G/I atacagctacocctaaatggt	1277
ABCD3	11	(intron 4 395)	aaagcatttcaagaatacac G/A ttgagcatgtttattagaag	1278
ABCD3	12	(exon 7 555)	gacaacagaatagctaacc A/G gaccagctgcttacacaaga	1279
ABCD3	13	(intron 7 124)	aaatattaatgcttttata A/G gaaattagagttgttgtaa	1280

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ABCD3	14	(intron 7 838)	ggcacagttgacccagata /G acagtttgagacaaaagaa	1281
ABCD3	15	(intron 8 1150)	aacttgaataactactagc A/C catatattgtctagatagt	1282
ABCD3	16	(intron 9 1493)	tcatcttctccataggctt A/G ggtgaggagagagatagaa	1283
ABCD3	17	(intron 13 1534)	tctgttgagttggggatcct A/G tggaaacctcttctctcact	1284
ABCD3	18	(intron 16 4310)	gaaagtgaatgcagtagt G/I ttagccagcttgatttaga	1285
ABCD3	19	(intron 20 273)	ttctaaagtctcagagaac I/A ctgtagctcatattctcigg	1286
ABCD3	20	(intron 20 1664)	ctcaaaagaaaaaataaa A/C aaaaacacatgatccataa	1287
ABCD3	21	(intron 20 6693)	cttaagggttctgtttact C/I tgagcaattagtatttccca	1288
ABCD3	22	(intron 21 7171)	atcataaacagagaaataat A/G tottaaatgagctctgaaaa	1289
ABCD3	23	(intron 22 1220)	ctagaaatcaaaaggcattta A/G aatatagccaagcctttatg	1290
ABCD3	24	(intron 22 1358)	agtagcaaaataatcacc G/A ccagtgatcatgtgaaggag	1291
ABCD3	25	(intron 4 4448 4461)	taactttctgtagtttagcg (I)11-14 aactgttttaacttttaggg	1292
ABCD3	26	(intron 5 268)	gtttttggcattttttttt I/ Δ aaccttcagtcagggttttc	1293
ABCD3	27	(intron 5 891 902)	ttgtgttaaacacctgtagtg (I)10-13 acaaatgcaaatatagtg	1294
ABCD3	28	(intron 7 1226 1227)	ggcaatgggggtgatac (I)13-15 caggttcgatctgggctaa	1295
ABCD3	29	(intron 7 1226 1227)	ggcaatgggggtgatac (I)13-15 caggttcgatctgggctaa	1296
ABCD3	30	(intron 8 1129)	cagatttactttttttttt I/ Δ aacttgaatacttactagc	1297
ABCD3	31	(intron 13 1595 1596)	tgaacataataaagcacac (IA) gttatcataataactttatg	1298
ABCD3	32	(intron 13 1595 1596)	tgaacataataaagcacac gttatcataataactttatg	1299
ABCD3	33	(intron 16 7337 7351)	ttaattcttcacagactga (I)13-15 caggttcgatctgggctaa	1300
ABCD3	34	(intron 18 12)	gttctcaggttaagacctag C/ Δ ttgagttattttgtatctaa	1301
ABCD3	35	(intron 20 1652 1670)	ccaagactctctcctcaaaag (A)17-20 cacatgatccataatagagg	1302
ABCD3	36	(intron 20 2262 2273)	ttaatcattttttgaaatc (I)11-13 aacttaaatagcaactatc	1303
ABCD3	37	(3' untranslated region 2072 2079)	taaaataaagttagacttag (I)18-9 aaaaaaaacaaagcaaca	1304
ABCD3	38	(3' untranslated region 2080 2091)	gttgagcttagttttttttt (A)10-11 caaagcaacaataactag	1305
ABCD3	39	(3' untranslated region 3349 3368)	acttatttctctgctcagatt (A)16-19 ctcatatctctatataaac	1306
ABCD4	1	(intron 1 276)	tggcattctttttttgaaaa G/A aagaacctcaggtgcacaaa	1307
ABCD4	2	(intron 1 329)	cttctcagttcttgacaccc I/C gtggcccaatgcaaggctcc	1308
ABCD4	3	(intron 3 171)	ttaagcacgttgatcttgct A/G ttggccacgtgggactgat	1309
ABCD4	4	(intron 3 449)	octacccctcattcagtagg G/A gggctaccacctgctcactc	1310
ABCD4	5	(intron 5 273)	gacaggggctacctgagagg G/I acaaggagtcagggtgagg	1311
ABCD4	6	(intron 7 240)	tagtttagtgccctagcgt G/A gggcctgaaattgtcaaatg	1312
ABCD4	7	(intron 7 267)	gaaattgtcaaatgaaatgaa I/C gccatctctctgtcgttg	1313
ABCD4	8	(coding region 910 (Ala 304 Thr))	tctatggagacatgagctcc G/A cagagcttagcaccttggtc	1314
ABCD4	9	(coding region 981 (Leu 327 Leu))	atcagctcttccaccagct C/A atcgacctgtccacagcct	1315
ABCD4	10	(coding region 1102 (Glu 367 Lys))	gcgaatcctggcgagagc G/A agtgggcttggacacgtga	1316
ABCD4	11	(intron 13 191)	tggattggcccaactactca I/C agcagctcctgaggcaggta	1317
ABCD4	12	(intron 13 262)	acgcgtatgtcaaacaccca A/G ggtcggattctggggccct	1318
ABCD4	13	(intron 17 848)	ccctctctcctctggtcccat C/G cttctcctgaggcaggct	1319
ABCD4	14	(intron 17 946)	gtggagagagaagcagcggc G/A gcagaggcagggttttcat	1320

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ABCD4	15	(intron 18 41)	ggcctaggaggagaaagaa C/I ccaaggcicagcctggcca	1321
ABCD4	16	(3' untranslated region 2001)	ggccaggctcaggtttcgt G/A ggggacactgaatctccag	1322
ABCG1	1	(5' flanking region -386)	gcaataatcattggctagag C/A tatgtgatgatgatcatt	1323
ABCG1	2	(intron 1 199)	caccaaatattgttgagctg C/I ctggatttggagatgcagt	1324
ABCG1	3	(intron 1 291)	acttgggtccgtgtgagg A/C tctgcacitcggtttctgtg	1325
ABCG1	4	(intron 1 318)	actcggttctgtgagg I/A gtcaggaggagtcacagtt	1326
ABCG1	5	(intron 1 468)	ggcccaacgggtttctaga I/C cctccagagagcccttgg	1327
ABCG1	6	(intron 2 434)	ctgggtacaggttttctoc G/A gttgtctgcattatgatat	1328
ABCG1	7	(intron 3 1839)	ttaaaatgagttttttct C/G ctaaaacctttaggagattg	1329
ABCG1	8	(intron 3 3076)	tttgtcacttcctcctc C/I ggcctacttcctcctggggt	1330
ABCG1	9	(intron 3 3352)	gttccttggaggaaactgg G/A gtacacagtggttccagta	1331
ABCG1	10	(intron 3 8030)	acagtgaagcacaggcagc C/I gaagacacagcaggcaggtc	1332
ABCG1	11	(intron 3 8066)	aggtcaggtctgtgtgaca I/C tggcaggctgc a/g tgcagacc	1333
ABCG1	12	(intron 3 8092)	ggctgc a/g tgcagaccacct C/I gggccaggaggagagcaga	1334
ABCG1	13	(intron 3 8285)	ctgcacatgacitccctc C/I accacacctcacagaccaca	1335
ABCG1	14	(intron 3 8860)	cagggtgataggagttcaa I/C tggacacagattcagtttgc	1336
ABCG1	15	(intron 4 2319)	ggaggtgaacagaggagcaga G/A gcttggcattcttcaactcag	1337
ABCG1	16	(intron 4 2557)	gaagggaagaagcagcagca A/G gaaagaagccctcggccct	1338
ABCG1	17	(intron 5 139)	tgaaccagggcacctagag I/A ggcgcggctccgatcgt	1339
ABCG1	18	(intron 5 177)	gctgcctcctgcctccgcc A/C gggccacctggagcctcggg	1340
ABCG1	19	(intron 6 13)	cagttactgtaagtcgttt I/C ccagggtgtgtca g/a gaatct	1341
ABCG1	20	(intron 6 27)	gctgtt t/c ccagggtgtgtca G/A gaatcctccttctgtgttt	1342
ABCG1	21	(intron 6 1191)	gctaagcagagttaggccccc G/A gctagtcttgaatgagaga	1343
ABCG1	22	(intron 6 1449)	atgctggagccctcagtttc G/A gtaggcatacaagggttggc	1344
ABCG1	23	(intron 6 2282)	ctgcatacacagcagtttca C/I gatcctattatgggtltag	1345
ABCG1	24	(intron 6 3853)	cctgggttcagcaggggcc I/C cacacctgcaatgggtg c/t ct	1346
ABCG1	25	(intron 6 3871)	cc t/c cacacctgcaatgggtg C/I ctgggagagggtgcagatg	1347
ABCG1	26	(intron 6 4175)	tccaaagccagatttgg I/C ttttgggctcttttggat	1348
ABCG1	27	(intron 7 4)	ctgggtggaggagaaagta G/A ggaaggcggctgcttgggt	1349
ABCG1	28	(intron 7 576)	agctcaggaggtgtgtgaa C/I gccacacagtcaggagttt	1350
ABCG1	29	(intron 7 1426)	aattctccttcaacttaa A/G gaaataatttatagaaaaat	1351
ABCG1	30	(intron 7 2342)	agagccttcaatggggccc G/A agggacctgccatgacica	1352
ABCG1	31	(intron 7 2399)	gagggttgacagacagat A/G tgtcig c/g tgtgtccagctg	1353
ABCG1	32	(intron 7 2406)	tgcagacagat a/g tgtctg C/G tgtgtccagctgctgtgtt	1354
ABCG1	33	(intron 7 2911)	ccctctctgtgccactgtt G/C tcccaacacccagctgtct	1355
ABCG1	34	(intron 7 4363)	tataatagattcctagcaga A/G aacataattgtgagggaac	1356
ABCG1	35	(intron 7 4752)	gctttcagagccattaca C/I aagggtctatttattagg	1357
ABCG1	36	(intron 7 5026)	ccaggtctgtggatttcag G/A ccaaaaaggagcgttagcaag	1358
ABCG1	37	(intron 7 5532)	gggttaaatattccgggag C/I gccaaagtcagattatctgta	1359
ABCG1	38	(intron 7 5681)	gctaagtgcatggagagca I/C catgaataaatccttcagg	1360

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ABCG1	39	(intron 7 9243)	gcctgagagcgcggcagta G/A gaaggctgccagttggac	1361
ABCG1	40	(intron 7 11371)	ggcctctcttggagccctt I/G tctctccagccctgcgtct	1362
ABCG1	41	(intron 7 12420)	ggatttcgaatcacaac I/C ctagctctgtgtttcccc	1363
ABCG1	42	(intron 7 12985)	ctattggcaggtgtaaca I/C tgttttgatttggcaata	1364
ABCG1	43	(intron 7 20041)	acatggccgttcccttct I/C cctc g/a gaatggcctgaatt	1365
ABCG1	44	(intron 7 20046)	gcggcttcccttct I/C cctc G/A gaatggcctggaattcgatc	1366
ABCG1	45	(intron 7 21058)	acaagacttagaattgacc G/A tgattttaaaactattctaa	1367
ABCG1	46	(intron 7 26189)	tcttgatgtggccatgca C/I gggggcaagggtttgatgag	1368
ABCG1	47	(intron 7 27453)	atcatgtgtttgggggaaa G/C ctagggaccacacttggta	1369
ABCG1	48	(intron 7 29810)	atgtttctctggttttgt I/C tgtgtgactttccctttaa	1370
ABCG1	49	(intron 10 2116)	aaacaggcttgagtctctc G/A taaggacagggagaccttc	1371
ABCG1	50	(intron 13 1196)	tgaagaagaaatggatgagt G/A gaa a/c coaaagagagaaaat	1372
ABCG1	51	(intron 13 1200)	aagaaatgagtagt g/a gaa A/C coaaagagagaaaatgtgg	1373
ABCG1	52	(intron 13 2041)	aagcagagggttttccacc G/A gagactcaagaagctgtctc	1374
ABCG1	53	(intron 13 2490)	gtgtgagtagagctgagc A/I cacggggagccctccatcc	1375
ABCG1	54	(intron 13 2822)	cagcagctccgtgctgaag I/C cacagcaagccaggcccttg	1376
ABCG1	55	(intron 13 2850)	agccagcccttgccctgcc G/A gagctggaagaccagaaca	1377
ABCG1	56	(intron 13 2919)	gcctccagagtagctiaca C/I gggaccgaaggcagatggc	1378
ABCG1	57	(intron 13 3506)	ggcagctgggcctgcgaga I/C cctccctggagcgcgcgcg	1379
ABCG1	58	(intron 13 3538)	cgccgcgcgggaagcccccag G/A ggggctggagctaca a/g gtgg	1380
ABCG1	59	(intron 13 3554)	ccag g/a ggggctggagctaca A/G gtggccttgaggtttttg	1381
ABCG1	60	(intron 13 3721)	ccagctcatgggcaggggtg C/I gggggaagggccaccacag	1382
ABCG1	61	(intron 13 3921)	gaagaccagcagctgatcc A/G gctgggaagaggcctctgcc	1383
ABCG1	62	(intron 13 3979)	accacaccgcttttccaga C/I agccttccagaagcgtttc	1384
ABCG1	63	(intron 13 4291)	gagccgttgagtaggttcc G/A cttgctatggctcccagggg	1385
ABCG1	64	(intron 13 4968)	tattgactggacaccttctc C/I gtagggcactgggctagg	1386
ABCG1	65	(intron 16 672)	atcagtaacgggtcaactaac G/A gatgtgtgtagtggggcag	1387
ABCG1	66	(intron 16 891)	tggcccaactgttgaggatgt G/A ggtgaccagaggggccctgga	1388
ABCG1	67	(intron 18 1616)	ctggaggaagaacacagata A/C agtctaagacgtg c/t tgtcac	1389
ABCG1	68	(intron 18 1630)	aggata a/c agtctaagacgtg C/I tgtcacagattcagggctcc	1390
ABCG1	69	(intron 18 1674)	gcttccaaaggcccatccg G/I gttgttctctgagc c/t gagga	1391
ABCG1	70	(intron 18 1689)	atccg g/t gttgttctctgagc C/I gaggacgggtttcggaacgc	1392
ABCG1	71	(intron 19 446)	tggtgcacagtgaacacagc G/A gctgttctccagaacttta	1393
ABCG1	72	(intron 22 243)	accggagagaccatggcagg A/C ccaagtgtctggacgttgc	1394
ABCG1	73	(3' flanking region 1257)	atggggccacagccctgcc I/C cagaagcagatttggctcgc	1395
ABCG1	74	(3' flanking region 1438)	gggggaagagcttgggaacc A/G tgaaggctgttaggcctgcaa	1396
ABCG1	75	(3' flanking region 1518)	tgaagggtgaactgagtag G/C tgaaggattctgcagttgacg	1397
ABCG1	76	(intron 3 3754~3755)	ctcaacctgcacctccctg (G) cctccitgatttccctcatc	1398
ABCG1	76	(intron 3 3754~3755)	ctcaacctgcacctccctg cctccitgatttccctcatc	1399
ABCG1	77	(intron 3 7848~7854)	cagtttcagaatttggggg (A) 6-7 tccataagctgtcatactt	1400

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ABCG1	78	(intron 4 190~191)	tgctgagagctcccttgcc (C) tggttgactctcagggttct	1401
ABCG1	78	(intron 4 190~191)	tgctgagagctcccttgcc tggttgactctcagggttct	1402
ABCG1	79	(intron 4 198~206)	agctcccttgctgctgttga TCCTCAGGG/ Δ tttctactagaatgcctcga	1403
ABCG1	80	(5' untranslated region (-713)~(-741))	cgagctcaagctcgtctcc (CGC) 8-10 cccggggcatggcctgtct	1404
ABCG1	81	(intron 6 376~387)	ttctgctttagctcaagag (A) 10-12 tagccaggtttctgcgcag	1405
ABCG1	82	(intron 7 19944~19945)	ctgatgaggaggaggagg (CACCAGGACGACATCTGATGAGGAGGGGAGGGGG)	1406
ABCG1	82	(intron 7 19944~19945)	caccaggcagcagactcga	1407
ABCG1	82	(intron 7 19944~19945)	ctgatgaggaggaggagg	1408
ABCG1	83	(intron 7 25136~25137)	catgaacttccctgaccata (G) cccgttgaggagctaggct	1409
ABCG1	83	(intron 7 25136~25137)	catgaacttccctgaccata cccgttgaggagctaggct	1410
ABCG2	1	(intron 1 152)	tcatttgaagtggtgtgc G/A gtttaaaactgacagttaa	1411
ABCG2	2	(intron 1 614)	agctagctataataataac G/A ccagagtagtaaggaagaga	1412
ABCG2	3	(intron 1 10002)	ccctaatggtatataatg T/A cccaacatattcttttcgat	1413
ABCG2	4	(intron 1 10123)	acagtggctcctttgggtgc G/A tataccaaatccctgcata	1414
ABCG2	5	(intron 1 10768)	ataggaaataggaaacag G/A gctgaagaactcgcagga	1415
ABCG2	6	(intron 1 10791)	ctgaagaactctcaggaaa T/C g/a aaaatagttccctgtttt	1416
ABCG2	7	(intron 1 10792)	tgagaactctgcaggaaa t/c G/A aaaatagttccctgtttt	1417
ABCG2	8	(intron 1 14183)	tcacttaagctttgcaggg T/G gctcaggacagaaaagaga	1418
ABCG2	9	(intron 1 14934)	aagttcttttaaaatttc A/G tottgatcagtgagctatt	1419
ABCG2	10	(intron 1 14955)	ttcttgatcagtgagctatt G/T aaatcaagcaataagtatt	1420
ABCG2	11	(intron 1 17251)	ctgttgggaacagcaactc A/C atcataggcagagagaaagt	1421
ABCG2	12	(intron 1 17347)	attcaaacctgtttcaaaa G/A ttgttaagctcatctttaagg	1422
ABCG2	13	(intron 1 17626)	gaaggtagcaataaaacttc T/G acataaagctggagctata	1423
ABCG2	14	(intron 1 18369)	ctattgctttctgtgtgca G/T aagataaaaaactctccaga	1424
ABCG2	15	(coding region 34 (Val 12 Met))	atgtcgaagttttatccca G/A tgcacaaggaaacaccaat	1425
ABCG2	16	(intron 2 36)	tgtaaaagacagcttttta A/G tttaacctacagtgaaactca	1426
ABCG2	17	(intron 2 4230)	caacctaaattggaggccc C/T gggcgtggtgattgagaag	1427
ABCG2	18	(intron 2 4518)	gttgacagactttttatagtg A/C gggacactgacctgcagca	1428
ABCG2	19	(intron 2 6278)	atgtatgtaccacgtcttca T/C attcttaaggatgaacctca	1429
ABCG2	20	(intron 3 10)	ggcaaatcttctgtgata A/G gagagtataagtaagcgttt	1430
ABCG2	21	(coding region 421 (Gln 141 Lys))	tgacgttgagagaaaactta C/A attctcagcagctctctcgg	1431
ABCG2	22	(intron 6 3203)	tcctattctgttttaataaa A/G gaattgaatttaggtttgct	1432
ABCG2	23	(intron 6 3287)	gtcaggctgaactagagcaa A/G caatctaaaggcaagaatag	1433
ABCG2	24	(intron 9 5974)	tatactaataatgggtgt A/T taagtttttattctctaattg	1434
ABCG2	25	(intron 10 1908)	gaogcttatgtgcagctat G/T ttgatgtctggaaagctga	1435
ABCG2	26	(intron 10 2094)	ccctgaggcctgaggtatct G/A gattatttccagacttgcta	1436
ABCG2	27	(intron 11 20)	ttgtgagtagctttgtttct A/G ggaacgggctgtccagcag	1437
ABCG2	28	(intron 11 1447)	tgcttctcaaggaaagcccc C/T gtcaaggaaggaaagaagc	1438
ABCG2	29	(intron 12 49)	atgtcttttagtcttgcctat G/T ggtgaagttaagttgcacct	1439
ABCG2	30	(intron 12 1566)	tatgcagttacatggacaga C/T acaacattggagacagagg	1440

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ABCG2	31	(intron 13 40)	gctctgataaggaaatgttt C/I ttctcttcattcttctctgc	1440
ABCG2	32	(intron 13 1823)	ttactcaagcagccctgact C/I ttagtatttgctttttgttag	1441
ABCG2	33	(intron 14 497)	ctaataaacaacaacaagaa I/C gaagatttgcactgtaaat	1442
ABCG2	34	(intron 14 815)	taactcttggaacactctt A/G aaatttaaacgttttaacct	1443
ABCG2	35	(intron 15 110)	ccaggggcactgaattttt C/I gagctaacgttttctcatcc	1444
ABCG2	36	(intron 15 566)	gcgcacatagctagtgtgt I/A gttttaaatcttaacttggaa	1445
ABCG2	37	(intron 15 639)	aaacaagaacacttgaataa G/A ttgagaataaaacccccgtttt	1446
ABCG2	38	(intron 15 1197)	tgagtacgtgggattacagg C/I gccaccacacacaccciggt	1447
ABCG2	39	(5' flanking region (-998)~(-995))	gttggatgctacactcac TAC/ Δ aaagccgaigggcccggttcc	1448
ABCG2	40	(intron 13 405)	ctgctagtatttttttt I/ Δ aacatttttaattttatgttt	1449
ABCG2	41	(intron 13 692~702)	tcaatatgttctgcttacc (I)9-11 aatggttaacttaacttaaat	1450
ABCG2	42	(intron 15 645~650)	aaacacttgaataaG/Attgag (A)7-8 cccggttttcacataatgtt	1451
ABCG4	1	(intron 1 84)	ggcttgggttcccatgttc G/A gaaagtcctgcaccagtgagg	1452
ABCG4	2	(intron 2 77)	gaacacagaaggatattcga A/G agggcattgacccccatcct	1453
ABCG4	3	(coding region 679 (Leu 227 Leu))	tgagtccctcatgaagtc C/I tggcacagggggggccgtacc	1454
ABCG4	4	(intron 7 95)	ggcctctaggggtagagat C/I tcacgtgccttgccttccc	1455
ABCG4	5	(intron 7 158)	cttgccttgggaagtgt G/A tgaatctaaactgagctctc	1456
ABCG4	6	(intron 8 106)	ccccagggcatctgcaacca A/G tgggtctaggaagaacctc	1457
ABCG4	7	(intron 11 1120)	acagataagtga t/c ggtcat A/G tggccagggagggaaggagac	1458
ABCG4	8	(intron 11 1173)	ggggacagcttgaacaaga A/G tgtggaggcaggatggacac	1459
ABCG4	9	(3' untranslated region 2758)	gagtacagacacatacatg A/C gaacaggccatctcagccct	1460
ABCG5	1	(intron 3 40)	ccctggcccccccgccgc C/A cggggcttaggtctacactg	1461
ABCG5	2	(intron 4 841)	gcttggaggcatcttgaatg C/I gctcatccaaactggactg	1462
ABCG5	3	(intron 4 1145)	gagcaaatccagccccacgc G/A tgtaaaat c/a ctgataagtaa	1463
ABCG5	4	(intron 4 1154)	cagccacacgc g/a tgtaaaat C/A ctgataagtaattcagttggg	1464
ABCG5	5	(intron 4 1690)	acagagatggagaaggaggt I/C ggaatctacctggctgggt	1465
ABCG5	6	(intron 4 1806)	tttttcttcagaatatat I/C tatatctagtattttatgct	1466
ABCG5	7	(intron 4 1878)	atttcagatatgtccattct C/I tgggtgggtccaaagctacat	1467
ABCG5	8	(intron 4 2052)	gggtgtctgaaacaacact C/I attacatatgagtatcttc	1468
ABCG5	9	(intron 4 2108)	tcacctgggggtttctgcag A/I tagagtaatcagtaacagg	1469
ABCG5	10	(intron 4 2230)	agctcttgattagaataatc G/A gtaaaagaattttttttagtc	1470
ABCG5	11	(intron 4 2318)	ggagttacagggctttaagta G/C agcgaagaagaatttggagaa	1471
ABCG5	12	(intron 4 2367)	ttaaatgtgctgggggtta C/I aaattgggtcccaattaaag	1472
ABCG5	13	(intron 4 2464)	gattatatgtcttttgatgtg A/G actcacacigagattgtacc	1473
ABCG5	14	(intron 4 2586)	aaagcatttgaataataa G/A tticaaaacccaacacatta	1474
ABCG5	15	(intron 6 1318)	cagagacattcaagtgcat C/I gctacoccttgatcacaca	1475
ABCG5	16	(intron 9 164)	caactattgagttaccaaca I/C gttatatgaatgagctcac	1476
ABCG5	17	(intron 9 365)	gtaccgttagcttctctttg A/G agctgatttttagcacagcca	1477
ABCG5	18	(intron 10 64)	tcatggagcttagtgggactc G/A tgcagggaaggtccagggt	1478
ABCG5	19	(intron 10 2406)	tcaacaagctgcttactg G/A gttagtgtgacacattgtct	1479

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ABCG5	20	(intron 10 2442)	tgctaaagtaattatgtt t/g toctatgagagctgaaggag	1480
ABCG5	21	(intron 11 4150)	aaggccctgaatggctgtt G/I ctggctattgttccgagctc	1481
ABCG5	22	(intron 11 4623)	caacagaaagaattttata C/I cttttgattgacagaaaaa	1482
ABCG5	23	(intron 11 4737)	atttcacaaatgaatgttg t/g toggctctctctctctttt	1483
ABCG5	24	(intron 11 4791)	ggtagttctaaactttac G/A ttggtaaccttaactttctg	1484
ABCG5	25	(3' untranslated region 2578)	tgagattaaataaaaaac C/I gtaggaaatggctcaacagt	1485
ABCG5	26	(3' flanking region 1560)	catagcaactcagaagaac G/C tgtctaaagactgaggttc	1486
ABCG5	27	(intron 4 1078~1080)	ggcacagctccctgggagc AGG/Δ agaactcccgatagcagagt	1487
ABCG5	28	(intron 10 2321~2327)	agcgggttggtgagccctt TAACAT/Δ aggtaggtgtgtgtggct	1488
ABCG5	29	(intron 11 422~433)	ggatlaagactagtcagac (A)10-12 gcctgcaggaataaagactg	1489
ABCG5	30	(intron 11 3988~4004)	ctttttttgtagtgtgtcc (I)15-17 cttttctgtttctactctg	1490
ABCG5	31	(3' untranslated region 2719~2731)	tacctaataacttaagtat (A)11-13 cctaccgaaaaaataaaaa	1491
ABCG8	1	(5' untranslated region -19)	aagagagctcagcccgagg G/I cacagacctgtggccocat	1492
ABCG8	2	(intron 1 898)	ctttgactgaattcggat A/G tggcaggatttgaagcagga	1493
ABCG8	3	(intron 1 1548)	cttcacacctgaaggcca G/I gtgtaaattgagaaattcta	1494
ABCG8	4	(intron 1 1611)	tggtacggggagccacttc C/I agcccagaccacaacctgtc	1495
ABCG8	5	(intron 1 3245)	tggacaaatgaagcaatgtg t/c acagtacacggcggagggc	1496
ABCG8	6	(intron 1 3430)	gggttaggtgggaatggaa A/C tctggagtctactactcgtg	1497
ABCG8	7	(intron 1 3509)	tacacaaatcagcttaaga t/a ctctcatgtacacacacca	1498
ABCG8	8	(intron 1 3980)	gaataaaccctgtgtcaga C/I gcttgggtcagccctccctc	1499
ABCG8	9	(intron 1 4123)	aagggtttctggctccccc G/A taagtgttgttgggtgcat	1500
ABCG8	10	(intron 1 5354)	cagtttcaaggagccccc A/C atctctcctgtct t/c ccacag	1501
ABCG8	11	(intron 1 5368)	gcocct a/c atctctcctgtct t/c ccacagggcctccaggtatg	1502
ABCG8	12	(coding region 161 (Cys 54 Tyr))	ggaggtcagagacctcaact G/A ccaggtagaggccagccctgg	1503
ABCG8	13	(intron 2 86)	gaataaagggtggggcca C/A ctggcaggccctctgccc c/g c	1504
ABCG8	14	(intron 2 105)	a c/a ctggcaggccctctgccc C/G caaggacagagtcagttcca	1505
ABCG8	15	(intron 4 43)	gaccccgaggtccaaagac C/I acagtgtccatgcccgcctc	1506
ABCG8	16	(intron 6 1035)	caggagacagggccgcccct C/I gccctctgtactcacattct	1507
ABCG8	17	(intron 6 1085)	cacagaagggtcacctccct C/A cctgtctcagggtggcagcc	1508
ABCG8	18	(intron 6 1184)	gcacctgccgacctggccat C/I ggggaataatttaaagtaac	1509
ABCG8	19	(coding region 1199 (Thr 400 Lys))	tggggcgggtgacagattta C/A gacgtgatcccggttaattat	1510
ABCG8	20	(intron 8 137)	gaaaaaacacagcatccagca G/A ggcgttgggtggcttatgcct	1511
ABCG8	21	(intron 9 412)	ttctcttttcttccctta t/c tttttaggttactcaagagag	1512
ABCG8	22	(intron 10 343)	aggaaagcagaggttcagaga G/A gctacgtgggtctccaaggg	1513
ABCG8	23	(intron 10 614)	cttttaacggtttataataa t/c ggcagtgagggtgctgctt	1514
ABCG8	24	(coding region 1695 (Ala 565 Ala))	gcctcctcttcagcaatgc C/I ctctacaactccttctacct	1515
ABCG8	25	(intron 11 82)	tgcttctatctggagatgga C/I acttatoacttagatccaac	1516
ABCG8	26	(intron 1 2882~2893)	tctottagaatgataaga (I)11-13 gacagagctcacgctgtgg	1517
ABCG8	27	(intron 1 3654)	tttatcttccattttttt t/Δ ctgtataatttgggtcttt	1518
ABCG8	28	(intron 1 5045)	tcagagcacagaggtttttt t/Δ atagaactctctccggtcca	1519

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ABCG8	29	(intron 9 292~302)	tgcttacttgctctattt (A)10-12 tgagagacttgggcaatatg	1520
ABCG8	30	(intron 9 417~418)	ttctcttccctta t/c ttttt (I) aggttactcagagaggcaca	1521
ABCG8	30	(intron 9 417~418)	ttctcttccctta t/c ttttt aggttactcagagaggcaca	1522
ABCG8	31	(intron 10 28~34)	ggcagggttagagagaagtg (C)7-9 accaccagggttggggataa	1523
ABCG8	32	(3' untranslated region 2118)	tcctggggagagtgaggaca A/ Δ tgacctacagatgtctcagc	1524
ABCE1	1	(5' flanking region -158)	aactcagattctggccacct C/I cagcagctggcttgcacaac	1525
ABCE1	2	(intron 9 237)	ctgaattatagcaaatc C/I gtgctttataggaaagcaga	1526
ABCE1	3	(intron 9 4203)	ttgttaggagctgataca T/G taatttgacatatgagatgt	1527
ABCE1	4	(intron 10 1811)	ccagaaacttcagctttct C/I ttcaacttaatataggaaac	1528
ABCE1	5	(intron 17 2301)	atatcagaacacagatggta T/C gtgcagaacaggttgtacag	1529
ABCE1	6	(3' untranslated region 1810)	tgatgattagactgaactct G/C agaattatgaagccattt	1530
ABCE1	7	(intron 1 5349~5363)	ttgtctgggttggttggtgg (I)13-16 gagacigggtctgactctca	1531
ABCE1	8	(intron 1 5845~5854)	tacatttgcataaatttata (I)9-10 gcagataatcatttcactc	1532
ABCE1	9	(intron 5 836~851)	taatttcacatgattctgta (I)14-16 aggtatctctcgaactggcag	1533
ABCE1	10	(intron 8 1153~1169)	tccttcaaatattattgc (I)13-17 catagtttcatgtttgata	1534
ABCE1	11	(intron 9 1023~1024)	ttgtctgtttcaaatctct (I) attcatggccagcagctcg	1535
ABCE1	11	(intron 9 1023~1024)	ttgtctgtttcaaatctct attcatggccagcagctcg	1536
ABCE1	12	(intron 9 2338~2346)	agtgatagtagacactgggg (A)8-9 ctagttaaggaaaagtaata	1537
ABCE1	13	(intron 9 3213~3221)	ttcaatttccattgttac (I)8-9 ctggcagattactctgaa	1538
ABCE1	14	(intron 10 284~299)	tcctctgatttggcttct GCAGTATGAGT/AGI/ Δ atttgcattttcaaatiaa	1539
ABCE1	15	(intron 10 840~853)	tttttggtttcttcttctc (I)13-14 aatcttggaggaaatctttt	1540
ABCE1	16	(intron 16 1163~1172)	gattagaaatccaggttaaa (I)9-10 gtttgcacaaaaatattac	1541
ABCE1	17	(intron 16 1372~1382)	taaaatttaatacaaatga (I)10-11 ctcttagtctctcaaacctt	1542
ABCF1	1	(5' untranslated region -60)	gcagcccccctggggttcc C/I cggccggggaagcggaaata	1543
ABCF1	2	(intron 1 101)	gcagagacacgacggggccc C/G tggggagttacttgcgcag	1544
ABCF1	3	(intron 20 69)	tgactttaaccgacaccctc C/I ctctcttctcgggcagaaa	1545
ABCF1	4	(intron 23 35)	agtgtgccctcctccctgct C/A catgggagacaagctgtagt	1546
ABCF1	5	(intron 7 342~354)	acagagagagactcctctc (A)10-14 gaaaaaaaaaaaacattt	1547
ABCF1	6	(intron 7 356~369)	cgtctcaaaaaaaaag (A)13-15 catttcatcagacctgtctt	1548
ABCF1	7	(3' untranslated region 2425)	tcagccggcccgagagtgga A/ Δ gcttcttctccagaagtct	1549
ABCF1	8	(3' flanking region 1067~1068)	attaatttgataattgtct (I) aatatgtctactctagatt	1550
ABCF1	8	(3' flanking region 1067~1068)	attaatttgataattgtct aatatgtctactctagatt	1551
OAT1	1	(5' untranslated region -127)	gcagctcggagcagctccc G/A gagcaacccagctggcgagg	1552
OAT1	2	(5' untranslated region -20)	gaagccctcagccccagcc A/G ctggcttggcctggcccaa	1553
OAT1	3	(intron 3 150)	caatagacaacctttctc G/A ggctcatgcgccttgacc	1554
OAT1	4	(intron 4 211)	ttcttgcttccccactc A/C gttctccagctgctctc	1555
OAT1	5	(intron 5 33)	gagacttccatgataacct C/I ccagggttccacccccaaac	1556
OAT1	6	(intron 6 168)	gaaccagatccccagct C/I gactcagtcacagctctccac	1557
OAT1	7	(intron 1 58~71)	ggagatggggccttctgtt (A)13~15 gtacatggagaaatctg	1558
OAT1	8	(intron 3 1306~1319)	aataggttagagagagcag (A)12~15 tcaagagtgtgagaggcca	1559

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
OAT2	1	(intron 4 842)	ttgacctcaaaaagtgtttg G/A attacaggcatgggccaatg	1560
OAT2	2	(intron 5 183)	ccacatccatcattcgagac A/C a/c actcgtctcagctgcoatg	1561
OAT2	3	(intron 5 184)	caaatccaatcattcgagac a/c A/C actcgtctcagctgcoatga	1562
OAT2	4	(coding region 1269 (Ser423Ser))	actagacgtgtagtgtcttc C/I ggtgagccagtcgccatagg	1563
OAT2	5	(3' untranslated region 1792)	ataaatgtgtacatgagigt A/G tgaacacaaatcacataaggt	1564
OAT2	6	(3' flanking region 1386)	tgtagcagccacatcgcca G/A tttcacacctgagagagag	1565
OAT3	1	(5' flanking region -463)	ttcttgagaggaataatcccc T/C tccctactcgggagggtgcc	1566
OAT3	2	(5' untranslated region -16)	cttgccacacgtctgctc G/A tottgccacagtgccatgac	1567
OAT3	3	(coding region 153 (Pro51Pro))	ctgtccaccacgtgctccc G/A ccccaaatgcctccacagg	1568
OAT3	4	(intron 2 177)	gcaccaagacccttggttc T/C toccaactcagagtcaccaagca	1569
OAT3	5	(intron 2 6201)	gctcactctctctgttctt T/G tgcocccagcacagggttcttc	1570
OAT3	6	(intron 3 79)	tctgctccaccgtgacccc G/C caaagaggcaagagotggg	1571
OAT3	7	(coding region 723 (Thr241Ihr))	tggcggttggtgagttaac I/A ggtccattcccttcttgt	1572
OAT3	8	(intron 5 524)	tgaagtacaaaaggaagtt T/C aagagaaagcctgagctgg	1573
OAT3	9	(intron 7 386)	gaacaatgggttcagactc G/A aagacaaaattatgittat	1574
OAT3	10	(intron 9 81)	attgtcctgtctctaccca G/A gggagccatcctttatgaac	1575
OAT3	11	(5' flanking region (-661)~(-660))	tacatttggctcccccagggg (G) aagcggctatcaggagaga	1576
OAT3	11	(5' flanking region (-661)~(-660))	tacatttggctcccccagggg aagcggctatcaggagaga	1577
OAT3	12	(intron 8 211~212)	tctgacttgagctgggcaaa AA/Δ gtagtgggtatctggatag	1578
OATP1	1	(5' flanking region -916)	acagagttagatgttcaataa G/A tatttggttgtatctgtgaga	1579
OATP1	2	(5' flanking region -843)	tagtgaagcactatgcctt G/A atgtgtgtgtgttgggatt	1580
OATP1	3	(5' flanking region -526)	aaatgtgtccgtgtatgta I/C acatcgtacataattcc	1581
OATP1	4	(5' flanking region -172)	acaaacacactcaaatat G/A tgtgtatttaaaagtagcta	1582
OATP1	5	(intron 1 206)	ttgattcagggcaagttagtc C/G taatggccttgagagactt	1583
OATP1	6	(intron 1 454)	caacataacaaataatttctt G/A taagaaaaatggccaatttg	1584
OATP1	7	(intron 1 999)	gtttagcaaggttagatatt A/G atgtgagtgttaagacaaaa	1585
OATP1	8	(intron 1 1223)	ttgctagaagctagtaggac C/I agcittataaatacacagat	1586
OATP1	9	(intron 1 1326)	aactagttaggcaaccatg T/C gttttagg g/a aaagcaatg	1587
OATP1	10	(intron 1 1336)	gcacccatg t/c gttttagg G/A aaagcaatgaggctatgat	1588
OATP1	11	(intron 1 1498)	atagttgtccttaagaata C/I actctgagaaggtttatagt	1589
OATP1	12	(intron 1 5041)	ttatgtcccgaggagttag C/I tctctaaatgcataaggaga	1590
OATP1	13	(intron 1 9532)	aaagactgggagcacttccc A/G atgacaaatactagactaga	1591
OATP1	14	(intron 2 961)	aaaaagtatatagaaaatat A/G agtgtcactctcttctagt	1592
OATP1	15	(intron 2 1110)	gtctactagtgttoaatccc T/C tiagactttagcctgtatca	1593
OATP1	16	(intron 2 1419)	aagccctaaagaagatcgag I/C gcaatagcctatgtgagaag	1594
OATP1	17	(intron 2 3339)	tatgggttgcaaaaaactta T/C tctatatttgtttttttca	1595
OATP1	18	(intron 3 66)	caggaatatgaattgcactt T/C cctctotaggagcaatgctt	1596
OATP1	19	(intron 3 205)	tcagtttttcoaatttacac A/G atgggattttgggacctttt	1597
OATP1	20	(intron 3 6377)	aatgaatatagactttgagta C/I tggatttttagtgataaat	1598
OATP1	21	(intron 3 7238)	tgaagtcacatttttttaa G/A ttgtgtctctatcicata	1599

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
OATP1	22	(intron 4 1016)	ttttattctggattcatgtt /C gggaaattgcagtagtcca	1600
OATP1	23	(intron 5 110)	tcacaatgaatgagtagagt A/G tcttggcacagtggccttc	1601
OATP1	24	(intron 6 496)	agtctgaattataagcca A/G ttttatagttggttggacc	1602
OATP1	25	(intron 7 1934)	aagtgaaaggaaattaaaa G/C tgaagaacttggacctgaatg	1603
OATP1	26	(intron 7 2140)	tagaatgtaccaaagaatc A/G gcatctcaggatgggacc	1604
OATP1	27	(intron 7 2365)	tgaatcttcttataact C/T gatttcccccagactttac	1605
OATP1	28	(intron 8 88)	gcaactcctaagttgaagt G/C ttttaggatatattttgact	1606
OATP1	29	(intron 9 534)	tcataatttatttttaag G/A ttatctgggtttttacigaaa	1607
OATP1	30	(intron 9 1286)	tattctctgagataaatca I/C tgaaggagtggtatgtgt	1608
OATP1	31	(intron 11 215)	ttcaactctatctcgcia C/T ttttctcttatttcttag	1609
OATP1	32	(intron 11 663)	ttcttcttcttttggagctc I/A aaagttaggttcagttaatc	1610
OATP1	33	(intron 11 999)	atcatcactgcatgagagt A/G gaattatcactatttggat	1611
OATP1	34	(intron 11 16727)	tttcttttatttacaactt A/G ttacttttccagtgatga	1612
OATP1	35	(intron 12 48)	ctatcagaacaattattia I/G tattattttttattacactt	1613
OATP1	36	(intron 12 686)	tatgttttgataaactttgc C/A gtacaaataaagaaaattga	1614
OATP1	37	(intron 12 708)	tacaaataaagaaaattgaa A/G tatttccaaataaatcaagt	1615
OATP1	38	(intron 13 418)	tctctgtctccaaatcat A/G tatttctccctcttta c/a at	1616
OATP1	39	(intron 13 436)	at a/g tatttctccctcttta C/A attttgcgaacaacttcc	1617
OATP1	40	(3' untranslated region 2130)	gtctttaagaaccttaaaaa C/A cctttaaactcaaaaataaa	1618
OATP1	41	(3' flanking region 57)	agtgactaaagtttttcttta C/A aaacaagtctgaatcaaa	1619
OATP1	42	(3' flanking region 572)	aatacactatggttatttat G/A tgtactataaatggatgag	1620
OATP1	43	(3' flanking region 788)	atttctctaattgatcagatg C/I atcatatgaaaaaagaagc	1621
OATP1	44	(3' flanking region 1356)	aggagactgacataaatggg G/A gcagagacataatgaggtt	1622
OATP1	45	(5' untranslated region (-189)~(-188))	atttctaatctgtattaaa (A) ggttccaggtatttttcta	1623
OATP1	45	(5' untranslated region (-189)~(-188))	atttctaatctgtattaaa ggttccaggtatttttcta	1624
OATP1	46	(intron 4 725~726)	tgatctttaatagaggggaa AA/ Δ caggcaagtcactatagtt	1625
OATP1	47	(intron 4 1082~1083)	attgagtcaggaaacacaaa CA/ Δ gtitcaaaaatttgaaaaat	1626
OATP1	48	(intron 4 2301)	aatgtcatgtctttttttt I/ Δ aatgcagagtgtacaaagga	1627
OATP1	49	(intron 9 241~46)	attgtatgtcatgtgggtg TGTG/ Δ catgattgtcttttgatat	1628
OATP2	1	(5' flanking region -2574)	ggataagcgaacccctatgt A/G tcactgtcaggagagagga	1629
OATP2	2	(5' flanking region -1723)	tcttcacacttcaagacc A/G tgatatattcatcagactgt	1630
OATP2	3	(5' flanking region -1180)	tgtttatttaacaggcataa I/G ctttggctcctcagaccaga	1631
OATP2	4	(5' flanking region -811)	tatgtgcataatgtatata G/A gtaaaagtgtgtatatatgt	1632
OATP2	5	(intron 1 7188)	aatcatttgaatttaagaa A/G aaataatgttcagagaaaaa	1633
OATP2	6	(intron 1 7331)	gtgaaatagggaacaaagt I/C ccacttttttttctgaata	1634
OATP2	7	(intron 1 7391)	agagagatgtgaatagtat I/G tttctgggaagtaggggaa	1635
OATP2	8	(intron 1 7886)	ttgttagtagaaagaaaatc G/A aagcctaaaactaaaggag	1636
OATP2	9	(intron 1 7958)	tgtctattataataattttt I/A a/t aaaaaagatttcttaaat	1637
OATP2	10	(intron 1 7959)	tgtctattataataattttt t/a A/I aaaaaagatttcttaaat	1638
OATP2	11	(intron 1 8036)	ggaaaaaatggsgtgaatt A/I atcaaaaggcagctttattac	1639

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
OATP2	12	(intron 1 9164)	acattatattctataaaaa G/I agtcagttgaagtataaaagt	1640
OATP2	13	(intron 2 193)	tgattaaagtattttcttgcc G/A aaatttttgattgottaatag	1641
OATP2	14	(intron 2 1020)	ttgagtaacatttagcccaa G/A tggcagtcataaggaaaaag	1642
OATP2	15	(intron 2 14865)	agaggataatcataagag G/I tttatttgctaaagtgaca	1643
OATP2	16	(intron 2 14931)	gttagttaataacagaaaa A/I tatcagaaattttataaaaat	1644
OATP2	17	(intron 2 15417)	ttctaaataagtaagctaa A/I tttctatattataactacta	1645
OATP2	18	(intron 2 20823)	ttgtataagagatacaaac A/C aattctactaggggaaata	1646
OATP2	19	(intron 2 20852)	ctagggaataaagcttca G/C taaggaggiggcattaaagct	1647
OATP2	20	(intron 2 21360)	ttcaaaagcgtatttctca I/C tagtgcititttiggataaaa	1648
OATP2	21	(intron 2 21467)	tatacacataaactgtcc A/G gaagatgtgtgtataagccaa	1649
OATP2	22	(intron 2 21621)	tatcaatactatgaagaga A/G ctactattcttaactaggga	1650
OATP2	23	(intron 2 22760)	ttccccacctctgttggtt C/G tctcttaacttctctctg	1651
OATP2	24	(intron 2 23199)	ccatctgcacataacattta C/I aaatttatgcaattata a/g a	1652
OATP2	25	(intron 2 23218)	a c/t aaacttatggcaattata A/G aactcaatatactattact	1653
OATP2	26	(intron 2 23330)	gcocttcttctgttctct G/A taactgccttaactacatag	1654
OATP2	27	(intron 2 23673)	ctggagacggtagctcaaac I/C gaggaagaaaatagacattt	1655
OATP2	28	(intron 3 89)	gggtatacaactgggtaaat I/G tatctctcacaggaatttg	1656
OATP2	29	(intron 3 224)	tgcataaatattctataatgc A/G caaagaatgaigtaactgaa	1657
OATP2	30	(intron 4 97)	ccctttaaataggcagttac C/A ttttgagaatataccacta	1658
OATP2	31	(intron 4 568)	ttcatgatccaaattgtggc A/G acgtatttccaggccaacaag	1659
OATP2	32	(intron 4 599)	aggcaacaagatagaagaag A/G aaagaataaagaagcaacaa	1660
OATP2	33	(intron 4 753)	aaataagacattattccaag I/A taccagttcccggttaaaa	1661
OATP2	34	(intron 4 781)	ttccgggttaaaaatcccaa G/C tataattactgtggaaggaa	1662
OATP2	35	(intron 4 1196)	aaggaccacaactatgatca G/I cattgctctaaatatgocat	1663
OATP2	36	(intron 4 1229)	tatgccataatatgtgaacac I/C ttigcaccctggtattctac	1664
OATP2	37	(intron 4 1623)	catctagtgtgaatggatta G/C attttatttttactacattt	1665
OATP2	38	(coding region 388 (Asn130Asp))	attctaaaggaactaataatc A/G attcacagaaaaattcaaca	1666
OATP2	39	(coding region 452 (Asn151Ser))	taatcaaaatttttaccatca A/G tagagcatcacctgagatag	1667
OATP2	40	(intron 5 165)	ttatatatacacagtttgcgcc A/I ttaacaacacaggttttaaac	1668
OATP2	41	(intron 5 189)	acaacacaggttttaaacac G/A c g/a ttttcacttctatgcaaa	1669
OATP2	42	(intron 5 191)	acaacaggttttaaacac g/a c G/A ttttcacttctatgcaatt	1670
OATP2	43	(intron 5 507)	atataaactttgctttcattg C/I aaaaggcaaac a/g ttatatac	1671
OATP2	44	(intron 5 520)	ttcattg c/t aaaaggcaaac A/G ttatataatttaagaacttt	1672
OATP2	45	(intron 5 856)	agtcagtataaacctaatag A/G ataaaaacacaaaaaagaaa	1673
OATP2	46	(intron 5 1157)	acagataatttttacttgtt I/C gtgcttttctgtatgatg	1674
OATP2	47	(intron 5 1226)	cccttgattgtaataatctcc A/C c a/c tggcaagagtgaggccag	1675
OATP2	48	(intron 5 1228)	ttgattgtataaatctcc a/c c A/C tggcaagagtgaggccaggt	1676
OATP2	49	(intron 5 1304)	actgttctcggttgtaataaa G/I aagttcacacaagatctgatg	1677
OATP2	50	(intron 5 1348)	ttataaatgagaggttccct G/A caaaagctctcttgcctgcc	1678
OATP2	51	(intron 5 1407)	ttgctcttcttctatctcc G/A ccatgattgtgaggccccc	1679

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
OATP2	52	(coding region 521 (Val174Ala))	gtcaacatgtgatataatg /C gttcatgggtaataatgcttc	1680
OATP2	53	(coding region 571 (Leu191Leu))	ggagaccoccatagtagcca /C tggggctttcttaccattgat	1681
OATP2	54	(coding region 597 (Phe199Phe))	ctttcttaccattgaatttt C/I gctaaagaaggacattcttc	1682
OATP2	55	(intron 7 33)	agaacaaggaccatgataa C/I gttcttcaagcacacatgc	1683
OATP2	56	(intron 7 267)	caaaataacccaatgtaaaa /A gtcctccctcccaaacigact	1684
OATP2	57	(intron 7 1260)	gtaatcacaatttctctgc A/G ttacacttggtaaaacttt	1685
OATP2	58	(intron 7 2273)	ttctcagctctctatctagc C/I gattatgacctttagttaact	1686
OATP2	59	(intron 8 207)	gtggaagagaatttagtttg /C actttttagcaggaggaac	1687
OATP2	60	(intron 8 546)	togggaagaagtttctcccta /C gtaatttagaataatatt a/c t	1688
OATP2	61	(intron 8 565)	a t/c gtaatttagaataatatt A/C ttitggtaattatctatcta	1689
OATP2	62	(intron 8 668)	taagtaatgtaaattaggat G/I catcagcatttgcagctggcc	1690
OATP2	63	(intron 8 739)	tggagaaccattgagagtc A/G taacaaagagagaatgaacttg	1691
OATP2	64	(intron 9 112)	attttagtaatacaggataa G/C tataattttttgtattctt	1692
OATP2	65	(intron 9 266)	ttagaggtagtatctgtata A/G ttggatctttataatttagtg	1693
OATP2	66	(intron 9 305)	tgtcaagaatctgagacaaac C/G cttttgtaattataatcatt	1694
OATP2	67	(intron 11 10224)	tacacttgttccataaaaaa /C tctctatattattctcctagt	1695
OATP2	68	(intron 11 10359)	attaatagattcaacgtgag G/C ttcccttaaaccttttagccta	1696
OATP2	69	(intron 11 10916)	cttatatagaagaataatcca C/G aaaaactattttacacttttat	1697
OATP2	70	(intron 11 10997)	aatatattagtttgaacaag /C gagacttcaactaaataaat	1698
OATP2	71	(intron 11 11018)	gagacttcaactaaataaat G/A caatgtatttgcagcactgt	1699
OATP2	72	(intron 12 442)	aacatttccaaaacttttaac C/I ga c/t t c/a acagcatgactttta	1700
OATP2	73	(intron 12 445)	attccaaaacttttaac c/t ga C/I t c/a acagcatgacttttaata	1701
OATP2	74	(intron 12 447)	tccaaaacttttaac c/t ga c/t t C/A acagcatgacttttaata	1702
OATP2	75	(intron 12 907)	aatgaaaaaagagctggcaga /C tgaacacatactgaatgagag	1703
OATP2	76	(intron 13 65)	tatatatatatatatata C/I acacacacacacatatatta	1704
OATP2	77	(intron 13 870)	aattctgagatctctatttc G/A atgtatccaatctgtggcac	1705
OATP2	78	(intron 13 1935)	taaaaaaaaaaagctcgc /C ttacagcaattgagcccaag	1706
OATP2	79	(intron 13 2261)	aacgaatcttccaaattttt G/C aacttttatttaatacaaat	1707
OATP2	80	(intron 14 248)	tcaaggataataaccaactt G/A tcaaaaaatcagagataatag	1708
OATP2	81	(intron 14 2463)	atttgtttactaataatgaa C/G ctttctcaagacatatatttt	1709
OATP2	82	(intron 14 2857)	tcataatgtatttccagac A/I cctggcaagatgcctctcag	1710
OATP2	83	(intron 14 11458)	atctccagagctcctcgt C/I tccccaaagtccactgaacc	1711
OATP2	84	(3' untranslated region 2243)	ataataaaacaacactgtagg /C agaaaaaagagagtagctca	1712
OATP2	85	(3' untranslated region 2404)	tcttaataaaacaataatgagt A/G tcatacaggtagaggttaaa	1713
OATP2	86	(3' untranslated region 2515)	cagagatttgaactaataac /G aagccctgaagtctagcttg	1714
OATP2	87	(3' untranslated region 2539)	gocctgaagctctagcttgat A/G tatgtacaataataatcigt	1715
OATP2	88	(intron 1 457~458)	taatttggcaaacataaaaaa (A) cagggtgtctcaaaagtcacat	1716
OATP2	88	(intron 1 457~458)	taatttggcaaacataaaaaa cagggtgtctcaaaagtcacat	1717
OATP2	89	(intron 1 753~7538)	gatcagcattacaaccaaga (G) atggagaatgacatttcagga	1718
OATP2	89	(intron 1 753~7538)	gatcagcattacaaccaaga atggagaatgacatttcagga	1719

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
OATP2	90	(intron 1 10032~10035)	tgtgtatctatatactt AC11/Δ gtttcaaatctctccaca	1720
OATP2	91	(intron 1 10058~10061)	tccaattctctccacaaa T1A/Δ ttttctattaatgttaat	1721
OATP2	92	(intron 2 413~423)	acttatttaaaatctttt (A)11-13 caaaaacagagatttaaaaa	1722
OATP2	93	(intron 3 1595~1603)	ttgccaaagtaattcaagtc (I)8-10 gtatttaaacacacttttca	1723
OATP2	94	(intron 4 10~23)	ttcaaggagtagtaagtggt (A)12-14 cctctgtgccactatcagta	1724
OATP2	95	(intron 5 1567~1572)	gtcaataataaacttactgtta C11G1A/Δ aatttaaaaaaataagtag	1725
OATP2	96	(intron 5 1577~1585)	attacttctacttgaatt (A)9-10 taagttagaataatlaagagt	1726
OATP2	97	(intron 8 1939~1941)	ttcttaactcctctactc C11/Δ atttcaagcagaatgcaactg	1727
OATP2	98	(intron 10 3077~3078)	aaattctttatctactttt (C11) ttccctctttctctgtttc	1728
OATP2	98	(intron 10 3077~3078)	aaattctttatctactttt ttccctctttctctgtttc	1729
OATP2	99	(intron 11 11011)	aaaaag t/c gagacttcaactaa A/Δ tataat g/a caatgtatttga	1730
OATP2	100	(intron 12 1160~1169)	agcatgacatggttagatg (A)9-11 gaatttttaacattgttaa	1731
OATP2	101	(intron 12 1310~1312)	tcactcttaataataaatgt TGI/Δ ctactcaaaaggagaagtct	1732
OATP2	102	(intron 13 9~34)	tagagacactaggtatgag (A)24-27 tatatatatatatatata	1733
OATP2	103	(intron 13 35~64)	aaaaaaaaaaataaaaaa (IA)10-21 c/t acacacacacatatatt	1734
OATP2	104	(intron 13 1379~1387)	aaaattttcaccacaatc (A)8-10 caaagtaaagttatgaacac	1735
OATP2	105	(intron 13 1916~1928)	aattctottaaaataatgtt (A)11-13 gtctgc t/c tttaacgaattg	1736
OATP2	106	(intron 14 588~596)	caattatacttttaoctttt (A)8-10 cttaatttcaaatcatatat	1737
OATP8	1	(5' flanking region -1413)	aataggsgcttaataactct G/C aaacttaagtattctcatat	1738
OATP8	2	(intron 1 38962)	atgaatttagtttaaaaaa G/A caacttaactatactctc	1739
OATP8	3	(intron 2 253)	acagacttacocacaagaa T/G tctcttcccaaaaatgtcta	1740
OATP8	4	(intron 2 329)	actaatgtttgcaaattaa C/G ttttttaggaaaactttatctc	1741
OATP8	5	(intron 2 2568)	ccattctgtgtcttcttcc G/A tgaactatttttccatcagt	1742
OATP8	6	(intron 2 2679)	cctttattgtcttcttccca T/C gtitttaacttaaaataattta	1743
OATP8	7	(intron 2 2753)	caggaacatttcacaaagcc C/A cttaatttaattgaactcctc	1744
OATP8	8	(intron 2 3132)	tggtttaattgtaggagatt T/C accttcacagttaaatata	1745
OATP8	9	(intron 2 3193)	aatgtcttgggcataatttgc A/G ttcaatttggggca t/c tcagtt	1746
OATP8	10	(intron 2 3207)	atttgc a/g ttcaatttggggca T/C tcagtctactagatacaaa	1747
OATP8	11	(coding region 334 (Ser112A1a))	gaactgggaagtattttgaca T/G ctttaccacatttcttctatg	1748
OATP8	12	(intron 3 76)	agaattttattttatactt G/A taagtggcagtttaacctttt	1749
OATP8	13	(intron 3 2443)	tcaatttcaattgttgcctta C/T agttatagggtattctaaaga	1750
OATP8	14	(intron 4 67)	taatcacgtctataaagttt C/G tgatatcttttaacaaaaatt	1751
OATP8	15	(intron 4 91)	tattcttttaacaaaattgat T/A taagaacaaataggagaac	1752
OATP8	16	(intron 4 197)	ggtttgaactgcactgttgc G/A cttatatagcagcttttggcc	1753
OATP8	17	(intron 4 813)	tttaacagaataaaaaaaa I/A attttgtaacgacaaaaagaa	1754
OATP8	18	(intron 4 974)	atatgcacittaaaaataac C/G tggatttttttaaatatgtta	1755
OATP8	19	(intron 4 1003)	taaaatgttaattgtacataa G/T gaattattatgcataatttgt	1756
OATP8	20	(intron 6 155)	catttaataatcagaataaaa A/G agaaatttagctcctattta	1757
OATP8	21	(intron 6 750)	atccacatgggggttagatt T/G cctcttttctgcctctctcc	1758
OATP8	22	(intron 6 780)	gcctctctccatctgcacc C/T tctcttttctcagcaaaaa	1759

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
OATP8	23	(intron 6 1248)	ctatgccctgtaactcaca C/I ttccctttatttaaatgg	1760
OATP8	24	(intron 6 1500)	tgtgtctgtgttagcatat A/G ataactatcagggttgg	1761
OATP8	25	(intron 6 2008)	ataacataaagtgataaaga A/G tatcaaggcaggaaattag	1762
OATP8	26	(intron 6 2087)	actactcctccatacacac I/C aaactcatgtctccccag	1763
OATP8	27	(intron 6 12305)	tcactatgaggagcagcaa I/C cattatcattatttccocaga	1764
OATP8	28	(intron 7 363)	taacaaatgataccagccat C/G atactattctcgtgtaatag	1765
OATP8	29	(intron 7 411)	ccctttattttttagaacct G/A gggatgatattaaga c/a gta	1766
OATP8	30	(intron 7 428)	cct g/a gtggatgatattaaga C/A gtatatagatcactgtaata	1767
OATP8	31	(intron 7 634)	aaatkatatatacatat A/G taacttaoctaagtattca	1768
OATP8	32	(intron 7 1791)	tgttttttaagggtagta I/C gigaatagtaaacggaattt	1769
OATP8	33	(intron 7 2000)	agttgagcaaatgtctotca G/A giagcataaigtacactgaa	1770
OATP8	34	(intron 7 2043)	gittattgatccatttttta A/G tggatcaacatigtatggag	1771
OATP8	35	(intron 7 2171)	atttattttgagcaaggctc G/A c g/a actct c/t cttagaagcct	1772
OATP8	36	(intron 7 2173)	ttattttgagcaaggctc g/a c G/A actct c/t tiagaagcctcac	1773
OATP8	37	(intron 7 2179)	tgagcaaggctc g/a c g/a actct C/I tiagaagcctcacaaatca	1774
OATP8	38	(intron 7 2219)	atttgtaactttaagcttta I/G ataacttatatttacaatat	1775
OATP8	39	(intron 7 2261)	cagataattaataatatttt A/I tiattgaaatatgttatttt	1776
OATP8	40	(intron 8 150)	acaaaattctccatctgt A/G ata t/a catcgtgtgtcgcgt	1777
OATP8	41	(intron 8 154)	aattctccatctgt a/g ata I/A catcgtgtgtcgcattga	1778
OATP8	42	(intron 8 1303)	tttttttgatgagtgagctct C/I gctctgtgccaggctggg	1779
OATP8	43	(intron 8 1372)	aagctcgcctccaggctc I/G ccacctctctttaaagaaa	1780
OATP8	44	(coding region 1272 (Leu424Leu))	tcctctgtgtttcaacttct A/G tatttccctotatactcggga	1781
OATP8	45	(intron 10 63)	tcacagatttgatttaataa A/I tacttatcaaatcttctat	1782
OATP8	46	(intron 10 911)	cttgcccaataicctaccaa C/I gtattttaaacggcgtgga	1783
OATP8	47	(intron 10 972)	tcctagtttctctgaagata G/A gctacaacttttagtaaacit	1784
OATP8	48	(intron 10 1101)	tcctgtgtctctgtgtgtcc A/I g t/c agtgaagacctgaagag	1785
OATP8	49	(intron 10 1103)	ccgtgtctctgtgtgtcc a/t g I/C agtgaagacctgaagagag	1786
OATP8	50	(intron 10 2027)	cccaatttcatgagtggtc A/G g/a tttgtcccggtttcaaac	1787
OATP8	51	(intron 10 2028)	cccaatttcatgagtggtc A/G g/a tttgtcccggtttcaaac	1788
OATP8	52	(intron 10 2372)	tgattttggcaaatgtattt G/I ttaatatitcaaaaactatt	1789
OATP8	53	(intron 11 10538)	caacagagagatcaatgtataa I/G gaaatctcttaaatataaca	1790
OATP8	54	(intron 12 55)	ataaatattaatgtataata C/I taaagactgaatgcaattaa	1791
OATP8	55	(intron 12 1802)	taaatgaatcggtaaaa C/I tcaigtataaatcactgtca	1792
OATP8	56	(intron 12 2612)	ataggcatataactctttt C/A ttccctcgttatataggag	1793
OATP8	57	(coding region 1833 (Gly611Gly))	aacagctgtgagcacaagg G/A gctttaggtatataatc	1794
OATP8	58	(5' flanking region (-1587) ~ (-1587))	tacataacataactatata CTA/Δ gttatgtgtcgtgtatata	1795
OATP8	59	(5' untranslated region (-28) ~ (-11))	agcatcagcaacaataaaa ATA/TCACTTGGTATCIG/Δ tagtttaaatggaaccaac	1796
OATP8	60	(5' untranslated region (-7) ~ (-4))	tattcaacttggtatcgttag TTTA/Δ ataattgaccaacatcaaca	1797
OATP8	61	(intron 4 213~214)	ttc g/a cttatatgcagctttt (I) gtccaaccaaacagaggag	1798
OATP8	61	(intron 4 213~214)	ttc g/a cttatatgcagctttt gtccaaccaaacagaggag	1799

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
OATP8	62	(intron 4 505)	tataacttctctttataaa G/Δ atgcaaatgttatagcatt	1800
OATP8	63	(intron 4 616)	aatgaagtggagaaaaaa A/Δ tgattcaagttttctgtct	1801
OATP8	64	(intron 4 804~812)	acaiccatgtttaacagaat (A)9-11 t/a atttgtaacacaaaga	1802
OATP8	65	(intron 4 855)	agattgttaacacaaattag G/Δ aaactattatcaacacact	1803
OATP8	66	(intron 7 619~628)	ttttatataatgaattaaaa (A)4-5 catat a/g taattcttaactaag	1804
OATP8	67	(intron 7 1773~1779)	attttctatatattgaactg (T)7-8 aagggtagiga t/c gtaatatag	1805
OATP8	68	(intron 8 1270~1290)	tagtggccacactttctctc (T)19-23 gagatggagttot c/t gctctgt	1806
OATP8	69	(intron 10 665)	aaatcaaaaggtttttttt t/Δ ccaatgacacataatcctgt	1807
OATP8	70	(intron 11 247~250)	aaaaatcttaaggcacacac TGA/Δ tgacagttgaccttgattgta	1808
OATP8	71	(intron 12 1622~1630)	aaataaattgttggcatcta (T)8-10 atttttctaagggtogctgt	1809
OATP8	72	(3' untranslated region 2464~2465)	ccgtatgacctttaaaaaaa A/Δ tgaacacatttggatgatt	1810
TAP1	1	5' flanking - 673	agctaagagtcacaagcacc G/C ctttttccaccagccctggcg	1811
TAP1	2	5' flanking - 646	ccaccagcctggcgctgtg T/G tcccttcacggacacacttag	1812
TAP1	3	5' flanking - 563	ttgcaagcgtgtgctgtac A/C gggagacctccctggctccc	1813
TAP1	4	5' flanking - 236	gcttgcggcggcgctaac G/I tgtgtagggaagatcigccc	1814
TAP1	5	intron 3 + 408	aagaaactagggcacaagac C/I ctatagtcigaaactgcaca	1815
TAP1	6	exon 4 + 153	ccctcacatggtcacacctg A/G tcacctgacctgtcttttc	1816
TAP1	7	intron 4 + 289	gtattttttagcatccaag G/I ggcatagtcgtgtctctttc	1817
TAP1	8	intron 4 + 291	attttcttagcatccaagg C/G catagctgtgtctctttctc	1818
TAP1	9	intron 5 + 1139	ttccttcaggttaagactg C/I ggttctttgtgtccctcca	1819
TAP1	10	intron 7 + 375	gtctctgacctgtctttgc C/I gcttcttctatctctactcc	1820
TAP1	11	3' flanking + 71	agcgcacttttcagctcgg G/A tgtctctctcttttctatcac	1821
TAP1	12	3' flanking + 129	aactgcatacacttttccct T/C aagctttttaaattcctatga	1822
TAP1	13	3' flanking + 459	catcagggaggagccaggctc G/A tgtgacgtcagacagtgtcg	1823
TAP2	1	intron 3 + 8	ttctcttttggcaggtaggig G/A tgggcagctgggtccatttg	1824
TAP2	2	intron 4 + 104	cttcacccgtatgcacaggac C/I tggggatgcttttctcttgt	1825
TAP2	3	intron 10 + 219	gcagcagttgtctctctcc A/G tgggcagcccccgcaggtcc	1826
TAP2	4	intron11 + (317~319)	atgtgcccaggtagtatgt G/G/Δ tccatctattctctcttt	1827
TAP2	5	exon 12 + 19	agctgcaggagctggaattcc I/C gtgggagtcgacagtgctg	1828
TAP2	6	exon 12 + (356~357)	agggtgggtgggtgggtgg G/G/TGGTGGGTTGA ggcgtctgtgtccaggaaa	1829
OCIN1	1	intron1+6602	aggcgagccaggttatgtgg C/I gaaggataaggccctctccc	1830
OCIN1	2	intron1+6790	gacaaaaggagaaaaccttc C/I gtataggcaggttttgga	1831
OCIN1	3	intron1+14019	cacgtctccacclggggccc G/A ccatgtcacigttaaaccaca	1832
OCIN1	4	intron1+14136	ccggttttcttaagaaaagcc I/C ttctaaaggaccctcttia	1833
OCIN1	5	intron1+14266	agcttttccaaaagacactt G/I cggcacacataactccccaaa	1834
OCIN1	6	intron1+14412	cttggggcaaacggccactg C/I gttgtcatgtgctcttctgt	1835
OCIN1	7	intron1+15776	acataggagacactttcttc G/A gatctcagttatcagaacaa	1836
OCIN1	8	intron1+15817	ctgtgcttctcggaataagc A/G gactactctggactactgtaa	1837
OCIN1	9	intron1+15889	agagccagttttggagcccc G/A tctggcaagcaggcagcccc	1838
OCIN1	10	intron1+16063	accctgtctgtcgcagaat A/G aggtgtgatataataatgtg	1839

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
OC1N1	11	intron2+1105	atatctccacaagctcttg C/A gtacactgtccatgctttt	1840
OC1N1	12	intron3+1022	ctctgtcaagttgccagga T/C ggaatatattccaactctact	1841
OC1N1	13	intron3+1217	tcctcttctcaggaggaa G/A gagcgggcaagattttctt	1842
OC1N1	14	intron3+1596	aagccagagaagctctctcc G/A tgggaatgggaacaagggtg	1843
OC1N1	15	intron3+1720	ggagctccaagctccct G/A tgtgagcgggtgggcaggg	1844
OC1N1	16	intron3+2104	tatgagactogttgtgttg G/A ttctcaggctgaaagtta	1845
OC1N1	17	intron3+8323	ctttcccttttctaagt G/C tgatagtttgaactciaact	1846
OC1N1	18	intron4+926	tttttgaactcaaatia G/I actagacctcaggttgccc	1847
OC1N1	19	intron4+1055	caactgtctgacagatagc G/A caggtoaggtgggctcactc	1848
OC1N1	20	intron5+ (1197-1202)	caacaacaacaacaaca ACAACA/Δ ttggagtgcttaacacttc	1849
OC1N1	21	intron5+ (2071-2083)	gtctgtcattgtctatgc (T)11-13 caaaaaaagaactaaggca	1850
OC1N1	22	intron5+2781	tgatcattcttagaaaaag G/A acactcactttggagagga	1851
OC1N1	23	intron6+ (882-917)	tcctactctatgatggcagc (AC)15-18 gatgatctcagaactgta	1852
OC1N1	24	intron6+924	acacacacacacogatgat A/C gtcagaacttgtagatttag	1853
OC1N1	25	intron7+511	attattgatagtaataaaaa T/C acatatttcttaataaag	1854
OC1N1	26	exon8+124	ggtcaggaacatggcggttg G/A ggtcacatccacggcctcca	1855
OC1N1	27	intron8+3514	acacacacacacgaaacat G/A tatgaattctcaggaaaggt	1856
OC1N1	28	intron8+3902	aagcaagatgaggatcgtt T/C ttctctgtgtgagtaaagc	1857
OC1N1	29	intron8+ (4064-4089)	gtgaacataacttagttg (T)18-26 gagtctcatagccctgtgga	1858
OC1N1	30	3' flanking+115	aacaaatgattatatcag T/A attcctatccagaaaacctt	1859
OC1N2	1	5' flanking - 225	cgggcctagaggagcaggt C/I ggactggaccaccaagcct	1860
OC1N2	2	5' flanking - 124	gcctggcagagccgggcctc G/I ccaggctccaccagcagcgc	1861
OC1N2	3	5' flanking - 13	ggcgcctctgcctgccag C/G gggcgcgcccttggggccca	1862
OC1N2	4	intron 1 + 232	ggtagtcagtctggcctccc G/A tctgatggccactttgaag	1863
OC1N2	5	intron 1 + 314	atggccctgtgtgtccagga C/I ttactctagttgggttggg	1864
OC1N2	6	intron 1 + 5055	catgtgtacctagcagcat G/A tctgactgtgtatcacgtca	1865
OC1N2	7	intron 1 + 6437	gaagcttggcctcacaca G/C aggcggcacccttgcata	1866
OC1N2	8	intron 2 + (173-174)	tagtaagaagagcaacaaca T/C/Δ atcgaactccgtaattcttg	1867
OC1N2	9	intron 2 + 608	agcaggattattgtataatt C/A taaagcttttaactcaagga	1868
OC1N2	10	intron 2 + 4370	taattttatgatccaagt G/A cctctataatagatgtca	1869
OC1N2	11	intron 5 + 969	caccagaaagggtcctctg C/I gcaaaagtcaggcaggagt	1870
OC1N2	12	exon 10 + (1028-1044)	ttagcctctctgtttgtgtc (T)16-18 aaaaagaatcactctggca	1871
OC1N1	1	intron 1 + 7715	tagtccagracacacatgg G/I tctgtcttttgcctcct	1872
OC1N1	2	intron 2 + 97	ggtggagaacatgaccagtt G/A gaattactgcagaagctgc	1873
OC1N1	3	intron 2 + 797	gtggagttgtgtgacaact C/G tttaaaagagatgtggggagg	1874
OC1N1	4	intron 2 + 1768	cgtgaactggagaggtctg T/C gggcactgcgcgcgtgagct	1875
OC1N1	5	intron 3 + 1244	gcagatggtaaaggagcaga C/I gggaaagcagcaggtcaggg	1876
OC1N1	6	intron 4 + 865	agcgtccagtgtaggaaag G/I ctccacagggtggcaatccca	1877
OC1N1	7	intron 4 + 1028	gtcatctgtctctctccc A/G ctcttcattttttatgtac	1878
OC1N1	8	intron 4 + 1040	ctctcccaacttcttcatt T/G tatagtactattgtattat	1879

Table 1

Designation of Gene	Nb.	Location	Sequence	SEQ ID No
OC11	9	intron 4 + 1485	agcctgccttcctccctgct C/I gtccttgtgaacagggatc	1880
OC11	10	intron 4 + 1997	tgaggattacagcccaac G/A tgggaggcagcctgcact	1881
OC11	11	exon 5 + 9	tggtgtcgagggtgtgc C/I ggagtcctcgtgtgctgt	1882
OC11	12	exon 5 + 20	gggtgtcgggagtcct C/G ggtgtgtttatcacaaaa	1883
OC11	13	intron 6 + 379	gggaagtctcattctcat A/G tctaaacacctagagacc	1884
OC11	14	intron 6 + 2125	tattgacccaatctgttct C/A acaatgaatatgactgta	1885
OC11	15	intron 6 + (2935-2953)	tttctcatctggaggggc (T)18-20 cttcagtcctgacatcgc	1886
OC11	16	intron 7 + (6-7)	ttttatctcaccctggtaagt (TGGTAAGT) tggtaagtgtctgtttca	1887
OC11	16	intron 7 + (6-7)	ttttatctcaccctggtaagt tggtaagtgtctgtttca	1888
OC11	17	intron 7 + (1780-1781)	gtttcttttccctttttt (T) catggagaagaacagagaa	1889
OC11	17	intron 7 + (1780-1781)	gtttcttttccctttttt catggagaagaacagagaa	1890
OC11	18	intron 8 + 3247	ccaggccaacaattccatt G/I tcatggccacitggccaagg	1891
OC11	19	intron 8 + 10521	cccttaaccaatgaagcca G/A tggcagatccctcattctga	1892
OC11	20	intron 10 + 393	tcagattcttagtaacttt G/C ttcaaaaaattctttgaca	1893
OC11	21	3' flanking + 1755	tgaatgaigtgtttcaaatg T/C gtattaaaaatgtctctct	1894
OC11	22	3' flanking + 1799	ctttcttagaatctcttgg G/Δ caaaactcttgaggaaagcc	1895
OC12	1	intron 2 + 1329	tggcagcagaaggaagagg G/Δ ataaagtggaggcacaggc	1896
OC12	2	intron 2 + 1867	ccctgtcaaggtaagtact C/Δ attattctccccaaaggc	1897
OC12	3	intron 9 + (340-343)	cagcaggcccttaactctct C/C/Δ gctgattccaccttccctg	1898
OC12	4	intron 9 - 396	atcataatttattactttt A/G ttgtctagaatgatcaag	1899
OC12	5	intron 9 - 386	cattacttttattgtctaga A/C atgatccaagtcttgactt	1900
OC12	6	intron 9 - 86	atagaaaaatgctaaaaaa A/Δ gttttaaacaataaagg	1901
OC12	7	intron 10 + 1725	tgaagaggccttgaatcc G/A agcggaggctcacactcgc	1902
OC12	8	intron 10 - 195	caagataattttaggaataa C/I tctgtgacatgagttaica	1903
OC12	9	exon 11 + 328	gtttcttgagggtttttt T/Δ ccatcttgtattttttaa	1904
OC12	10	exon 11 + 427	aggcaacaataatagaaaa A/I gtgtgaaaaacagttaaagt	1905
OC12	11	exon 11 + 455	aaacagttaaagttggagag G/A agcatctattttctttaaaga	1906
OC12	12	3' flanking + 34	agaatgtatgtcaagaattt T/A agataggcctttcagtaaca	1907
NTCP	1	exon 1 + 307	tatggcatcatgccccctcac G/A gctttgtgtggcaaggt	1908
NTCP	2	intron 1 + 607	ccagcaccactccagata G/C gccagcccatctcagccac	1909
NTCP	3	intron 1 + 702	gcagaaatcagcaggctc G/A ctcctggagacgcagcacac	1910
NTCP	4	intron 1 + (3950-3966)	caacatccctaacaagcttgc (T)14-17 gagaataaggcatgtaaaaa	1911
NTCP	5	intron 1 + 9597	aagcacatattattcagct C/G tgagtgtcataattttttt	1912
NTCP	6	intron 2 + 4808	cctatggagaagcaactacc C/I ggggccacttgtctcagcag	1913
NTCP	7	intron 2 + 5032	acactggagactagcagag G/C cagctttcccccaggatca	1914
NTCP	8	intron 2 + 5046	gcagaggcagctttccacc A/I ggatcatatcaaatattgtg	1915
NTCP	9	intron 3 + (8-21)	gcctcaatggacggtagta (T)12-15 aagaagggtctcacctct	1916
NTCP	10	intron 4 + (484-495)	taataaacccagaataaag (A)10-13 gattctcaactctagttac	1917
NTCP	11	intron 4 + (728-754)	tgcactttaacacaatttt (A)25-27 caggacattcaaccacatt	1918
NTCP	12	intron 4 + 747	taaaaaaaaaaaaaaaaa A/C aaaaaacaggacattcaaa	1919

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
NTCP	13	intron 4 + 1339	coccatggaacactaaat C/A aaagcaacgtattctttgg	1920
NTCP	14	intron 4 + 1545	acacggacaagaaggta G/C atcaattgggggttgagggg	1921
NTCP	15	3' flanking + 559	caagacaatatagttttcgg G/A tatcagtttggcaaatgtgc	1922
PEP11	1	exon 1 + 25	ctgcaggagcacgtccgc C/T ggcaggtcgaggagccctg	1923
PEP11	2	intron 1 + 88	caaggccggagggcgga G/A ggtacgcggcgcggaagc	1924
PEP11	3	intron 1 + 106	agggttacgcggcgggga A/T gcggggcaccocgaagccc	1925
PEP11	4	intron 1 + 248	cgagttgcgactcctggccc G/A cccgccctggggcactgta	1926
PEP11	5	intron 1 + 326	tggagcggacagggaccag C/A gsgtgacggcagggcgga	1927
PEP11	6	intron 1 + 1238	tttagcatttccagcagatc C/T aatccgagagctgttagag	1928
PEP11	7	intron 1 + 3001	tottatctgagggaag C/T gtcagtaagaaaaagcagcc	1929
PEP11	8	intron 1 + 5673	tigggaagtggcacagccac G/C gggcacagggacagggcttt	1930
PEP11	9	intron 1 + 5679	agtccacagccaggggca C/G agggcacagggttccacag	1931
PEP11	10	intron 1 + 5917	aaattcacaaaatgtacttc C/T ataagaaggctcgttaaaag	1932
PEP11	11	intron 1 + 5966	ctaggcatttagaacttcta C/T aatctgcocctagtgacaag	1933
PEP11	12	intron 1 + 9255	tgttcattcagggcctcttc A/G gctatgatttttagatagtt	1934
PEP11	13	intron 1 + 10278	catgaccatgtaggcgga A/G aagcagccctgttagcagcag	1935
PEP11	14	intron 1 + 20251	agaagagccctgtgtttatt C/T agtgattgcaatgtgtggg	1936
PEP11	15	intron 1 + 20509	aaacacacctctgcatttg C/A gcittctaagatagcaatcc	1937
PEP11	16	intron 1 + 20532	tttctaagatagcaatcttg T/C tgacacaggtacaaatgaat	1938
PEP11	17	intron 3 + 55	agagcggaggtggccataac C/Δ agtctaactttgttcccc	1939
PEP11	18	intron 5 + 1720	atcctctcttactggaaa C/A aataaagctacaaaagaacc	1940
PEP11	19	intron 5 + 1790	gtactgttttatgttttcc G/A gatgtaaatattagatgg	1941
PEP11	20	intron 5 + 1860	agtttcatttgactatcac G/A ctgcattcctctgtgagctggc	1942
PEP11	21	intron 5 + 1943	aggccactgagggaaactg G/A ggaagaagagagggccttctac	1943
PEP11	22	intron 8 + 1478	tgtttcagatcttagtagt A/G catggaataggaccgttttc	1944
PEP11	23	intron 8 + 1898	ttaaatatttagtgtaaaag A/G aaacatagactcaatcttt	1945
PEP11	24	intron 10 + 388	ttaaatagtttagacatttt C/T gattttctaagaaaaactgc	1946
PEP11	25	intron 11 + 985	atccataaggtactcagtag C/T tggcctgtatgaagaactoa	1947
PEP11	26	intron 11 + (1022-1045)	ctcaaacaggggtagatttc (T) 20-24 gagtcaagagctcactctg	1948
PEP11	27	intron 11 + 1320	tttgagccactgcacotggc C/T aatttccigactttctatga	1949
PEP11	28	exon 16 + 107	tggagagatggtagacacttg G/C cccaatgtctcaagtaagta	1950
PEP11	29	intron 18 + 6048	tttgttgggtttttttt T/Δ gttgtgtgtttgtttgtt	1951
PEP11	30	intron 18 + (6141-6142)	tcactgcagcctccggcccc (T) gsgttcaagcaattatcctg	1952
PEP11	30	intron 18 + (6141-6142)	tcactgcagcctccggcccc gsgttcaagcaattatcctg	1953
PEP11	31	intron 18 + (6241-6242)	tatttttagtagagagggg (G) ttccaccatattggccagcg	1954
PEP11	31	intron 18 + (6241-6242)	tatttttagtagagagggg ttccaccatattggccagcg	1955
PEP11	32	intron 18 + 12102	gtgggaattctagctaaggg C/T cgtgtggatctgtctcaggt	1956
PEP11	33	intron 18 + 12203	gaccctgagtttaattcatag C/A cattttctccagcacctaa	1957
PEP11	34	intron 18 + 12307	gaaggttaaatattctttt A/G cactctgagggtgtacacta	1958
PEP11	35	intron 20 + 79	tcacaaacacttaggacata A/G tatgatttaactagagtgat	1959

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
PEP11	36	exon 23 + (348-370)	tcctttttctttttcttttc (1)18-23 gagacagagttttgctcttg	1960
PEP11	37	exon 23 + 790	ccacattggtcatcttccct A/G toacacaatgatgtatttt	1961
PEP11	38	3' flanking + 2	aaataaatttctgttcttaa G/A cctaagtgttcatgtatctc	1962
EPHX1	1	intron 1 + 110	tgcaaaatgtgttacttag C/T tttctagtcataaaatatig	1963
EPHX1	2	intron 1 + 143	aaatattgttgagctcttc G/A ctgtctggccagtcaccca	1964
EPHX1	3	intron 1 + 1097	aatccagagagagataga T/G tggaaattcaagggtggaca	1965
EPHX1	4	intron 1 + 1717	ttocaagaacagcagagggg T/C gctctggggcgtgttttc	1966
EPHX1	5	intron 1 + 1772	aactcgtatgtttctctcc G/T tctgggtctaaactgcagtg	1967
EPHX1	6	intron 1 + 2054	gaaatgtacaggcaacact A/G tggacacagaaagtagattia	1968
EPHX1	7	intron 2 + 1414	atttccaaaatctgtttggg G/T gtaactgaacacacttgggaa	1969
EPHX1	8	exon 3 + 174	taacctcaactcaagactaa G/A attgaaggtagtttggcaaa	1970
EPHX1	9	intron 3 + 6583	ctgtcaatccatgaagggg G/C ggcggggcactaaagggtgg	1971
EPHX1	10	intron 4 + 34	agagggttccataactgcccc G/A tctctgccaaagggtggccc	1972
EPHX1	11	intron 4 + 63	aagggtggcccggtgttcc C/T accaggctctctctcggcg	1973
EPHX1	12	intron 5 + 154	gcagtgccctgaggcacgttg G/A cttggatcctctctgtctgtia	1974
EPHX1	13	intron 5 + 276	tgttgaccaaagctciggga T/C agccctgacagaaactcccc	1975
EPHX1	14	exon 6 + 130	gattgtggagcigtgtiaacc C/T gtcaaggagaaaggtattctia	1976
EPHX1	15	intron 8 + 206	gggtgccttggtctccggggcg C/A cctcagtaacctctccocagt	1977
EPHX1	16	intron 8 + 353	tggccctccagaaaagaga A/G ggcctcagtgaggggagag	1978
EPHX1	17	3' flanking + 708	aggtgcagactatgaactc A/G gccctgaagagggtgagagag	1979
EPHX2	1	5' flanking - (523-522)	aaagtacattggatatgcccc (C) tccccggcccccaacacgg	1980
EPHX2	1	5' flanking - (523-522)	aaagtacattggatatgcccc tccccggcccccaacacgg	1981
EPHX2	2	5' flanking - 522	aaagtacattggatatgcccc T/C cccccggcccccaacacgtt	1982
EPHX2	3	5' flanking - 521	aaagtacattggatatgcccc C/T cccccggcccccaacacgtt	1983
EPHX2	4	5' flanking - 516	actggatatgccccctcccc G/C ccccccaacacaggtcttatg	1984
EPHX2	5	5' flanking - 515	ctggatatgccccctcccc G/C ccccccaacacaggtcttatg	1985
EPHX2	6	intron 1 - 74	tggctgtcttcacatgaata T/C gaacagtgctgtttccatg	1986
EPHX2	7	intron 3 + 72	gagcattaggctcagaatcca T/C tgaagtgaagctttgagatca	1987
EPHX2	8	intron 4 + 473	gtgtgtctactttaatct A/G caaaagggtgatigaatggag	1988
EPHX2	9	intron 5 + 276	caagatgggatgttcaagg C/T catctgaacctcaactttga	1989
EPHX2	10	intron 8 + 8	tctgtctctcccggtgggtg T/C gctgtcttcagctgtcttia	1990
EPHX2	11	intron 9 + 1573	atgtcatgaagactgatga C/T gatggacgctgcactgtctc	1991
EPHX2	12	intron 10 + 207	gaacaggtgggatgagct T/C gtttatttgtcttttaatga	1992
EPHX2	13	intron 12 + 911	tgaagagacctcacatgtc G/T catccacatactacagga	1993
EPHX2	14	intron 12 + 2425	atcttctcagctcagcaaac C/T gaggtcagagggttacc	1994
EPHX2	15	intron 12 + 2460	ttaaccccaactggcccaag G/A ccaggtacatgattgggtca	1995
EPHX2	16	intron 12 - 281	aagtccttcaagagattat T/C ataagtagtaccttctcatt	1996
EPHX2	17	intron 12 - 268	agattattataagtagtacc T/G tctcattataggaatatga	1997
EPHX2	18	exon 13 + 50	cttgatcgagcttcaaaa G/T cctcttcagagcaagcgtg	1998
EPHX2	19	intron 13 + 1739	tgtcgttaacagggtttica G/T atgagcatatttctcttgta	1999

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
EPHX2	20	exon 14 + 33	atgcataaagctctgtgaagc G/A ggaagagacatgcttggga	2000
EPHX2	21	intron 14 + 314	ggattgagagcttacctcta T/C ggggtcaacctogtgtatgc	2001
EPHX2	22	intron 14 + 878	attccottattccttcacac C/T gctgtcacatcattca	2002
EPHX2	23	intron 14 + 948	gcacagcctgggtatgaagc I/C gggcgicgaigtgcagctac	2003
EPHX2	24	intron 15 + 259	agagggttttcactacttt C/T agtcatggctcctcagagaa	2004
EPHX2	25	intron 16 + 459	tctcatttgtcaacagaa G/C atgagttccaatctctgtgg	2005
EPHX2	26	intron 16 + 645	gtaagtgaacacactgtac G/A tgcagacttctgcacagac	2006
EPHX2	27	intron 16 + 985	gtcattatcatcatatgacc G/A atgaaaatgaccaaactgca	2007
EPHX2	28	3' flanking + 12	aggtagccttacacatct I/C gcattggatggcagcattgt	2008
EPHX2	29	3' flanking + 374	tgttcacggagaatgcacgg C/T atgggatgaacctttccc	2009
EPHX2	30	3' flanking + 544	tagccacctgctttctccc G/A gcttccctagcagagtgg	2010
COMT	1	5' flanking - 1287	cgtatataattccattct G/A agtcagaataactagaaat	2011
COMT	2	5' flanking - 1217	tgtgagtatgggaaggga G/A cttttctgtgtgtcccc	2012
COMT	3	5' flanking - 503	cagggtctcaggaggacga G/A tgtgtatcctccattgtctc	2013
COMT	4	5' flanking - 425	gagaagttgggaagtctggc C/T agtggggcgggtgcctgttg	2014
COMT	5	5' flanking - 277	ccagcccaagtttccccc C/T tgggaagggggtactatttg	2015
COMT	6	intron 1 + 12058	ctggccatggaaaggagg G/A agggggcccgacggggcca	2016
COMT	7	intron 1 + 12070	agggagggaggggggcccg A/G cggggccacagttaaaggagt	2017
COMT	8	intron 1 + 18831	tgtgtatgttcttggtaaac C/T agcccttgtgtttacacatc	2018
COMT	9	intron 2 + 832	ctctcctttggccacccgt G/C actaccccactccgggcc	2019
COMT	10	intron 3 + 90	ggagaagctgttatccccc A/G ttccagggggtgggaacc	2020
COMT	11	intron 3 + 425	ccccagggtgggggttcgg I/G gattcagagaggcgactct	2021
COMT	12	intron 3 + 671	ggctctgtcttttggaga G/A gtggggggcgtgcctgggg	2022
COMT	13	intron 3 + 676	ctgctctttgggagaggtgg G/I gggcctgtcctggggatcca	2023
COMT	14	intron 5 + 75	tcagctcagcctctccaaa G/C agccaggcattccagtagag	2024
COMT	15	intron 5 + 310	accagacacacaggggcagaa C/I ggcacaggaccaaggagatg	2025
COMT	16	intron 5 + 346	agatggggtggggaaggcc G/A ctctggggccagcctgtct	2026
COMT	17	intron 5 + 3023	aaggcagcccgctgtctaa G/A gcttagggcattgtctcct	2027
GAMT	1	intron 1 + 429	ctcgaaagctgagctcagg G/A agacagctgtccccgggttg	2028
GAMT	2	intron 5 + 1411	ggtgacctgtgcatccccc G/A accagagagcaggtggccc	2029
GAMT	3	3' flanking + 626	cactgacctcttgccttga G/A agaaggcggctcctgtgt	2030
PNMT	1	5' flanking - 367	aagagtgaaatggctgcggg G/A gcttagagaaagagagatgg	2031
PNMT	2	intron 1 + 35	ctgaggcacaggacaaga G/I gctgtoggggagtgaagca	2032
HNMT	1	5' flanking - 211	cagagcagatgacagcttt C/I cgttaaagatttcacigtctg	2033
HNMT	2	intron 1 + 5409	aatatactatataattgg A/G acatttcattgtggcctagt	2034
HNMT	3	intron 2 + 2561	cacttgtcttgacaagaa A/G agaagcctacaagaaaag	2035
HNMT	4	intron 2 + 2895	caatcagaaatgaagaaa A/C ctccaagaaaaatttaagtt	2036
HNMT	5	intron 2 + 3977	accaacttggaaagttaaa G/A ttatgcattgtatgtatgt	2037
HNMT	6	intron 2 + 5296	ttacatagtgagtttggag I/C ccaggaattttatttcctt	2038
HNMT	7	intron 2 + 13317	caacctcatgaattcttag C/I tgggattgggtccctataaca	2039

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
HNMT	8	Intron 2 + 14682	gtatagagcaaatgagttc A/ Δ ggagagatttaaataccctta	2040
HNMT	9	Intron 2 + 15406	gtctatgcattcatgcatcc G/A tctaaccagctgtctaccta	2041
HNMT	10	Intron 2 + 28943	atgtgacttaaaccttcaggt A/G tatcaataccttgaatgt	2042
HNMT	11	Intron 4 + 49	cagaaagagacttttccaga A/G tatatatataaigaatatct	2043
HNMT	12	Intron 4 + (1942-1943)	tttgagaaaaatttaaggta (A) tctttatggccacattcca	2044
HNMT	12	Intron 4 + (1942-1943)	tttgagaaaaatttaaggta tctttatggccacattcca	2045
HNMT	13	Intron 4 + 2405	cctgtgacaaagcagataa C/A ctcatgcttttatttagtcca	2046
HNMT	14	Intron 5 + (80-81)	cctgtgtttgaagaagcctt (T) atatatatttgccttcaat	2047
HNMT	14	Intron 5 + (80-81)	cctgtgtttgaagaagcctt atatatatttgccttcaat	2048
HNMT	15	Intron 5 + 235	ctttcttttgggaaaatag I/C ctttgccttctatatagaa	2049
HNMT	16	Intron 5 + (702-703)	tacttacaggttgattttag (AT) acacagcagactctgtcttc	2050
HNMT	16	Intron 5 + (702-703)	tacttacaggttgattttag acacagcagactctgtcttc	2051
HNMT	17	Intron 5 + 749	ttacacacagaccatactt I/G aacacataatgtcacaaaat	2052
HNMT	18	Intron 5 + 1101	gtaggcagcctatcttgat I/G ataticataatcatacaga	2053
HNMT	19	Intron 5 + 1137	acagaaaaagatattgtagac G/A gaataacaatttcattgaga	2054
HNMT	20	Intron 5 + 1348	agggagcagtaaatgtcca C/G aagtaactlgagaactgattta	2055
HNMT	21	Intron 5 + 1673	caaaaagaaggagtaaaga C/G tcaacaatcagtttagctttt	2056
HNMT	22	Intron 5 + 2022	attttatttgggctttcta C/I gctctctctctaaagccta	2057
HNMT	23	Intron 5 + 2285	tgtcactacttaactcttaa G/C atccagagtaaatgatggag	2058
HNMT	24	Intron 5 + 4159	tccagttgaccagcaacc C/I tottatagagtagttttaa	2059
HNMT	25	Intron 5 + 4501	aatgatccacaaaattacta C/G toattgttttcttccaatga	2060
HNMT	26	Intron 5 + 5251	cacacacacacacacacaca C/G caaatggagcagccagaca	2061
HNMT	27	Intron 5 + 5802	gaaaagaataatctgctta C/I atcatgttgaaaaacaaagt	2062
HNMT	28	Intron 5 + 6189	tcaatttccacttctccta G/C agcatatctgcagttacct	2063
HNMT	29	Intron 5 + 6297	gtttggttcatctcttgag I/A taaattagatcttggaactt	2064
HNMT	30	3' flanking + 458	tatgtcactctcaagaactc C/I taaagacaaagagtcactt	2065
HNMT	31	3' flanking + 993	cigaaaatgaacactgaacc G/A ttaatcactatgatgtac	2066
HNMT	32	3' flanking + 1793	gtggagcacagcattttagg G/A ctgtatatttgccttattata	2067
HNMT	1	5' flanking - 228	ataatttctcagcagctc A/I agtgcctcctctggtotaca	2068
HNMT	2	Intron 1 + 44	ccccactaatgtgagtcata I/C agatggagtcctcagggcaag	2069
HNMT	3	Intron 1 + 149	ggataaaaacgaatatgtt A/G tagcattccacagtttaca	2070
HNMT	4	Intron 2 + 158	agataggcccatgtgtgtgc G/A tgttagtaaatgtgtgtac	2071
HNMT	5	Intron 2 + 433	gctgtagccatccagccta I/C agaacttggctgtgaggttg	2072
HNMT	6	Intron 2 + 10826	atcatctgacttgtaagttc C/I agttctgttgtaactcaagt	2073
HNMT	7	Intron 2 + 13630	atttcattgagggaagtcca I/C ggtagaagcagcgtctctagg	2074
HNMT	8	3' flanking + 71	ggctcagttgggtgggcccc A/G tggttcattcaggacgggac	2075
PEMT	1	Intron 1 + (297-299)	attgtgtgactcagaggtt tGI/ Δ cogtgttagcttttgggatt	2076
PEMT	2	Intron 1 + 817	tcatgaagcctgttaaggac A/G tctctgccccacagccttc	2077
PEMT	3	Intron 1 + 830	agggcacatctctgccccaa G/A cagcttctaataccagttctt	2078
PEMT	4	Intron 1 + 1035	gagttctcigaaggagctaa I/C accagttagttgttttgaaga	2079

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
PENT	5	intron 1 + 15/3	agtgccagggagagactaac C/I ggggtgtgaggggtggcgt	2080
PENT	6	intron 1 + 1759	gatttttctaagaagaa A/G gaaagaaacatacaacatac	2081
PENT	7	intron 1 + 2768	gcatctgtgtccacagg C/A gggcacctccaggattcag	2082
PENT	8	intron 1 + 2785	ggccggggcaccctccaggat T/C cagaagatgactccagtagg	2083
PENT	9	exon 2 + 162	agtcagcagacotctggc C/I gtggggtagctcctttcc	2084
PENT	10	intron 2 + 4598	cagtggtttttttttttt t/ Δ cttaattttttgtgtgtg	2085
PENT	11	intron 4 + 39	actgtccagacgggagiatc C/I cactgtgtgtgagcccccac	2086
PENT	12	intron 4 + 1317	acgtgccagctggcccca G/A cctctgacatgggctctg	2087
PENT	13	intron 4 + 1355	ctggagccaggctgcagccg A/C agtgcctggccatccttggcg	2088
PENT	14	intron 4 + 5925	gtccaggcactgtggcccta C/I gtggagatctccagtctca	2089
PENT	15	intron 4 + 6028	ggcagtggtccaaggaccag G/C atggacccctctcttcacc	2090
PENT	16	intron 4 + 6078	atcigtaccctcgggactc C/I acctggttcgtgcccacac	2091
PENT	17	intron 4 + 6089	cgggactctacgtggttc A/G tgccatcaccccccgcagat	2092
PENT	18	intron 4 + 6379	tcagggtccctccctccat G/A cctctcacccctgccccttc	2093
PENT	19	intron 4 + 7339	tgtaaagaatccigccaaga C/I ggcagatgcacacggggtca	2094
PENT	20	intron 4 + 7619	ctctgcacatgigtctccag A/G gaggaaagcatttgacagg	2095
PENT	21	intron 4 + 8858	ggcatgtgtgtgtgtgtgta T/G gtgtgtgagtgtgtcatgt	2096
PENT	22	intron 4 + 9029	ttcttgaccagaaagogtc G/A tctctgcccaggccctcttg	2097
PENT	23	intron 4 + 9056	gcaaggccctcttgcaattg C/I gggaaagcigagctgagctg	2098
PENT	24	intron 4 + 9512	ctagcttgggcagcagcatt A/G cctgtgtgtgtgtgtgcaact	2099
PENT	25	intron 4 + 9523	agcagaattactctgtgtgc T/C gctggcactggccctgtgtggg	2100
PENT	26	intron 4 + 9622	gacaagagtacacaaaggt G/A tctcgaaactgggtcagctca	2101
PENT	27	intron 4 + 10776	ccattctgggtctcttttg G/A aggtgaatgaatccatg	2102
PENT	28	intron 4 + 10912	tcgtcccaattgtctcaga G/C gtgcaacaaggcccttcagga	2103
PENT	29	intron 4 + 11590	ggacactggccctgagtcaga G/C gtgtgtgtctctcttcagcag	2104
PENT	30	intron 4 + 12090	ggccaggccaccctaccag G/C ctgagtcaccactgtccagc	2105
PENT	31	intron 4 + 12263	taccgccttccagatgga G/A cgggctgctcatgggactta	2106
PENT	32	intron 4 + 12448	tcgtgtccctctctctgtt G/A tagtttccgtgggtataaatc	2107
PENT	33	intron 4 + 12730	tggaccagtgccgccacca C/I ggccaaggacctgtgtgttc	2108
PENT	34	intron 4 + 13240	gggtccagggcacacacagcgg T/C cccagtacacctgtcgttt	2109
PENT	35	intron 4 + 13494	tcogtgaactcagagatgg T/C acctccctgcgaggtggggc	2110
PENT	36	intron 4 + 13817	aactctccctgtctgtcag A/G cagatcttgagacctggcc	2111
PENT	37	intron 4 + 14773	ccgccctgtcttcatgtccc C/I ctatgctctcactgcctgg	2112
PENT	38	intron 4 + 14951	gtcttgaggccctccacc G/A gggcctgggtggccctcaca	2113
PENT	39	intron 4 + 16896	gctgtgactgtcttggagac T/C gggctttggcgggcttgggtg	2114
PENT	40	intron 4 + 19439	ccaggagcccttgaggcagc G/A gggcttctcaaccacacac	2115
PENT	41	intron 4 + 19557	attttgcagcatgtcagt C/I cctttcataatgaagcaagg	2116
PENT	42	intron 4 + 20051	acagacatggggagccacg A/G catctgcagacgcatattgat	2117
PENT	43	intron 4 + 20816	tggactctctggcgtccatc C/I agccacttcagtgcgacgtg	2118
PENT	44	intron 4 + 21196	ggctggctggggccctggat C/G atogtgacagggcttttagtg	2119

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
PEMT	45	Intron 4 + 21528	acaggtagggagccgaggctc G/I ggaggtggccgggctgagc	2120
PEMT	46	Intron 4 + 21596	cgcctcccccgtctctggc C/I gtacgagaagtgccocact	2121
PEMT	47	Intron 4 + 22672	agcctccactgctctgtgg C/I tagggggagggggcgggctc	2122
PEMT	48	Intron 4 + 22713	tctaaagctgtctcttgt A/I ctgaaacaaacacactctt	2123
PEMT	49	Intron 4 + 23010	tgcggggcagcggggaggga G/A ggcgagtggtccccaagt	2124
PEMT	50	Intron 4 + 23588	gtcagggccctgcatccc C/I gcagcaagttcttggggcggg	2125
PEMT	51	Intron 4 + 23627	gaacttgccctgagccaggga C/I ggtgaggtgggacgccttc	2126
PEMT	52	Intron 4 + 23941	tgagggttgggactctaca G/A aggagatggactcacgggg	2127
PEMT	53	Intron 4 + 24091	gacactcttcactgtcagc G/I ctgagacagcccttgcct	2128
PEMT	54	Intron 4 + 25348	caggccagttggatctctac G/A tagagtgaagcatctcagc	2129
PEMT	55	Intron 4 + 25603	taagcagttaacactgatgc G/A tgatgaaaattccaaacgca	2130
PEMT	56	Intron 4 + 31540	ctccaggtagggcaggaaacac I/C gtgaggagcatgcaactgc	2131
PEMT	57	Intron 4 + 31637	gtgggtgggagccaggac G/A gtgagggttcaaggtgtg	2132
PEMT	58	Intron 4 + 31642	ctggggagccaggacaggga G/A gggcttcaagggtgttgt	2133
PEMT	59	Intron 4 + 35593	ggaggagctgaagagactgg G/A gctcgggatacagtgattca	2134
PEMT	60	Intron 4 + 35647	acttgaggcaacacacgac C/A tgtcgtgctgaggagagac	2135
PEMT	61	Intron 4 + 35862	tccagtgtgtgtctgtcc C/I cgtctcagccgagcaactcag	2136
PEMT	62	Intron 4 + 35882	cgtctcagccgagcactca I/G cggccagggtgctggactc	2137
PEMT	63	Intron 4 + 37141	ccacagccggatgcttga I/C actctcagctcagggtcgtg	2138
PEMT	64	Intron 4 + 38862	tgaggagacacotcagaca C/G caaggacgggcatgccaatgg	2139
PEMT	65	Intron 4 + 38872	acctcagacagcaagacagg G/I catgcatgggtcccgccag	2140
PEMT	66	Intron 4 + 39140	atgtctcaatctccctccc C/I gggaaatctaggcacaggctc	2141
PEMT	67	Intron 4 + 39635	caggccagagcaggtggg G/I cctcctcacaggagcaggcc	2142
PEMT	68	Intron 4 + 39713	actctgagcatgtgtgtccc C/I tctcttctccaggggcagca	2143
PEMT	69	Intron 4 + 40436	cctgtgtgtcttcggaccc C/A gaggcagacagaggagccct	2144
PEMT	70	Intron 4 + 47485	acaatgactgttgagccct C/I gaggagcgtgtcacgtgg	2145
PEMT	71	Intron 4 + 48131	actgggggatactgaatccc G/A cctcctgatgccagtgagc	2146
PEMT	72	Intron 4 + 48558	cacagtgtgaactgttaggc C/G acagccacatcttgcggag	2147
PEMT	73	Intron 4 + 48702	gaaatggggcggttoggga G/A gcaaaagcaggaaaggcagaa	2148
PEMT	74	Intron 4 + 50302	gcatgtgcatggcagaggc I/C gttccatctgagtgaggacc	2149
PEMT	75	Intron 4 + 54102	ggcgggtgtctctgcagcc A/I tgggtcctctggcagttct	2150
PEMT	76	Intron 4 + 54220	ccagggagacagatctctcc G/A ccagagctctcttctgctt	2151
PEMT	77	Intron 4 + 54371	gcagataatgtcagctggg G/A tgcattgtgtgtgtgtccc	2152
PEMT	78	exon 5 + 79	tggcctgtactctctaaagc G/C tcacatcctgtctctgaac	2153
PEMT	79	Intron 5 - 6796	ggaggagtcagctctcttac A/C gatgtggtctccagcttcc	2154
PEMT	80	Intron 5 - 6636	ttttctctctcacttttg I/C gttcagagcagaggtgtgc	2155
PEMT	81	Intron 5 - 6448	gttggcccaagctctgacag G/A accctcgggacacagctctcg	2156
PEMT	82	Intron 5 - 5218	ggagccctggtgaagaagc C/G ttacgacaaagccttgagg	2157
PEMT	83	Intron 5 - 4824	ggacagccgggggttgagc G/A gctgcatgaaggaggagg	2158
PEMT	84	Intron 5 - 4249	tcaccagagtgattctctcg C/A ggcagggtgctggggtagcc	2159

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
PEMT	85	intron 5 - 4230	gagcaggctgcctgggtag C/I cactggcggggtccatgag	2160
PEMT	86	intron 5 - 4182	ggagagtaaggggtggggg G/A cacttagcacagggaagctg	2161
PEMT	87	intron 5 - 3369	ccaggtagggccgtgtgcct G/C tggcctgtgtgtggccag	2162
PEMT	88	intron 5 - 2625	cagggaagctgggcccctgaa C/I gagcigggttttggggccac	2163
PEMT	89	intron 5 - 1200	attatgtgagcatgggaag A/I gcacatttgatcacacatgt	2164
PEMT	90	intron 6 + 606	gctgtgtagacggccacca A/G tgacctgatgatggcagca	2165
PEMT	91	intron 6 + 1229	tttggccaggaagggggac G/A gcaccagagagctcggat	2166
PEMT	92	intron 7 + 716	atggagatgtgtcccccgg C/G ggtcagaggaactcggctc	2167
PEMT	93	intron 7 + 1537	ctctgggggacgataagcc G/A cctccagaggacatcagcca	2168
PEMT	94	intron 7 + 1718	gggtccaggggtgtctgagc T/C ccccgccatgtaggaccca	2169
PEMT	95	intron 7 + 2695	ggcttgggggacccctggac C/I catttttagaanaacacctt	2170
PEMT	96	intron 8 + 140	ccagggtccaggtcagag C/I ggcctaggtagcttaacaatg	2171
PEMT	97	3' flanking + 179	tacttagggcgctcagggg C/I tcacctggccatggccatgg	2172
PEMT	98	3' flanking + 394	gatgacactgtcaticotaa A/G tgaatggcctgtgtgaccc	2173
ALDH1A1	1	intron 1 + 564	cattattcttcagccaagt T/C tgttgccattggagcagatg	2174
ALDH1A1	2	intron 1 + 710	gtctgagagtaactctgaa C/I ttgttcgttttcaacatgct	2175
ALDH1A1	3	intron 1 - 3868	ccctttttatccagaata C/G agcctaaacttcttctctg	2176
ALDH1A1	4	intron 2 + 2933	taagtatgtctactatatt T/C gatagatactatactata	2177
ALDH1A1	5	intron 2 - 1646	caatgttaactaatgaatg C/I gcaaatatgcactgtatatg	2178
ALDH1A1	6	exon 3 + 54	caggcttttcagattggatc C/I cogtggcgtactatggatgc	2179
ALDH1A1	7	intron 3 + 157	taggccccttaacattgaac T/G atttcaaatagtaatctgc	2180
ALDH1A1	8	intron 3 + 339	tgagtctctagaatgat G/A ttaggtttattcaagcattt	2181
ALDH1A1	9	intron 3 + 655	agcagtttagatgagtcagag C/A ataataatgttgggggaggg	2182
ALDH1A1	10	intron 3 + 735	gaagccaatttaacataaac C/A aataccaagatcaggtttca	2183
ALDH1A1	11	intron 3 + 863	gcagtagtgttaatcaaac G/A accattttattactcaaatat	2184
ALDH1A1	12	intron 3 + 1757	agatgacaagatttcttcta T/A ttcaaaaattccctagcaca	2185
ALDH1A1	13	intron 5 + 90	ttcttaaaaacagatggatg C/A ttatgtatttgtttaaatgtg	2186
ALDH1A1	14	intron 6 + 213	caggaagccaaacacaaagg T/C ttgggtcaaacacagtcacact	2187
ALDH1A1	15	intron 6 + 1323	ttttgaaattaaattcttata C/I tghtaacttttaaacitttta	2188
ALDH1A1	16	intron 7 + 638	gcaaaagaaagtggtgggaag C/A atactgtaccatgcacaaaa	2189
ALDH1A1	17	intron 9 + (1462-1463)	aatggaaattctatgttttt (I) gtgtgattattttatctatc	2190
ALDH1A1	18	intron 9 + (1462-1463)	aatggaaattctatgttttt gtgtgattattttatctatc	2191
ALDH1A1	19	intron 9 + 1757	tgatctagattttgtttct A/G taaatgaatagatccagtg	2192
ALDH1A1	20	intron 12 - 1383	aatcccaacttattactctcc T/G gagagotttcaagtgcciatat	2193
ALDH1A1	21	3' flanking + 40	ttttaagtaacaagtttgggt T/C acagtgatttcttcttgca	2194
ALDH1A2	1	5' flanking - 716	cagggtatccttcttgagc C/G cgaggcagggggactcgcga	2195
ALDH1A2	2	intron 1 + 314	cggctccogactgcoggggg G/ Δ aaggcgtgggaaccgcttag	2196
ALDH1A2	3	intron 1 + (664-675)	ttttgaactgaagaacttac (T)11-13 ataacgaagcttgacatctt	2197
ALDH1A2	4	intron 1 + 1370	gcctgacgcttagaagtttt A/G tttttatgagggtctctaaccc	2198
ALDH1A2	5	intron 1 + 1557	ggtaacgtttttcagaattta A/ Δ tttagaagctcttccagttc	2199

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ALDH1A2	6	intron 1 + 1934	taagctcttttagtagactt C/G taaattttttaagacaaga	2200
ALDH1A2	7	intron 1 + (1971-1980)	agcatagtgacagaagcta (T)9-11 aaacgtgaagagacaagot	2201
ALDH1A2	8	intron 1 + 2295	tactgtaagacaataagta I/C tgtttttgtctgtctaaac	2202
ALDH1A2	9	intron 1 + 2387	ttagggaccacatagagta C/T tacttaaaataaaigaccag	2203
ALDH1A2	10	intron 1 + 2841	aggaatgtgctttttaaac I/ Δ agatgggttagtcaaggag	2204
ALDH1A2	11	intron 1 + 3035	gaattttataattttgtata A/G ctagattataggaatacac	2205
ALDH1A2	12	intron 1 + 3319	aagagttatgtttttttt I/ Δ ctgcatctgattataagg	2206
ALDH1A2	13	intron 1 + 3474	tgtctttttattttatcat I/C taaactctgtttttctgggg	2207
ALDH1A2	14	intron 1 + 4186	cttccaaacctttacttaa G/C attgtctgttttggtoataa	2208
ALDH1A2	15	intron 1 + 4222	cataaattgcagtcacaaat A/G catgttaatatagaggacttca	2209
ALDH1A2	16	intron 1 + 4254	aggacttcaggtttttttt I/ Δ aaatacttttcaataactat	2210
ALDH1A2	17	intron 1 + 4397	cccttcacactacatggcct A/G tgttaacatgigaattatc	2211
ALDH1A2	18	intron 1 + 5935	aaotccagggttgcaaataga I/C gttctggtatttttaagtag	2212
ALDH1A2	19	intron 1 + 6206	ttttgaagccctctctagca I/G ttctttaattttttattga	2213
ALDH1A2	20	intron 1 + 9559	agataaattgatgaattatt C/T acitcigtctgtcatagat	2214
ALDH1A2	21	intron 1 + (9631-9632)	taaaaagaatttctaaaga (AAGA) ccttttttgaataactct	2215
ALDH1A2	21	intron 1 + (9631-9632)	taaaaagaatttctaaaga ccttttttgaataactct	2216
ALDH1A2	22	intron 1 + 12731	ctgaatatagaacctttcag T/A gtacottgacagacagtga	2217
ALDH1A2	23	intron 1 + 13442	cagtgctaaagatcacgc G/A gaatacaaaatgtttcatat	2218
ALDH1A2	24	intron 1 + (14173-14176)	tctaaaaataataataaata AAA/ Δ gaaaaataaagtttaagat	2219
ALDH1A2	25	intron 1 + 14586	actcattttattgttcaaac G/G cttcttcaaccttaggatat	2220
ALDH1A2	26	intron 1 + 14595	ttggttcaaaccttcttca A/G ccttaggatatgaattgagg	2221
ALDH1A2	27	intron 1 + 14711	gtttgagacattacttcta A/G ttaactgaagatgctagtt	2222
ALDH1A2	28	intron 1 + (15327-15337)	gaagacacagtagaagac (T)9-11 aacctagcaatactattga	2223
ALDH1A2	29	intron 1 + 17258	atcagtaacaatgtgttgggc A/G tacaacacttaatttataat	2224
ALDH1A2	30	intron 1 + 18277	taatacaaatcatttgaagc A/G tttaactattaaaaaacaacaa	2225
ALDH1A2	31	intron 1 + 18734	ctttgagacactactgcatt T/A taagtctgttaagatgtgg	2226
ALDH1A2	32	intron 1 + 19081	ttaatcacctcaactctttaa C/T gaatttctgtatttttcttt	2227
ALDH1A2	33	intron 1 + 21514	aatcaggataggggggttc G/A tictttatctgcacacaaat	2228
ALDH1A2	34	intron 1 + 21732	cattttaaaatagtgctta A/G taggacttggcgtttaaagt	2229
ALDH1A2	35	intron 1 + 21865	tggcataggtttaaaaatgt C/T tgtttaggactcttttcca	2230
ALDH1A2	36	intron 1 + 26282	taagaaggagagaaaaaaa A/ Δ ctaactgagacttttcagg	2231
ALDH1A2	37	intron 1 + 27805	ggatgatgtctacccaagaa I/C tgcacacttccagacagtac	2232
ALDH1A2	38	intron 1 + 28204	tcacttcatttttttaactgt C/G ctctctaaatgigtgttaa	2233
ALDH1A2	39	intron 1 + 28521	tccttgttacacttctttaa I/C cggggtatcagataactctc	2234
ALDH1A2	40	intron 1 + 49478	gaataaaggataggacat G/T ggtaagaccactttttccct	2235
ALDH1A2	41	intron 1 + 49834	gccttcaattttctcatgt G/T taatagagagaaaaacctgc	2236
ALDH1A2	42	intron 1 + 50351	gaotcaggtttcataagtt C/G agaaatttcacttggtgct	2237
ALDH1A2	43	intron 1 + 51181	tgtttattaccatagtagtic C/T gtaacacttggcgttgaact	2238
ALDH1A2	44	intron 3 + 654	ttaacctctcttgagtaaaa G/A gaatccttcagaaccagagg	2239

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ALDH1A2	45	intron 3 + 668	gtaaaggatcctcagaa C/I cagaggagtggtacggacc	2240
ALDH1A2	46	intron 3 + 712	catacactctgcctcgatt G/I cctgtcattctgtgagcca	2241
ALDH1A2	47	intron 3 + 1273	tattcatactgtgaaaaagg I/A gtttcaggtgaagaaattc	2242
ALDH1A2	48	intron 3 + 1743	ccacacctaatgagattcc C/I gttttaaacacictcaagct	2243
ALDH1A2	49	intron 3 + 2891	tgacataatactcattgt A/G gttttactaggaaactagac	2244
ALDH1A2	50	intron 3 + 2919	ctaggaaactagaccacactg G/A cagtactagaaatcttttta	2245
ALDH1A2	51	intron 3 + 3054	tgaaaggttcggggactta G/C tatctcacttctctcttcc	2246
ALDH1A2	52	intron 4 + 290	cattgtgctagattaggtgc I/C gggtaggtatgaagggca	2247
ALDH1A2	53	intron 4 + 380	ctcttgccctcctcgaaca I/C ataagatctactctttggaa	2248
ALDH1A2	54	intron 4 + 461	gattaaggctgatttcaagt G/I tottttaataattttctct	2249
ALDH1A2	55	intron 4 + 506	tcataattctcgaaggcc G/A tgaattactttcataatcta	2250
ALDH1A2	56	intron 4 + 1952	tgggtcccaactccactgt C/G attcattattaaaaacaaca	2251
ALDH1A2	57	intron 4 + 2079	ctctatttggcctaaaggta C/I ctgggttttcttttacttcc	2252
ALDH1A2	58	intron 4 + 2519	ttgggtcataagagctctct C/G catggtgtctcacaacagatg	2253
ALDH1A2	59	intron 4 + (2840-2851)	tttgtctctgcatacttggc (I)11-13 cacagtgaagtctggaatat	2254
ALDH1A2	60	intron 4 + 7231	aataggatacaataacacaa A/I gatagtgattcagactctaa	2255
ALDH1A2	61	intron 4 + 7958	taaaatcgtttttatgttta C/I taggtatataaaatttgccta	2256
ALDH1A2	62	intron 4 + 8090	ctgattttatcactgttta C/I agatgcttagtcatactca	2257
ALDH1A2	63	intron 4 + 12823	tgttagcctgtagctaaatg C/I ttttcaaatatgtgaacggt	2258
ALDH1A2	64	intron 4 + 12939	atagggtccacttttaaga I/C tttgtctacattttctctcc	2259
ALDH1A2	65	intron 4 + 14935	tattgatggaggtcttttta I/G aaatgacttttaccctctt	2260
ALDH1A2	66	intron 4 + 15321	gcatttgggtgtctgagaga C/I atatocagaataatgctatg	2261
ALDH1A2	67	intron 4 + 15412	tttcaagtttatttctgttt I/G tttttttttttttttttttt	2262
ALDH1A2	68	intron 5 + 1888	aatccaaacatctgtaacttt G/I tagtggacaagatttaigt	2263
ALDH1A2	69	intron 7 + 9166	gaaaagctacttttattcaaa G/A ataaaagtattttaagaaa	2264
ALDH1A2	70	intron 7 + 9914	aagctggagaaaatactagg C/I ttctctcaacagtgatttcc	2265
ALDH1A2	71	intron 7 + 18942	tttggaggagggaactaatcc G/A tgaactttaggtttatctctt	2266
ALDH1A2	72	intron 7 + 19820	ttccacctctatttttaggtt A/G ggggaggtggcttgctacag	2267
ALDH1A2	73	intron 7 + 19826	ctctatttttaggttagggga G/A gggcttgctacagtttttag	2268
ALDH1A2	74	intron 7 + 19913	cgtaaatcttcagttattt A/G tttaaaaataccagtttgaa	2269
ALDH1A2	75	intron 7 + (20110-20111)	catgattttatctctaacta (ACTA) tgcctaagtcacaaagattctgc	2270
ALDH1A2	75	intron 7 + (20110-20111)	catgattttatctctaacta tgcctaagtcacaaagattctgc	2271
ALDH1A2	76	intron 7 + 21857	acaatgaaataaagaagg A/I gaagagggaaggaagcagaga	2272
ALDH1A2	77	intron 7 + 21929	tacaagacacagcactcttt A/G actagtttacttgggaactct	2273
ALDH1A2	78	intron 7 + 23308	gggttgacttcggaaacct G/I tgggtttatacaaaagactag	2274
ALDH1A2	79	intron 7 + 23554	gacatttggtaaacaccagg C/I tgttttaggagtgctcctgtcc	2275
ALDH1A2	80	intron 7 + (23701-23703)	catctgagatttgcttctgt G/G/Δ tttaocaggttagtggtgtgc	2276
ALDH1A2	81	intron 7 + 26479	gatacatgaacaatttttt I/C atcctcatgatacttttcaa	2277
ALDH1A2	82	intron 7 + 26561	taaaggccacaatgcagiga I/C tgaatctccagttacattt	2278
ALDH1A2	83	intron 7 + 26662	tttctttagtctcttccatca C/I gaaactaaagctgtcttcca	2279

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ALDH1A2	84	intron 8 + 76	tttatatctccacttttgat G/A ggacactagcaaaagatat	2280
ALDH1A2	85	intron 8 + (700-711)	acatctcattcagtgatc (T)11-12 ccctccactgttgccagcc	2281
ALDH1A2	86	intron 8 + 724	ttttttccctccactgt I/C gccagccagagctgttcc	2282
ALDH1A2	87	intron 8 + 800	cagattctgaatttcagc C/A ccagcttggaatttgcagag	2283
ALDH1A2	88	intron 8 + 1251	gattctgtgaaaattgaga G/A gatctggcaacctgggectc	2284
ALDH1A2	89	intron 8 + 1627	ggccctcccccaggaaga G/A gtgagaacatggctgttcc	2285
ALDH1A2	90	exon 9 + 141	tgagcgggccaagagccg G/A tagtgggagtcctttgac	2286
ALDH1A2	91	intron 9 + 778	aacagcttgacagatccc I/C tgtagctgtgaaagttag	2287
ALDH1A2	92	intron 9 + 801	tagcttgtaaaagttagga A/G gtaagggttggtcacttc	2288
ALDH1A2	93	intron 9 + 868	tcgaaggctcgtgtactt I/C agtgggtgggaggccac	2289
ALDH1A2	94	intron 9 + 1338	aattttgctctttttact A/G tcaatacaattgctaaagt	2290
ALDH1A2	95	intron 10 + (227-229)	ctatgtcttaigtattia TTA/Δ gccaacagacaatcagaat	2291
ALDH1A2	96	intron 10 + 316	ctaaatgtgggtcactgga I/C gttaacaggagagagaatc	2292
ALDH1A2	97	intron 10 + 368	ctttacatctgtgcaagga G/A ggacaaggagcaaatcagcc	2293
ALDH1A2	98	intron 10 + 660	gttaacttgatgaatgt G/A gaaagcaggttaagggaatga	2294
ALDH1A2	99	intron 11 + 104	tgggaataccaaaagcaac C/I aaagttaccagaaaagggg	2295
ALDH1A2	100	intron 11 + 229	aaacttctaaaagaatacc A/G tgcagtcagattatgtgt	2296
ALDH1A2	101	intron 12 + 117	catacttcaacaacattt C/I gtggagacatgtactata	2297
ALDH1A2	102	intron 12 + 691	gatagggaagatcactgtga A/G ctggaaaaatctgggaacc	2298
ALDH1A2	103	intron 12 + 1934	catotttctagatgtcatg I/C ttgtttgtttgttctct	2299
ALDH1A2	104	intron 12 + 1973	ctacttaccoccaaacatg I/A ttctctttcttaaatgacc	2300
ALDH1A2	105	intron 12 + 2722	ccagagtgactccagtatac C/A tcactgcccaggaccacag	2301
ALDH1A2	106	intron 12 + 3855	cacttgaagaacacataat I/C gtgagttttgtatgtgta	2302
ALDH1A2	107	intron 12 + 4185	ttgttttaagcgaataaac I/C ataggacaggaagaacagcc	2303
ALDH1A2	108	intron 12 + 4991	acaggaaacttagacatgc A/G accactcccacccctcgtc	2304
ALDH1A2	109	intron 12 + (5018-5019)	cccacctccgtctgtgggg (G) aggaagcacactactgtcc	2305
ALDH1A2	109	intron 12 + (5018-5019)	cccacctccgtctgtgggg aggaagcacactactgtcc	2306
ALDH1A2	110	intron 12 + (5051-5052)	actgtcccaagaactaata (A) ctgaaccagtgctgcttgt	2307
ALDH1A2	110	intron 12 + (5051-5052)	actgtcccaagaactaata ctgaaccagtgctgcttgt	2308
ALDH1A2	111	intron 12 + (5300-5302)	ttaaagttttaaaaaactt CCI/Δ taaaaactactcatgagatg	2309
ALDH1A2	112	intron 12 + 5405	catcccaggaacttctgttc G/C caggtgataaactgcactc	2310
ALDH1A2	113	intron 12 + 5435	aactgcacctcccaggact C/A ccgtgcactcaaatgaagc	2311
ALDH1A2	114	3' flanking + 449	tttggcgggaaacaaattt I/C caagttgtaaagccaaatt	2312
ALDH1A2	115	3' flanking + 597	acctgggattctctgaccc A/C atctgttttcttttaocca	2313
ALDH1A2	116	3' flanking + 669	atagagactggaagtcacca T/C gtgcagttcacccgtctga	2314
ALDH1A2	117	3' flanking + 1122	cgtgtccactgagctcttc I/G gtcacaccccaattttgccc	2315
ALDH1A2	118	3' flanking + 2214	tgcagctgtaaaagaatac I/C gtaaatgtgacctactac	2316
ALDH1A3	1	5' flanking - 1425	cagttgttagccagccgatat C/I ggtaaggctgccccgtcgc	2317
ALDH1A3	2	5' flanking - 1379	ccattatccctttccccgg C/I ctacagttgtgcactccagc	2318
ALDH1A3	3	5' flanking - 1270	aacttacccctctatccagc T/A ctatccagaaggacaccagg	2319

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ALDH1A3	4	5' flanking - (1214-1213)	acggaggcctcaaacagga (55A) aaataagagagacccctcccc	2320
ALDH1A3	4	5' flanking - (1214-1213)	acggaggcctcaaacagga aaataagagagacccctcccc	2321
ALDH1A3	5	5' flanking - 1103	gcacagctttgtcaggagt C/I cgtgcctcggctttgttc	2322
ALDH1A3	6	intron 1 + 986	gccttaactttcccaccctt I/G gcttctcttgattttgt	2323
ALDH1A3	7	intron 1 + 1462	gtacaggatttcaaaatact G/A tatatagaaccagacagta	2324
ALDH1A3	8	intron 1 + 1661	cctgttgtttgttggtgc G/A caacotttgcagttaaagg	2325
ALDH1A3	9	intron 1 + 2360	agaggatagaagtcctctt A/G atttagaggcctcttctt	2326
ALDH1A3	10	intron 1 + 2516	tgaacaatatctttttga G/A tttagctgagtggcctgttg	2327
ALDH1A3	11	intron 1 + 2624	cctgagacaccttacagtc C/I gtcctgttccatgtcattc	2328
ALDH1A3	12	intron 1 + 3255	tttcatctttctacaattg G/C cccctcttctcgtgctgact	2329
ALDH1A3	13	intron 1 + (3643-3656)	gcttcagaggtttttgtggg (I) 12-14 aaatttatcaacttttaa	2330
ALDH1A3	14	intron 1 + 4265	caaaaggccctctcttttaa I/G atgacatttaataagacaatt	2331
ALDH1A3	15	intron 1 + 5187	caagatggataagacgtcac C/I taaggtccttagcatgtga	2332
ALDH1A3	16	intron 2 + 43	ctctaaagtaattcaattatg G/I atgaocaaagagataaggaaa	2333
ALDH1A3	17	intron 2 + 127	cagggcctgggttagctgg I/C gaattggcatgttggttctca	2334
ALDH1A3	18	intron 2 + (285-300)	agaaagggttttttttttc (I) 16-17 atcaattatttggacctgga	2335
ALDH1A3	19	intron 2 + 778	cgtgtcagagttaggttgg A/G tttttatcttggccatgatt	2336
ALDH1A3	20	intron 2 + 1216	actcgttagagtcacictctg A/C ctgggtgcacatccactc	2337
ALDH1A3	21	intron 3 + 81	accatgggttatgggaaaaa A/C gatcaggctccttggtttgt	2338
ALDH1A3	22	intron 3 + 236	gtcagcttcttgaccgaagt I/G gtgtgtataggaagattgag	2339
ALDH1A3	23	intron 3 + 1467	ggcccaggttagggaggga G/I atctctttctggccttga	2340
ALDH1A3	24	intron 3 + 1725	ccacatgttcccggttag A/G gtatctcctccacagggtaa	2341
ALDH1A3	25	intron 3 + 3777	gcagaagtagatgccccca A/G ttacgtctgtgcattactag	2342
ALDH1A3	26	intron 3 + 3829	caagtcactgggccttagc G/C tccgtgcctgcaccttgaag	2343
ALDH1A3	27	intron 3 + 4299	tcaatttccacagccacct G/A gccagcctggccgagaagga	2344
ALDH1A3	28	intron 4 + 84	agagcccccctgactgitt C/G cctaaaggcaccattcccaac	2345
ALDH1A3	29	intron 4 + 126	ccactccctctccaaaatggt A/G ctgccaattcttcttctaa	2346
ALDH1A3	30	intron 6 + (290-291)	tagagaattttcaggggggg (G) tcaaccaagaggaggccaaa	2347
ALDH1A3	30	intron 6 + (290-291)	tagagaattttcaggggggg tcaaccaagaggaggccaaa	2348
ALDH1A3	31	intron 6 + 705	aacagctgttgatgagccaa I/G ttccactttcttgggtga	2349
ALDH1A3	32	intron 7 + 56	ggggcgtgttatitgacacc C/I gtgagcttttcttctgacag	2350
ALDH1A3	33	intron 7 + 1107	gatctgttactctctcttgg A/G gacagacactgcctgttga	2351
ALDH1A3	34	intron 7 + 1610	aagagccacacagaaacc C/G cctactgtggcgtttggaaat	2352
ALDH1A3	35	intron 7 + 1820	caactgtagtgtgaggct I/C agaccaagatccccaggatg	2353
ALDH1A3	36	intron 8 + 963	gagaaggacagaggaggga C/I acaggctctcagaaggaaa	2354
ALDH1A3	37	intron 8 + 1824	accattcttatccactaagc G/A tatccccaagatcttattc	2355
ALDH1A3	38	intron 8 + 2384	cgctcccttcgcccctcccc C/A tccagtggacttggcagttgg	2356
ALDH1A3	39	intron 9 + 24	atccccctgtgtgtgaa A/C ccaatgtgtgttcttagggg	2357
ALDH1A3	40	intron 9 + 91	gcctaacagggtccctctccg I/C gaaaggaatgctgacctgtc	2358
ALDH1A3	41	intron 9 + 219	actgaggcatggaggagg C/G gctattccaggggcagaagg	2359

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ALDH1A3	42	intron 9 + 435	ccagacggagagagagcctggg G/A caggagaatgtatctccagg	2360
ALDH1A3	43	intron 9 + 1472	ttgacttttagggccagata C/I accgatttttccaaagagaa	2361
ALDH1A3	44	intron 9 + 2038	taacaatgtttcttccagg G/A cttccaggagggtgtggagt	2362
ALDH1A3	45	intron 9 + 2124	caaacagggtctccagatg G/A cataigccocaggccaggg	2363
ALDH1A3	46	intron 9 + 2154	agcagccaggaggagocicg G/C gttggcgagggccctgtgt	2364
ALDH1A3	47	intron 9 + 2197	ctttggccctccaggagg G/A gaagagcagctcagcagcat	2365
ALDH1A3	48	intron 9 + 2466	ttcttagttctctcatgttc C/I cttcagaatgttttctgttg	2366
ALDH1A3	49	intron 9 + 3655	gattgtcaagtggcagca C/I ggttiagccctctctccig	2367
ALDH1A3	50	intron 9 + 3954	gggtggcctttgacaaactg C/G tcagtagcgtgttcaaacg	2368
ALDH1A3	51	exon 10 + 88	tagaatgcggggctcagcc A/G tggaaagacaaggggctcttc	2369
ALDH1A3	52	intron 10 + 8	tgccaaagaggagggtacaag G/A gggctgtgcaaggctacga	2370
ALDH1A3	53	intron 10 + 307	ctctcgtatttttaacaca A/C cgggtccocagagtcagtcac	2371
ALDH1A3	54	intron 10 + 378	gtgggtttgccaggaaica G/A ttcaagaacctgtggattca	2372
ALDH1A3	55	intron 10 + 975	aatattgtctctctctcc C/G ctggtagttattatggaaac	2373
ALDH1A3	56	intron 10 + 1088	cagtccagagagccagggg C/I cttctccagatgactctgag	2374
ALDH1A3	57	intron 11 + 105	ttgtttacattgtattat A/G taccagccctgtctcagtg	2375
ALDH1A3	58	intron 11 + 274	agggtccagtaacctgtgcc I/G gggccctgtgtctgtacig	2376
ALDH1A3	59	intron 11 + 1088	cagtgccaggagccagggg I/A cttctccagatgactctgag	2377
ALDH1A3	60	intron 12 + 96	ctccaatctctgacacccc G/A tccccccacacccgcgc	2378
ALDH1A3	61	intron 12 + 1537	ggcccttggttggggccttt G/I tgtgctctcttttgagatt	2379
ALDH1A3	62	intron 12 + 1660	gtcccccctccacccctcagtc C/Δ tgcctttagtccatccctg	2380
ALDH1A3	63	intron 12 + 5642	tcgtgtcgaactgtctgttc I/C ctcatgccccctaggctggc	2381
ALDH1A3	64	exon 13 + 104	gggctctctctcaaacatc C/C gacgggggaatgtggcagat	2382
ALDH1A3	65	exon 13 + 281	ataggttgtctgtgaatcg C/I agtctgcttggggaggag	2383
ALDH1A3	66	3' flanking + 743	gtgagcaggaaactgttagga G/A aaggatatatttccctcattt	2384
ALDH1A3	67	3' flanking + 1145	gcctccagctacccccc A/G cctcaggagggttcattcca	2385
ALDH1A3	68	3' flanking + 1185	aacctagggtgtctgagaatc I/C gggtaggattaccagcaaaa	2386
ALDH1A3	69	3' flanking + 1600	acaccacgctgcaaatg I/C tgggaactgtcgggtggcaa	2387
ALDH1A3	70	3' flanking + 1847	caggagccctggcgctgccc C/G ggttctgtgaaatggcagtg	2388
ALDH1B1	1	intron 1 + 134	cgttgcaactgtaggactctc C/I ccacgtccctaatccatc	2389
ALDH1B1	2	intron 1 + 367	gcagttcccgcgatagaga A/G ggtccggctctcccgctgt	2390
ALDH1B1	3	intron 1 + 405	tgtgggtgaaactgtaaaaa C/I tgcctgtattcaggaggata	2391
ALDH1B1	4	intron 1 + 2002	cttcaactaatctgggaaca C/I tacactctgtttaatttca	2392
ALDH1B1	5	intron 1 + 2157	tggaaagctgaaaaaggat G/I ctgagacctgtgttggggg	2393
ALDH1B1	6	exon 2 + 192	ccgacgtcaacccctaccac I/C ggggaggtcatgtgggcacgt	2394
ALDH1B1	7	exon 2 + 265	cgtgaaagcagcccggaag C/I ctcccgctggggctcccat	2395
ALDH1B1	8	exon 2 + 329	ggggggccgctgctgaacc G/I cctggcagacctagtggagc	2396
ALDH1B1	9	exon 2 + 614	acttggcccgccactgcaca C/I aggcaacactgtgttatga	2397
ALDH1B1	10	3' flanking + 168	aaagtgaactgtgaagacc G/A tagagaaaaactctgttcc	2398
ALDH1L1	1	intron 1 + 252	cgcagcgcaggactggccc G/C ccgaggtatctggccggcgcg	2399

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ALDH1L1	2	intron 1 + 544	ctcaggggctgcgctgaagt C/I ccagctccagccactgcgct	2400
ALDH1L1	3	intron 1 - 6596	cagatttttttaagggtca C/G tagccactgaggatatttt	2401
ALDH1L1	4	intron 1 - 6513	caattatggtttatcttagg G/A acatgtttatagagatagta	2402
ALDH1L1	5	intron 1 - 6478	atagtattcttacttagctt G/A cattctaaatttgttccct	2403
ALDH1L1	6	intron 2 + 240	gtgcattataggctctaggag A/G agggctatagagaagccag	2404
ALDH1L1	7	intron 2 + 1326	gaggagagaccggagagga G/C agccagtccagtcaggccc	2405
ALDH1L1	8	intron 3 + 386	gtctactctaacctccact G/A ccgtctctcggcagcacaca	2406
ALDH1L1	9	intron 4 + 271	ggcccttcaatagacaag G/C aaggctaaaggcaggagctg	2407
ALDH1L1	10	intron 4 + 356	taggattctattctcttc C/I ttccctcgttgattctcctt	2408
ALDH1L1	11	intron 4 + 608	gtgctctgataggctgtctc A/C gtccatgtctctctgtggg	2409
ALDH1L1	12	intron 4 + 664	ggtcacatggcctgagggc A/G gggcggtcagtcacctggg	2410
ALDH1L1	13	intron 4 + 785	gaggcctgttgcctcctgcc C/G gaggacaggctggcaggagc	2411
ALDH1L1	14	intron 4 + 874	ccctggggagccctgtgtgt I/G tgggcgcagcagaagagca	2412
ALDH1L1	15	intron 4 + 1349	tcctcagagctctgtctc G/A tgggcccagactccttgct	2413
ALDH1L1	16	intron 4 + 1799	ctggggctgggaaggagca G/A ggtcctattgtggggatag	2414
ALDH1L1	17	intron 4 + 1815	ggcagggtcctattgtcggg G/A atagcaaccacitggatctc	2415
ALDH1L1	18	intron 5 + 272	aaagccacacaggagataag A/G gtggagttagggggcaaaa	2416
ALDH1L1	19	intron 5 + 301	tagggggcaaaacgtcagcc G/A tagtgcagcagcttcaag	2417
ALDH1L1	20	intron 5 + 343	caaggtgtgaggagcagtg G/A ggtctctggagcaatagcca	2418
ALDH1L1	21	intron 6 + 926	cctccctgggtactgtgtt C/I gggggcttctctcaccac	2419
ALDH1L1	22	exon 7 + 41	aacctgaacacttcagcc I/C ggtcccgaggaggagacgtt	2420
ALDH1L1	23	intron 7 + 305	cctagaatcagagagaagcc C/I tccaggaggccctgggttca	2421
ALDH1L1	24	intron 7 + 837	gtccggacaacaccctagtg C/I gtgtaccocccagccgtgtt	2422
ALDH1L1	25	intron 7 + 866	ccagcagctgttgtgtgt C/I ggctaccagagtagggcgt	2423
ALDH1L1	26	intron 7 + 884	tcggcctaccagagtagg C/I gtggcagtatgggcccctggc	2424
ALDH1L1	27	intron 7 + 1118	aatgttcagaaaatcatgc G/C aggcagtaaggccagagagaa	2425
ALDH1L1	28	intron 7 + 1168	aaagtaaggttcaggagaa G/A tctagcctggggctgtctcc	2426
ALDH1L1	29	intron 7 + 1451	caggccaccacagcatctg I/C ccagagacctgcaaaagacag	2427
ALDH1L1	30	intron 7 + 1489	caggaatgcaagaaggcaa I/C taagtgtcttaagaggagc	2428
ALDH1L1	31	intron 7 + 1579	tcagggtggaggaggagtg G/A gagagaccagctgaggcac	2429
ALDH1L1	32	intron 7 + 1691	ctgctcggccttagcttgc A/C gaaagctccagaacatctt	2430
ALDH1L1	33	intron 8 + 1632	tcaggtttgcatttgttcc I/C gtgcacattcagagttccag	2431
ALDH1L1	34	intron 8 + 1799	gtcaagtctctctctagct G/C ttccagctgcagccccctaa	2432
ALDH1L1	35	intron 8 + 1986	ggtagggggcctggccctgt G/I gcgttcaggagaaacgtcc	2433
ALDH1L1	36	intron 8 + 2002	ctgtggctgttcaggagagac A/G ctccaagagcctgtgtggg	2434
ALDH1L1	37	intron 8 + 2627	aaagagagagccgggggtg C/I ttgtccaggggttggggga	2435
ALDH1L1	38	intron 8 + 2646	gcttgtgccaggggttgggg G/A aactgttcttgattggcct	2436
ALDH1L1	39	intron 8 + 2925	ctgtgcctccataggtcc C/G agactgaatccttcagagga	2437
ALDH1L1	40	exon 9 + 4	caggtctgttcttcagaggt G/I ttggcagcggatcctccc	2438
ALDH1L1	41	exon 10 + 109	cagctgttagtgaggagct G/I cgaggggacatgaggagg	2439

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ALDH1L1	42	intron 10 + (671-672)	tggcattttctctgtctga (AG) gtctctttagccaccctaa	2440
ALDH1L1	42	intron 10 + (671-672)	tggcattttctctgtctga gtctctttagccaccctaa	2441
ALDH1L1	43	intron 11 + 8	caccgatgaagtgtgagtg C/A agggccagcacccttctcc	2442
ALDH1L1	44	intron 11 + 447	atagccaaagcagccctat G/A gtatatacacacagtgaacat	2443
ALDH1L1	45	intron 11 + 601	ctcaaatgagtcatttgag A/G ggagttaatgaaagactcat	2444
ALDH1L1	46	intron 11 + 639	catctgcaaaaggagagagg G/A ggggtaggagcacagacag	2445
ALDH1L1	47	intron 12 + 66	ctggcagttggcacgggggg G/Δ acttctgtgaggccctttt	2446
ALDH1L1	48	intron 12 + 478	ctattaaaaaagagagaggg A/Δ tttaagccaggagagaggg	2447
ALDH1L1	49	intron 12 + 684	tctggagagagagaggggtg C/I ggcagatgagccgagagaca	2448
ALDH1L1	50	intron 12 + 767	cgctagggagtgcaagcca A/G gtatggcgtgtgtcccaacg	2449
ALDH1L1	51	intron 12 + 1014	tcataggttcagtcacctt C/I gcaagccctcaattotaga	2450
ALDH1L1	52	intron 12 + 1359	ctggttcgctcagctcag C/I acagcagaggtgggtctag	2451
ALDH1L1	53	intron 12 + 1734	ggtagtcaggtgtgtgtg G/I tcagtagggccggccgagcc	2452
ALDH1L1	54	intron 12 + 1901	ttcagcagcctaactgaatt G/A acaatagaatagtcctgcaa	2453
ALDH1L1	55	intron 12 - 470	gggatggggccacctctcca I/C ctctggagatgccaggctca	2454
ALDH1L1	56	intron 12 - 334	aaggcagcctcttgggcca I/C gaccttctgtctgtcag	2455
ALDH1L1	57	intron 12 - 325	ctttgggcatgacctt I/C goigtctgcagcaagtgggt	2456
ALDH1L1	58	intron 12 - 221	gaaggagcagaggaagatc G/C aggaagagagagaggagacag	2457
ALDH1L1	59	intron 12 - 4	cccgcttccctcaccctgg I/C caggttggcagatctcatgg	2458
ALDH1L1	60	intron 13 + 34	tcacacccagtgtgagcca I/C gcagactggcccagccatat	2459
ALDH1L1	61	intron 13 + 58	gactggccagccatatagg A/G gaactccaggccagccacag	2460
ALDH1L1	62	intron 13 + 125	ccacaactgtgtgttgaa I/C gacacotgtttattagcttg	2461
ALDH1L1	63	intron 13 + 126	cacaactgtgtgttgaaat G/A acacctgtttattagcttgt	2462
ALDH1L1	64	intron 13 + 281	acotgcatccagacaggttc I/G ggtgtgacagagttcagtt	2463
ALDH1L1	65	intron 13 + 299	tgggtgtttacagagttca A/G ttccgtgtggtatccaggct	2464
ALDH1L1	66	intron 14 + 121	cattatcaaacagccatcc A/G tgtctctgtgagcaacctgc	2465
ALDH1L1	67	intron 14 + 167	gccaggcatgtgtgaagga C/I tigaggacaattgtatttaa	2466
ALDH1L1	68	intron 14 + 205	taatctcccagtaaacctgg A/C tcagtccaggtccacgttggg	2467
ALDH1L1	69	intron 14 + 219	caotggatcagtcaggtcca C/G ggtgggaacaagagataaac	2468
ALDH1L1	70	intron 14 + 2275	ttctcatgtgtatcatccg I/C cagacctctgtctccagcct	2469
ALDH1L1	71	intron 14 + 2431	agaatgactagtgatcaga C/G cttagagagcccccgcgg	2470
ALDH1L1	72	intron 14 + 2660	agccaagcatttcttgggga C/I accaagaaccttgccttgg	2471
ALDH1L1	73	intron 14 + 2740	aactcaccctcaccgtcca I/C gcagctccccagagagctca	2472
ALDH1L1	74	intron 14 + 2756	tcactcagctccccagag I/C gtcagagagcagagagagggg	2473
ALDH1L1	75	intron 14 + 2805	ccgcacagcaggaagaatggc I/C ccaagggagggagggacggg	2474
ALDH1L1	76	intron 14 + (3636-3637)	ttctctgggtgtgtgtggg (G) tgtgggcagctccctatc	2475
ALDH1L1	76	intron 14 + (3636-3637)	ttctctgggtgtgtgtggg tgtgggcagctccctatc	2476
ALDH1L1	77	intron 14 + 4347	tcaggacacaaacacagcagg C/I gtgagctgcctctcagaggg	2477
ALDH1L1	78	intron 15 + 380	atgtcccttatgtgtgttcc A/G agaccagagatcctgagag	2478
ALDH1L1	79	intron 15 + (1055-1056)	ggcacaatctgcagctactc (C) tccagctgtgtgtgtggct	2479

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ALDH1L1	79	intron 15 + (1055-1056)	gccacaatctgcagctactc tccagcttctctgctgggct	2480
ALDH1L1	80	intron 17 + 15	gaaagggtcgtggctgggg G/C tggagcagaggaggcctgc	2481
ALDH1L1	81	intron 17 + 44	aggagggtcgtctgtagtg C/T gcctgggacatggcagtgct	2482
ALDH1L1	82	intron 17 + 51	gtgtctgtagtgcgctgg G/A acatggcagctgtgtccaca	2483
ALDH1L1	83	intron 17 - (2224-2223)	ctgggtgcatctccagact C/T Δ gtcaataaaccacaatatga	2484
ALDH1L1	84	intron 18 + 140	agcgtcaatcaagcatagc G/A tggcaggcagcaggttagg	2485
ALDH1L1	85	intron 19 + (51-52)	tggttcacitgggacacagc GG/ Δ ctggciggaggsggttggag	2486
ALDH1L1	86	intron 19 + 399	tcaggtcagcctgggctga C/A catggacaggggccctggag	2487
ALDH1L1	87	intron 19 + 608	ccaccagatttaccacta A/G ccacacctgggaagagcagc	2488
ALDH1L1	88	intron 19 + (669-670)	atgggccatctcagtgcccc (C) ttgggaggtttgtaatgct	2489
ALDH1L1	88	intron 19 + (669-670)	atgggccatctcagtgcccc ttgggaggtttgtaatgct	2490
ALDH1L1	89	intron 19 + 1794	gtccctgtctgggggtcttaa G/C ggagtcagagacttccaca	2491
ALDH1L1	90	intron 19 + 1969	tgaicgggtgctgggttggg G/T cgacaggacagggagcagaga	2492
ALDH1L1	91	intron 19 + 1972	tcgggtgctgggttggggc A/G caggacagggagcagagaata	2493
ALDH1L1	92	intron 19 + 2083	tgagaagagcagaggsgtgt G/T cgggtgtctcagagtcacacc	2494
ALDH1L1	93	intron 19 + 2119	acacctgtctcagttagg C/T tgattagggtgcagagttt	2495
ALDH1L1	94	intron 20 + 1388	tiacctcttccacatccc C/T tggactgtgagttccatgag	2496
ALDH1L1	95	intron 20 + 1564	ccagggaacaggaacagtg G/A ggagccatcaccccgcctg	2497
ALDH1L1	96	intron 20 + 1873	tcagtttaaaacatattt G/A tgaatgtatgaaaaatatg	2498
ALDH1L1	97	intron 20 + 2427	actaggattggatggacttg G/C gatcagggtctcagctctgic	2499
ALDH1L1	98	intron 20 + 2458	cagctctgcacatgccaac C/T ggcggcccatcttccatcaa	2500
ALDH1L1	99	intron 20 + 2544	ccaggctggagagccatctg C/T agcgtgttgacacccatcac	2501
ALDH1L1	100	intron 20 + 2573	gacaccatcacacgggtgc C/T gtgaccgggtgcttatgtog	2502
ALDH1L1	101	intron 20 + 2574	aacccatcacacgggtgccc G/A tgaccgggtgcttatgtcgg	2503
ALDH1L1	102	exon 21 + 33	agccaactgttttcacagac G/A tggaaagaccacatgttcata	2504
ALDH1L1	103	exon 21 + 87	ctctggggcctgctcatgac A/G tctctcgggttctcgtatggg	2505
ALDH1L1	104	intron 21 + 323	ccatgcattaaacccccc C/G aacttgagttggttgaata	2506
ALDH1L1	105	intron 21 + 361	ataatcagagatttattta C/G tcacggcttaggttcaatga	2507
ALDH1L1	106	intron 21 + 478	gtcttcggggaggtcttctc C/A ggttggcagctcggggttg	2508
ALDH1L1	107	intron 21 + 1086	caaccaatcttgccccgg C/T gctgcagcccgccacatttt	2509
ALDH1L1	108	intron 22 + 235	ggccttggaggagacacitc A/C gcaaggagcacttggggcc	2510
ALDH1L1	109	intron 22 + 313	atagcagaggaggagtggcc G/A tgaagaccagggggccgtg	2511
ALDH1L1	110	intron 22 + 1214	tgggccaattatgaatcct G/C cccgagttccctcaagctccc	2512
ALDH1L1	111	intron 22 + 1226	tgaatctccccaggttccc I/G cagctccctcctaaacctag	2513
ALDH1L1	112	intron 22 + 1623	ggggtctccacatgtccaga C/G aaggcgtgggagctgggga	2514
ALDH1L1	113	intron 22 + 1698	attctggggagctctggccc A/G ctatccactgccagggataa	2515
ALDH1L1	114	3' flanking + 145	gagagacagaggagaatggg C/T gtgggtcatctcagggccca	2516
ALDH1L1	115	3' flanking + 239	tgggaacaggtgggaagac G/A gggattgagctgggtgacc	2517
ALDH1L1	116	3' flanking + 288	ggagagcagctcagactccct C/T agcagatggggcgggcccct	2518
ALDH1L1	117	3' flanking + 1513	agggtggctcagaccocgg A/C gtgcctcgtggcatgtccagc	2519

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ALDH1L1	118	3' flanking + 1707	cagtgaggacttgccctagca C/I gtgccacttataccagaaca	2520
ALDH1L1	119	3' flanking + 1709	gtgggacttgccctagca C/I gcaacttataccagaaca	2521
ALDH1L1	120	3' flanking + 1745	acagatgagtcacatgcaac C/I gcttctgagttccctttgt	2522
ALDH1L1	121	3' flanking + 1843	cigcctctcagccacagcc G/A ggcgcctcacactctccca	2523
ALDH2	1	intron 3 + 1766	aaattggtgctcactcgc C/ Δ tggccctctctctctctc	2524
ALDH2	2	intron 8 + 52	gaaggtagccctggccact G/C tctgtgtgctccagccgac	2525
ALDH2	3	intron 8 + 69	ctgtgtgtggtccagcc G/A atcctgtgccccccagtg	2526
ALDH2	4	intron 9 + 5197	gctttttagaacttgcc C/A atttccagttgtctgttg	2527
ALDH2	5	intron 11 + 114	gagctgggctcagtttctcc I/C gggtcagggtgtgctga	2528
ALDH2	6	3' flanking + 411	ggatagatttctgcccctc I/C tctgtgtgggttaacagct	2529
ALDH2	7	3' flanking + (432-433)	tctgtgtgggttaaacagct IC/ Δ tgttcatgcatttactttt	2530
ALDH2	8	3' flanking + 488	ccaataagaatgtgctgaa G/I gtttcatgcatttactttg	2531
ALDH3A1	1	5' flanking - 758	cigcagcgagggtgagggtgg C/A gggaagcgcctggtagagg	2532
ALDH3A1	2	5' flanking - 308	agtctggaagctgggaagg C/I tccatgccaggctgaatcaa	2533
ALDH3A1	3	5' flanking - 294	gaagagctccatgccaggct G/A aatcaatcagcagccccac	2534
ALDH3A1	4	5' flanking - 3	gtccctctgtgctcttgcc G/A ttccaggagccccagttacc	2535
ALDH3A1	5	intron 1 + 2323	actgtctctttcttcgga C/I ctttgggatgtttacaatac	2536
ALDH3A1	6	intron 1 + 2499	cccgatttgccactatactt I/C cgtgtatgtgttagcaggat	2537
ALDH3A1	7	intron 1 + 2943	caggggctagcaaggcagcc A/G agggccagggctctgagta	2538
ALDH3A1	8	intron 5 + 72	cacacatgactgcactcat G/C ctgtgggtccactctgagta	2539
ALDH3A1	9	intron 7 + 633	cgctgggggtctctgccc G/A tccactctgggtttttcc	2540
ALDH3A1	10	exon 8 + 36	cggacgtgacccccagtc C/G cggtagtcaagaggagatc	2541
ALDH3A1	11	intron 9 + (40-41)	gtgcctctctctgggcccc (C) agggctgggcacacaccc	2542
ALDH3A1	11	intron 9 + (40-41)	gtgcctctctctgggcccc agggctgggcacacactccac	2543
ALDH3A1	12	intron 9 + 322	cacagtgtagatccctggg G/ Δ acaccctagacattggccac	2544
ALDH3A2	1	intron 1 + 39	gggtgagggaactggccc C/I cgcgcgcacttgtagactg	2545
ALDH3A2	2	intron 3 + 2491	tgcgggaagaataatggcac I/A gctgagttctacatgcagtt	2546
ALDH3A2	3	intron 3 + 2595	ttctgtacatcaacttgtga I/A agattgagggccagttctgtt	2547
ALDH3A2	4	intron 3 + 2775	taocgcttggccctgacca G/A ggttaattcttcaataact	2548
ALDH3A2	5	intron 3 + 3424	aggcaattcgcacacaccc G/A cgtctcatgcattttccctg	2549
ALDH3A2	6	intron 3 + 3676	atgttaagagattgtgat G/A ttagacgttaggattttatt	2550
ALDH3A2	7	intron 4 + 481	tagaaaaaagagggtttcag G/I ttctctctgctaaatccggt	2551
ALDH3A2	8	intron 4 + 769	atcctcctttataccctgaac G/A tottgaggcagagccaaaa	2552
ALDH3A2	9	intron 4 + 796	aggcagagcaaaagccaca A/G ccaggagagctcgtaccgaa	2553
ALDH3A2	10	intron 5 + 254	attagttggccatactt I/G ttttaaaaaagttaataaat	2554
ALDH3A2	11	intron 6 + 137	aatcctgtttctgtgtatc I/C gtacctgtagctttgttat	2555
ALDH3A2	12	intron 6 + 923	aggctaataagtgtaagag G/A aagggtctatctgtattgc	2556
ALDH3A2	13	intron 7 + 331	tgtttttcgtatgttaatcc A/ Δ caggcattgtcgaataaca	2557
ALDH3A2	14	intron 8 + 643	tttagaacatgacactgcctg C/I cctccacatgtgagatga	2558
ALDH3A2	15	intron 8 + 666	ctccacatgtagatgact G/A actcagctttttatttctcc	2559

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ALDH3A2	16	intron 9 + 2129	tgatttcattttttaaaaaa G/I gttgacatttgaattcatg	2560
ALDH3A2	17	exon 10 + (1894-1895)	ttgctgtctactaataca CA/Δ tctgcttcaaaatgaacata	2561
ALDH3A2	18	3' flanking + 31	gtatttgcacattttttt I/Δ ctcatttttaaatcttagc	2562
ALDH3A2	19	3' flanking + 106	ggtgttgggggtgggtt G/A gtagctatagtaaatagggt	2563
ALDH3A2	20	3' flanking + 1630	aaaagacgttggaacacaa A/G ttaatcatgtcttaocgtat	2564
ALDH3B1	1	5' flanking - 1455	ctgcctgtccacaccacag C/I agcttgcacatcatcccccac	2565
ALDH3B1	2	intron 1 + 464	catgaatgactcttggaag A/G atcattcttagcaatggact	2566
ALDH3B1	3	intron 1 + 2269	aaatggaatccaaacagcaa G/C agacotccctcaccggtca	2567
ALDH3B1	4	intron 2 + 1349	actgagcttctgocaccgc C/I gctcgcggccttcattgaga	2568
ALDH3B1	5	intron 2 + 1820	tcogtgtgaagacaccttc C/G cccagcctcagtggtctagga	2569
ALDH3B1	6	intron 2 + 2046	aacctcaggogctgctcag C/G caggagacacgctggcccc	2570
ALDH3B1	7	intron 2 + 2939	aagcacgcactgaacatgga G/A tgagtgaagtgaacgaatgaa	2571
ALDH3B1	8	intron 3 + 7	tgcccaagaacotgttgagc C/I ggcgggctgagggcggcag	2572
ALDH3B1	9	intron 4 + 36	goccttcoggtcaccttc I/C cggctcaggcctcaggggcc	2573
ALDH3B1	10	intron 6 + (116-117)	attctctctctctctct C/I/Δ ggaccaggctggggcagctc	2574
ALDH3B1	11	intron 6 + 263	cagacctataogtgaccc I/C gctgccccccaggctcttag	2575
ALDH3B1	12	intron 6 + 1298	gtagacagagctggactcca I/G ccttgggtgataaggatcc	2576
ALDH3B1	13	intron 6 + 1411	gocagggtcacacagcagg C/I gggagagccaaaggggttig	2577
ALDH3B1	14	exon 7 + 185	acotgggtggcccccga C/I gtcctatgacgcccctgagat	2578
ALDH3B1	15	exon 7 + 339	tgogggcattgttggctgc G/A gctgtggccattggggggcc	2579
ALDH3B1	16	intron 7 + 249	ccagggtccaggggctcagc G/A tgctaagatgaactcccatc	2580
ALDH3B1	17	intron 7 + 277	atgaatcccatccaccac C/I ggcctatcctgaaagctgta	2581
ALDH3B1	18	intron 7 + 498	gaaccaaggctcggggattct C/I tggctccacagggccctgag	2582
ALDH3B1	19	intron 8 + 14	cagccagggtgggggtgcgc C/I gggctgggcaggggtcaggag	2583
ALDH3B1	20	intron 8 + 49	caggagcccgagtgaggcag C/I acaagtggtggcagcaggagg	2584
ALDH3B1	21	intron 8 + 111	tcaggactttgggatgtgg A/I cctcttggctctgtctctgc	2585
ALDH3B1	22	intron 8 + 3219	atcctgatggggctcaaggc A/G gctcagccacatcctgttc	2586
ALDH3B1	23	exon 9 + 33	gtgtgacccagaccagcag C/I gggggcttctgtgggaacga	2587
ALDH3B1	24	intron 9 + 946	tcocaggccccgagctgac C/A cttcttgggtggccgtggccc	2588
ALDH3B1	25	intron 9 + 1067	aggctcccaagcctgggtc C/I ctcttggccccccactct	2589
ALDH3B1	26	exon 10 + 137	cgcacatgcgcgcgcgcct G/A aggaatgctgtgtggccat	2590
ALDH3B1	27	exon 10 + 397	cgcctcccaaccatgagagcc G/A aggtggagggcatgggaac	2591
ALDH3B1	28	exon 10 + 1198	ctcttcccatgtctcat C/I ctcttggggcccatccatc	2592
ALDH3B1	29	exon 10 + 1475	cagggttgagacctgatttc G/A totctgtctctgtgctga	2593
ALDH3B1	30	3' flanking + 15	ctgggaactacttacatctc A/G gtgatttcttctgtgcat	2594
ALDH3B1	31	3' flanking + 60	caacaggaactctggaacaa G/C ccttggcgttggtaacaat	2595
ALDH3B2	1	intron 1 + 98	agggaggggatgtgtccc G/A tggccgttgggtcagggggc	2596
ALDH3B2	2	intron 1 + 157	atggctgcaggggccatggg I/C acggggcttgcagggagag	2597
ALDH3B2	3	intron 1 + 354	tctgtgaacagaagaagatt C/G ggtcgggggacacagggctg	2598
ALDH3B2	4	intron 1 + 851	tatgaacaggtccatcaggcc I/G cacccttcctgtgtgttat	2599

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ALDH3B2	5	intron 1 + 894	ctagcatctgccccacag /G gctttgcacacgttggttc	2600
ALDH3B2	6	intron 1 - 463	aaagaacctccagttccct C/G gtttagtcccaagaaggagg	2601
ALDH3B2	7	exon 2 + 61	gccttaactgaggcgac G/A cggcggcgagttccggcg	2602
ALDH3B2	8	intron 2 + 8	ggacctgcataaagtgaggcc A/G tggagagtgggcccgccag	2603
ALDH3B2	9	intron 2 + 23	ggccctgagagatggccc G/C ggcagggtggagcagcgt	2604
ALDH3B2	10	intron 2 + (180-181)	ttcaacttcgaacactaca (A) gccacctgtgatcaggct	2605
ALDH3B2	10	intron 2 + (180-181)	ttcaacttcgaacactaca gccacctgtgatcaggct	2606
ALDH3B2	11	exon 3 + 72	gactaagctcaagaacct /G caggcttgatgaaggatga	2607
ALDH3B2	12	intron 8 + 375	ctgagcatctcaacctac C/T gtcgcactcaaggctgcg	2608
ALDH3B2	13	intron 8 + 463	aatcaccocatggacccc G/A accgtcactgagagggtgct	2609
ALDH3B2	14	exon 9 + 33	atgctggagcggaccagcag C/A ggcagcttggaggcaatga	2610
ALDH3B2	15	exon 10 + 428	agggtcctcacacccca C/T cctcccaattccagocctt	2611
ALDH5A1	1	5' flanking - 1303	gaaatgattaaacttact G/A ttatcactctgccatagt	2612
ALDH5A1	2	5' flanking - 301	gtgaaaaggtgacagcagtc C/T gcagggtgcatctactggcga	2613
ALDH5A1	3	5' flanking - 221	ggctgcgcagggagagaagc C/T ggcggcgcttagggcaagg	2614
ALDH5A1	4	5' flanking - 175	aggcggcggcggggtgcag C/G gagaagaacggagagagg	2615
ALDH5A1	5	5' flanking - 174	ggcggcggcggggtgcagc G/A agaaagacggagagagg	2616
ALDH5A1	6	exon 1 + 106	ggcgctgtgtccctgcctcc G/C ggcctggccggccggccggcc	2617
ALDH5A1	7	intron 1 + 326	ctaaacgttggaggggcgagg G/A agaaaggaggagggtgtcag	2618
ALDH5A1	8	intron 1 + 5551	gtctgtacaaaaaaatttt /G ttttaattagcagcagcatga	2619
ALDH5A1	9	intron 1 + 5555	gtacaaaaaaatttttt /Δ aatiagcagcagcatcat	2620
ALDH5A1	10	intron 2 + 306	gttttgggtgttttttt /Δ aaactgtttttgtacattt	2621
ALDH5A1	11	exon 3 + 107	cggagacattatocacccc C/T ggcaaggacagggggggcc	2622
ALDH5A1	12	intron 3 + 201	gtggtggcagtgagtggat G/T atgcatttttaagtccgtga	2623
ALDH5A1	13	exon 4 + 42	atcacccggaagtgaggcc C/T gccctggcagcggcgctgtac	2624
ALDH5A1	14	intron 4 + 2306	atcgtgttataaatcagtt /C tctaggtataaaatccttg	2625
ALDH5A1	15	intron 4 + (2334-2346)	tataaaatccttggcgcaca (I)11-13 acttgattatcctaagtga	2626
ALDH5A1	16	intron 4 + 2456	tataagtaacttttttt /Δ acctagatacacaaaagtgt	2627
ALDH5A1	17	intron 4 + 2501	tttggttttttcccccctt A/G totttaagaacaaataatgt	2628
ALDH5A1	18	intron 4 - (64-46)	atctattattttctttt (I)16-18 cagtttggtaaatgttggc	2629
ALDH5A1	19	intron 4 - 27	ttcagtttggtaaatgttg G/C cacatgtttgtgtttctct	2630
ALDH5A1	20	intron 5 + (4621-4624)	tttgaatagataaacactta C/TΔ tatgttgaataaataagac	2631
ALDH5A1	21	intron 5 + (4677-4678)	accatgacaagttcacctt (C) acccaaacctgactcactc	2632
ALDH5A1	21	intron 5 + (4677-4678)	accatgacaagttcacctt acccaaacctgactcactc	2633
ALDH5A1	22	intron 7 + (432-443)	aaaaaatgattttaaaggc (A)10-12 tgaatacaaaaaagtcattt	2634
ALDH5A1	23	intron 7 + (3243-3244)	capctctgtgtgtgtgt G/TΔ ccccaaacacactgtcgtga	2635
ALDH5A1	24	intron 7 + 4987	tttttgaataaagaaaaaa A/Δ tggactagtattatgttttc	2636
ALDH5A1	25	intron 8 + 2717	gatcaactggaactcacagg C/T gtgttaggagacgtgcagcc	2637
ALDH5A1	26	3' flanking + 2711	cagtggatgcttgggaag G/A agccagcatgtgaatgatg	2638
ALDH5A1	27	3' flanking + 2777	gtccatgggtggtggttata G/A aatgtttgtaagctgaact	2639

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ALDH8A1	1	5' flanking - 1303	ctctaaagcagaacaagag G/C aaagcatgggagatatacca	2640
ALDH8A1	2	5' flanking - (1273-1270)	ggagtatacaaaacaactt AAT/Δ gttacttgaatgacttgca	2641
ALDH8A1	3	intron 1 + 437	tgcattgtccctccctcccc A/T cctacttcaatcactcogtgg	2642
ALDH8A1	4	intron 1 + 835	gttccacccccaaaaatcagc I/Δ cttctagtgctacacacct	2643
ALDH8A1	5	intron 1 + 1294	atattcttctgctcgatcct I/C gttctgttctagtatcttt	2644
ALDH8A1	6	intron 1 + 1447	gagtcattggaacaccttaag A/G aagtatittgtctctttcca	2645
ALDH8A1	7	intron 1 + 2536	agtcttgcaactctcttcta I/C gttaggcactgacataggt	2646
ALDH8A1	8	intron 1 + 2703	caggagagaagaggttccct G/T ataaaggatatagcaagtag	2647
ALDH8A1	9	intron 1 + 2802	gcaacaatgctaattgggigt I/C tolttaggaatgaagaaaag	2648
ALDH8A1	10	intron 2 + 2333	gtttgtttgtttgtttgttt G/Δ ttttttcagccaaactgtaa	2649
ALDH8A1	11	intron 4 + 138	gactctccctctgtaactgc A/G totctcagttctattctt	2650
ALDH8A1	12	intron 4 + 200	aaagagaacattcttgcct I/C aatttctatttgtgtctt	2651
ALDH8A1	13	intron 5 + 291	ggcaagtcagtgtaacctgc G/A ccccttcattggcctgaacc	2652
ALDH8A1	14	intron 7 + 209	tcccggttcaagcgattct C/A ctgcctcagccctcccgagta	2653
ALDH8A1	15	intron 8 + 287	gcctctgagcagcttggac C/T acaggtgaggccacacct	2654
ALDH8A1	16	intron 9 + 877	gatatcaaatataaacata C/T agacatatitggaggcctaaa	2655
ALDH8A1	17	intron 9 + 885	aataataacatacacacata I/G ttggaggcgaagaggagttaa	2656
ALDH8A1	18	intron 11 + 40	ttttgtcttttctttaaaga A/C atttctttaaagatattcag	2657
ALDH8A1	19	3' flanking + 520	ctgcgaagttttcttttagc C/T cotcttttatccacaatac	2658
ALDH8A1	20	3' flanking + 1026	cgtgttgtoagcgtgggtct I/C gaactcctgacctcaggtga	2659
ALDH8A1	21	3' flanking + 1035	caggctggctctcgaactcct G/C acctcaggtgatccgctgc	2660
ALDH8A1	1	5' flanking - (837-836)	gctgaacattgttaatat (AT) tcattagccaattgtgttcc	2661
ALDH8A1	1	5' flanking - (837-836)	gctgaacattgttaatat tcattagccaattgtgttcc	2662
ALDH8A1	2	5' flanking - 702	gggatctgaagccttgccta C/T atgtgtcacacatgtttttg	2663
ALDH8A1	3	5' flanking - 642	gcacatctaggagaagtga G/A cagccactgtggcccggtt	2664
ALDH8A1	4	5' flanking - 84	atgctctctgagagcgtcag G/T tgcctccacattcactga	2665
ALDH8A1	5	intron 1 + 5437	gcattggtgaaatgagcg I/C gttctttgttttctatgtga	2666
ALDH8A1	6	intron 1 + (5836-5855)	gtgagaatccatataaaaa (CAAAA) 4-5 atgaggtgtgtgagacctg	2667
ALDH8A1	7	exon 3 + 146	cactacacaggtgcggggccc G/T gtggagtggtgtgagtgctg	2668
ALDH8A1	8	intron 4 + 1033	aggtctttttgtatgtcac C/T ccacggccaggcagcagtg	2669
ALDH8A1	9	intron 4 + 1037	ctttttgtctatgtcacccca C/T ggccaggcagcagcagtgctg	2670
ALDH8A1	10	intron 4 + 1662	ttctctctgagaccagaac G/A totgtatagatgatgaggtta	2671
ALDH8A1	11	intron 4 + 2046	agctctgggcaatttaaacag A/C cttagacagataaaacttcctt	2672
ALDH8A1	12	intron 6 + 1146	ttttccagatgcagaagact C/G ccttttctctctctctctg	2673
ALDH8A1	13	intron 6 + 1744	ttcttcttcttcttctt C/T tttcttttttaacatgtact	2674
ALDH8A1	14	intron 6 + 9802	tgaagtgaattcttaacttt A/T ctgtttattagctctatgaa	2675
ALDH8A1	15	exon 7 + (1089-1098)	tacagtgcagacctgtttt (A) 9-10 tgcgtcaaaacccaaaaataa	2676
ALDH8A1	16	3' flanking + 848	ctcagctgagtcctccctgac I/C ttaatcaacttttagtgaagaa	2677
ALDH9A1	1	exon 1 + 121	actgtgtgggtatggcggg G/A tgggtgggagaatgtgtgt	2678
ALDH9A1	2	intron 1 + 67	cgcggatttcccgccagcc C/G ccgttctgtgtgtgtgcag	2679

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ALDH9A1	3	intron 1 + 103	tgacgcttgacitgagcac A/G agacagtgacagtggagagt	2680
ALDH9A1	4	intron 1 + 1818	gaatttttgagaaaaaaa A/Δ tgttccttttaggttgctt	2681
ALDH9A1	5	intron 2 + 5891	tcaggacaggaaagtaaga G/A gtttacatttctaatttct	2682
ALDH9A1	6	intron 2 + 6398	atcaaaaaaacctgtctgat T/G atcgtctctgaacctgct	2683
ALDH9A1	7	intron 2 + 9677	atgaccttgagtttgct A/G tttctttgtttttcttgct	2684
ALDH9A1	8	intron 2 + 9991	ggagagaaggaggacctac C/T ctggcttctaattttcat	2685
ALDH9A1	9	intron 2 + 10198	ttgtcagagacatcttgat A/G atccttaactactatcag	2686
ALDH9A1	10	intron 2 + 10256	ttagtataaacctttttt I/Δ gtaaggatggagaataatag	2687
ALDH9A1	11	intron 2 + 11382	catattcaattctttatgt T/G ctttagaccaagaaggca	2688
ALDH9A1	12	intron 2 + 11455	taaacctttaagctcatat C/T ggacctctatigaattct	2689
ALDH9A1	13	intron 2 + 12044	atttaagtgaaagctattt C/T tagttttaaaaaatigagcag	2690
ALDH9A1	14	intron 3 + 334	ctatttagcaaacctttttt I/Δ gacagtgataaagtttca	2691
ALDH9A1	15	intron 3 + 368	gtttcaacaattgatattg G/Δ aaggttgtagggcctagga	2692
ALDH9A1	16	intron 4 + 191	cctcaaggagcctatagtt T/A aggttgtaacacaatcatgic	2693
ALDH9A1	17	intron 4 + 557	tagaaaaattgtaattgta A/G aaagcattactgttaggaca	2694
ALDH9A1	18	intron 5 + 830	agttcaagatgatttttag G/C ttcaggcctagttgactta	2695
ALDH9A1	19	intron 5 + 838	atgatttttagtttcagg G/T ctattgacttagcatgcaa	2696
ALDH9A1	20	intron 6 + 120	agaaaagttgcacaaatagt A/C caaagaattcccattgacct	2697
ALDH9A1	21	intron 6 + 2569	attaaatctgtttaaata I/G ttttttggggagaggacac	2698
ALDH9A1	22	intron 8 + 1414	cagatctcaaaaaattagc T/C agggatgtgtgtgcacatg	2699
ALDH9A1	23	intron 9 + 664	aaagttcacattttttttt I/Δ ataacttcattggtcaagagc	2700
ALDH9A1	24	intron 9 + 2170	taatgcacacattttttttt I/Δ cttcataggggacatocacag	2701
ALDH9A1	25	exon 11 + 587	aaacaaaaaaacaaaaaa A/Δ ccttgctcctttataggctc	2702
ADH1	1	(5' flanking region -55)	atcatgtgtggactggaat C/T eggtgttattcaagcaaaaa	2703
ADH1	2	(intron 1 268)	acatttgcgtaaaagcgata A/G ttatttcaagctaatcatg	2704
ADH1	3	(intron 3 443)	aatgga g/c gctaatgctat G/A gctgaatgagcatgaccttt	2705
ADH1	4	(intron 6 56)	tacaacttgaggagatgcat T/G aggcgcagaaatataatgtt	2706
ADH1	5	(intron 8 74)	gtctagcagaaaatgaaaag G/A tggaaaggatgagaaaaatta	2707
ADH2	1	(intron 2 340)	ctatttttaaaagctgcat T/C cttacataagacttaaatat	2708
ADH2	2	(intron 3 91)	aaggcaatgagagacgaaaag T/G gottgcacaaggtcacccgg	2709
ADH2	3	(intron 3 205)	atgtattgtacccttcaacc A/G ttatgtacagatatactact	2710
ADH2	4	(intron 7 108)	acaattgacaagcaagatt T/C tgaacacaaatcaaaaaataa	2711
ADH2	5	(intron 3 1721*1723)	aotgcatagaaaatttaagaa GAA/Δ ctgttttattctctctccag	2712
ADH2	6	(3' untranslated region 2305~2306)	gttaatgctttccactctc AG/Δ gggaaggatttgcatttga	2713
ADH3	1	(5' flanking region -254)	tgaagagaagaagcagaaa C/G ttgagagaggaggaggaagag	2714
ADH3	2	(intron 2 355)	tatgcatcttcctatattat A/G caagacaaaaatttttaggat	2715
ADH3	3	(intron 3 32)	acactcagggaacatgctt G/A gtccaccatcacagatttag	2716
ADH3	4	(intron 4 6)	ctgcttgaaaaatgagtaag C/T tctgtatgctttctttgac	2717
ADH3	5	(coding region 453 (Thr 151 Thr))	agcaactctcccatgaac A/G gtgtgatgagaaatgcagt	2718
ADH3	6	(coding region 815 (Arg 272 Gln))	ttcgtttgaagtcacgtgc A/G gcttgcacaccatggtatgat	2719

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ADH4	1	(5' flanking region -482)	acagccagacacccagacc A/G tcaggcctgggttaaggact	2720
ADH4	2	(5' flanking region -437)	catcagctggacacaaaaa G/A tagctcttagcagtgacta	2721
ADH4	3	(5' flanking region -234)	actcaagcataigtgaacc A/G agtacctgaaagaatttgt	2722
ADH4	4	(5' untranslated region -361)	ggttaagttaattggcgatt C/G tggaggatagaatttccctt	2723
ADH4	5	(5' untranslated region -253)	ttcaataaagaaaaagaa I/A ttaaaaaatcttggagctca	2724
ADH4	6	(intron 1 707)	ttatatgtgaattaaaaat A/G taatttgagctagaaaaaa	2725
ADH4	7	(intron 5 619)	tcaagaggatctcaaat I/C ggacatctcaacctgttat	2726
ADH4	8	(intron 5 1755)	tttaaggcacacaattactca I/C taataaaaaatttaaaaaat	2727
ADH4	9	(intron 5 3425)	actgagactctggagcaata I/C attaagaatcatcatgaaca	2728
ADH4	10	(intron 1 1181*1189)	ggtaaatcttaatacacctg (T)9-11 caagaaataaaaaatgtaat	2729
ADH4	11	(intron 5 2828)	tccagtcacaaagtcacctaa A/Δ ttccaggagtggttctcc	2730
ADH4	12	(intron 7 15)	ttgggtgctagttttttt I/Δ ctctatagctttaaatctt	2731
ADH5	1	(5' flanking region -115)	taactgctgttaagttaac G/A g/a ggaagcccttccgacaa	2732
ADH5	2	(5' flanking region -114)	aactgctgttaagttaac g/a G/A ggaagcccttccgacaaa	2733
ADH6	1	(intron 3 249)	tgaacitggacttgaaagta C/A aatgagacacaaaatttatg	2734
ADH6	2	(intron 6 1072)	taacctctactgtattgc A/G tcactttctacacaggcagct	2735
ADH6	3	(coding region 885 (Val 295 Val))	gtctgtgtgtgtgtgggt G/A ttccctgccagtgttcaact	2736
ADH6	4	(intron 7 1292)	gttgagaacacactgcctagt C/A cagtctgtgtgtctagaatt	2737
ADH6	5	(intron 7 1616)	ctatcacagaataatccca I/C agaacaataagcagattacg	2738
ADH7	1	(5' flanking region -528)	tgtgcagacacagaagttt I/C acttaactttcacacctaa	2739
ADH7	2	(intron 1 361)	tcagttagcatgtgtgcact C/T gcigcagtagtttcaatgga	2740
ADH7	3	(intron 3 183)	aacctcaaccttttagaggc A/G aacctacagggtgtttataaa	2741
ADH7	4	(intron 4 76)	tgaattgaaatatttaaac G/A tgtatttgatgatacaaca	2742
ADH7	5	(intron 6 615)	tggcatagcgtaagagact I/A ggaataatggaataaagcca	2743
ADH7	6	(intron 8 532)	aagtciaaccatatacccaa I/C ttagtatgccattgtactat	2744
ADH7	7	(intron 8 651)	gcctgtatttatttoagta G/A gccacaaaatttccatttt	2745
ADH7	8	(intron 8 727)	ttcagatccctgtaagccag G/A tattattttaccattttta	2746
ADH7	9	(intron 8 1207)	tctccacatttggctagcc I/C acaggatcatcatattatga	2747
ADH7	10	(intron 8 1691)	tccctcatctcatggccac G/A ctcatgttttaattcagtc	2748
ADH7	11	(3' untranslated region 1364)	atttaccattttgtaaggcta I/C aattgtatctttttaagaaaa	2749
ADH7	12	(3' untranslated region 1498)	gatataagtaaatgcctcc I/C agagtaataatcoacttaaca	2750
ADH7	13	(3' untranslated region 1584)	aaacactgttatgatttaa C/G ttggattacatttgaagac	2751
ADH7	14	(3' untranslated region 1818)	aatataaacatagagctaga A/G tcatattatcatacttaca	2752
ADH7	15	(3' untranslated region 865)	tacatcaaaagaataaatic C/T aagaaggaataaacacattt	2753
HEP27	1	(5' flanking region -191)	tcagcaactctgtgttagot A/T aaggttttgaatgcaccaa	2754
HEP27	2	(5' untranslated region -163)	gaaccataaatccgttaoa C/A atttttggaacttgaagag	2755
HEP27	3	(intron 1 1941)	aaatttaacctaacagcct G/C actctcgcacatttctgtt	2756
HEP27	4	(coding region 289 (Ala 97 Thr))	ttgtgtgcacgtggggag G/A ctgaggaccgggagcagctg	2757
HEP27	5	(intron 4 1070)	tgtctcagttcacagata I/C gactctttttctcgaaactg	2758
HEP27	6	(3' flanking region 362)	agctttgtgtgtgtcatt A/G tctgaactgggctgtctggg	2759

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
UG11A1	1	(5' flanking region -1337)	tctttcccttttgactcaa A/C taagtcatcagaatttccccc	2760
UG11A1	2	(coding region 211 (Gly 71Arg))	cctcgtgtacatcagagac G/A gagcattttacaccttgaag	2761
UG11A1	3	(intron 1 2925)	gcatttgggaaggagaaatc I/G aattaaagccfcaaaataaa	2762
UG11A1	4	(intron 1 3442)	agactggccttttccagat G/I agcttcagtgtaagagtgagg	2763
UG11A1	5	(intron 1 3512)	ttaagttaagccatttaccac C/I gctcagaagaagaacttga	2764
UG11A1	6	(intron 1 3665)	tcttgctacaaacccaaaaa I/C gcagcatgggtgtggggagg	2765
UG11A1	7	(intron 2 15)	cagacagtaagaagattcta I/C accatggcctcatatctatt	2766
UG11A1	8	(intron 4 574)	agattttaaactccaattta C/I ataaaaagttgcataatag	2767
UG11A1	9	(3' flanking region 125)	tatagaggttcacacacac C/I gcttcattggctgtgcatg	2768
UG12A1	1	(5' flanking region -1602)	ataacatcttctcagagaa A/C cttaaalggaaatacactca	2769
UG12A1	2	(5' flanking region -1480)	taoagattatctttgtgat G/C ggagagcttagaagagacat	2770
UG12A1	3	(5' flanking region -1406)	atttcagaagatttattaac A/I tgaaggatcacctcig c/t tt	2771
UG12A1	4	(5' flanking region -1388)	acatgaagaaggatcacctcig C/I ttatcacagacataatgat	2772
UG12A1	5	(5' flanking region -935)	aaattatcaatctctttgg G/A cagtggttctcttttttttg	2773
UG12A1	6	(intron 1 535)	cattgatcagggtgatttat C/I catgctaagccttatttaatt	2774
UG12A1	7	(intron 1 642)	tatatgatcatgttgatac A/C ttatatacatattttgtcta	2775
UG12A1	8	(intron 1 1448)	agtgcttacaggcaacatc C/I acatagcagtcigtgctgg	2776
UG12A1	9	(intron 1 2000)	gacacattagcttcttttct A/G cagatctctgtctcctaaaca	2777
UG12A1	10	(intron 1 3118)	cttaaaatttcttaataaaa I/G cattgcaacaaatttatatac	2778
UG12A1	11	(intron 1 3191)	ataaatagaacaactcccta A/I gtttaactctcgcagtgga	2779
UG12A1	12	(intron 1 3770)	atcacagataaatttactat C/I cattaaaggagtaggtcatca	2780
UG12A1	13	(intron 1 4584)	tgaattggtagaactcttga A/C aaattctctagtatcattcc	2781
UG12A1	14	(intron 1 4854)	taactctgcatctgttaata G/A cctatacacttggtgctgtcc	2782
UG12A1	15	(intron 1 -19146)	ctgttttaaatctcattcaa C/I ggccacatgggttaaaataaa	2783
UG12A1	16	(intron 1 -19085)	tagacaagaagaccctttcaat A/C aacaaagtttagaaatgtgtt	2784
UG12A1	17	(intron 1 -18346)	atggcaatatttttagaat G/A ttaactcccaataatgaata	2785
UG12A1	18	(intron 1 -18218)	tatatcattattttaactta I/G agatagcactagccctaatt	2786
UG12A1	19	(intron 1 -17937)	ctctaataatttggactca C/I catacttattcagcaactatc	2787
UG12A1	20	(intron 1 -12585)	ttccacacagggacaagtca A/G cagagaaatttttcttgct	2788
UG12A1	21	(intron 1 -11430)	aacaaaggtttattttctta C/G agttctggtgctagacgtc	2789
UG12A1	22	(intron 1 -10761)	tttaaatatgcagtattt I/G ccacttttaaaaactatatac	2790
UG12A1	23	(intron 1 -381)	aaatccctccctctctctc C/I ttcccagggcccccactctac	2791
UG12A1	24	(intron 1 -329)	ttcccttctctctttctcc A/G tctctctctctctctctctc	2792
UG12A1	25	(intron 1 -41)	ttttctcctcagcaaacata I/A agctaattttccctccatcca	2793
UG12A1	26	(intron 2 263)	cacttgatagctgacttgg I/C gggacagaaaccaccatcat	2794
UG12A1	27	(intron 2 454)	agaaagcccatgcaataag G/C cagggttttttaggttttaatt	2795
UG12A1	28	(intron 2 554)	aaaaacttttttaggttgaac A/I atggtagtttagttttctga	2796
UG12A1	29	(intron 2 1113)	ctcaggaagcgtctatgta A/I tgtttattataggaaataat	2797
UG12A1	30	(coding region 922 (Gly308Arg))	gtgttggttggttttctcig G/A gatcaatgggtcaaaaacctt	2798
UG12A1	31	(intron 3 -217)	aagcttagaagtgataaata I/C caaaacaataatactatact	2799

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
UG12A1	32	(intron 3 -194)	aaacaataactactactg g/a tagactattagtacaagact	2800
UG12A1	33	(coding region 1171 (Val391Ile))	acggagtccctatggggg g/a ttcccatgtttgctgacag	2801
UG12A1	34	(intron 5 1546)	tttttaaaatcagaaactc A/G g/a ttatgggtattcttcaaa	2802
UG12A1	35	(intron 5 1547)	tttttaaaatcagaaactc a/g G/A ttatgggtattcttcaaa	2803
UG12A1	36	(intron 5 2505)	taattgacttttattatc g/a tacatgttgataaagtcata	2804
UG12A1	37	(intron 5 2639)	tagactattacaagtgtt A/G gttgtgacaattttgttca	2805
UG12A1	38	(intron 5 4009)	gaatccaggctgaactttt C/A ttccagacacaaacaaaat	2806
UG12A1	39	(intron 5 4311)	atacagacacgttcctttt G/A tcacaaacatcacagtgtt	2807
UG12A1	40	(intron 5 4616)	actttttatgtctacattt G/C atcacactgtgttaagcata	2808
UG12A1	41	(intron 5 4717)	tgcagaattatatttttc C/A acgtaactatggccttaaac	2809
UG12A1	42	(coding region 1524 (Gln508Gln))	gctatattttgttcatac A/G tttgtttgttttctctgca	2810
UG12A1	43	(3' untranslated region 1683)	aaggagtttaacaaaacac G/A tcgccatcctgtttccaaa	2811
UG12A1	44	(3' flanking region 685)	aactagaaaataatatac I/C ttttataaaatttttagtca	2812
UG12A1	45	(intron 1 (-18967) (-18965))	ctcccaattagattgattag TAI/ Δ gaggttcctgggttaactggt	2813
UG12A1	46	(intron 1 (-18862) (-18803))	aataacttttccccccttc (AC) 14-17 atgcttactggcctatttat	2814
UG12A1	47	(intron 1 (-17463) (-17447))	aaacttagaacctctattc (A) 16-27 gtaagaaaatggcagagaa	2815
UG12A1	48	(intron 1 -10860)	atccaatgcaacttttttt I/ Δ gtaatggcagaattagaaca	2816
UG12A1	49	(intron 2 528 538)	ctgttaggaacaacttgggt (A) 8-10 ctttttgggttgacA/tatgg	2817
UG12A1	50	(intron 2 1514 1533)	tttgtgtgtgtgtgtgtt (GI) 9-11 tatttttaatgaattaatatc	2818
UG12A1	51	(intron 5 916 917)	gcttagtatattatataat AA/ Δ gtctatatataatagcttagt	2819
UG12A1	52	(intron 5 1163)	caatatattgtcattttt I/ Δ cicacattttactcgtttcc	2820
UG12A1	53	(intron 5 3819 3838)	agacagacagacacacaaac (AC) 8-12 tcaacacatgtaaacactc	2821
UG12A1	54	(intron 5 4785)	tacttccaatgaaaataaaa A/ Δ caaaaattgtctaatcttg	2822
UG12B15	1	(5' flanking region -277)	cgaacagcaggcaggacctct C/A acttgccactgtttttaaca	2823
UG12B15	2	(intron 1 670)	catcaagaagaaataggggcc A/T aattaaggagagacacatat	2824
UG12B15	3	(intron 1 775)	ctaattatattaagaactta A/C gatgaaccaagacagtagta	2825
UG12B15	4	(intron 2 2183)	cagagtttcaccatgttggc C/T aggcgtggcttgaactcctg	2826
UG12B15	5	(intron 2 2430)	tattccaagaagaataagact C/G ttgccaanaagatcaagtg	2827
UG12B15	6	(intron 2 4806)	aaaaattacccaatagct C/T ctga c/g ttctcatcttagat	2828
UG12B15	7	(intron 3 129)	ctaattatctcagacatctg I/C tcaaa g/a caaaaacatatatg	2829
UG12B15	8	(intron 3 424)	caataacaataagcaggat I/C gaaaaacttgaatgcat	2830
UG12B15	9	(intron 3 493)	ggc t/a gttttactccatg C/T attggaataggctctatttag	2831
UG12B15	10	(intron 3 906)	gcctctcgaatgatctat G/A caagttttgtcgaaaaaac	2832
UG12B15	11	(intron 3 1036)	tcagtcccttagtttggtag I/C agacatggtaagaciggct	2833
UG12B15	12	(intron 3 1544)	aataaataatagggttatta C/G taatttgcacttttttatt	2834
UG12B15	13	(intron 3 5550)	gtgtgtgtaatcaatgtgtg C/T tgccttgggcagtaoctca	2835
UG12B15	14	(intron 3 5720)	ttttttaaaagtttaattttt C/A ttggggatttccctgcaggg	2836
UG12B15	15	(intron 4 134)	atcaaatttaactactttat A/G tttattttccagctcttagta	2837
UG12B15	16	(intron 5 6627)	ttttaatgttgatatttta I/C atttatccttcagctataaa	2838
UG12B15	17	(coding region 1568 (Lys23Thr))	tttccgaagacttgcacaaa A/C aggaagaagaagaagaag	2839

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
UGT2B15	18	(3' untranslated region 1761)	ggaatttaacgtacttag C/T tgaattattctatgic a/t at	2840
UGT2B15	19	(3' untranslated region 1779)	ag c/t tgaattattctatgic A/T atgatttttaagctatgaaa	2841
UGT2B15	20	(intron 2 1980~1981)	aaagagtagcagaataaagg (A66) caaaggataaataactagt	2842
UGT2B15	20	(intron 2 1980~1981)	aaagagtagcagaataaagg acaaggataaataactagt	2843
UGT2B15	21	(intron 3 605~618)	ctagccaagtagatttagag (A)11-15 cttgtctgtctgtgactt	2844
UGT2B15	22	(3' untranslated region 1957~1968)	aagtataatttaaaaaagc (A)11-14 tacaactctttttttaaac	2845
UGT8	1	(coding region 677(Pro226Leu))	gcagaagtaaacactgtgc C/T ggagaagtccatgtatgatt	2846
UGT8	2	(coding region 741(Ala247Ala))	atgctgtactgaactagc A/G ctggaattcccaagaccac	2847
UGT8	3	(intron 2 53~54)	tigacaataataatctctt G1/Δ ttatgtcacaggtccagta	2848
GSTA1	1	(5' flanking region -266)	ttgcaaaaagagcaaatct C/A ggtgaatgtattgtgtaa	2849
GSTA1	2	(intron 2 1220)	gagacacaggcttctctaa A/C tatgacaacacataactag	2850
GSTA1	3	(intron 4 1813)	aaaggacccactggagggtg A/C attattttgccatcacctga	2851
GSTA1	4	(intron 5 732)	gagagtggtgtcatgaagg I/C ggagtcactgcccaaggag	2852
GSTA1	5	(intron 6 333)	ttatccataatgtgccaca A/G tgagcgggtctgagcagagc	2853
GSTA1	6	(3' flanking region 412)	ctttctatgcatttgcaaa A/C caatgattctgtctgtgtg	2854
GSTA4	1	(intron 1 280)	gcattggtgaagggtggct C/T ggatgtccccgggcoctggc	2855
GSTA4	2	(intron 3 176)	ggaaatcaccttctattcaa I/C agttocataaaaagctggcgc	2856
GSTA4	3	(intron 4 94)	acaccacatttacttaagt C/G ttacatagtttagtgatca	2857
GSTA4	4	(intron 5 1062)	cacactgtgcacatgcaga C/T acccatggcattcccaaggt	2858
GSTA4	5	(coding region 487 (Thr 163 Ala))	cagatgtgatttactocaa A/G coattttagctctetagaagag	2859
GSTA4	6	(intron 6 595)	tgagctctgagacaaatga G/A agatgtt a/g gcaccctaaaca	2860
GSTA4	7	(intron 6 630)	taacatcaccccaaaaggt I/A cotacattctctcttctgag	2861
GSTA4	8	(intron 6 3943)	ttctctagttatctataoc I/C tttttgttagccttaagtt	2862
GSTA4	9	(3' untranslated region 1099)	taataacacccgaatgtcta G/A taaatgactctctctctgagc	2863
GSTA4	10	(intron 5 370~371)	gttgtgaaacagtgctctca (TA) gctgacatctctctctgataa	2864
GSTA4	10	(intron 5 370~371)	gttgtgaaacagtgctctca gcigacatctctctctgataa	2865
GSTM1	1	(5' flanking region -694)	taggaagtggtctaatitaca C/T agtacttagccagatgaccg	2866
GSTM1	2	(5' flanking region -661)	gatgaccgaaggactcagta C/T ccgagggcccttaacagaaa	2867
GSTM1	3	(5' flanking region -658)	gaccgaaggactcagtaacc G/A agggcccttaacagaaaaa	2868
GSTM1	4	(5' flanking region -656)	ccgaaggactcagtaaccga G/A gggcccttaacagaaaaaca	2869
GSTM1	5	(5' flanking region -537)	tagaggggactaagccct G/C ggatagctttcggatcaga	2870
GSTM1	6	(5' flanking region -525)	taagccctggagtagcttt C/G ggatcagagaagatcctgct	2871
GSTM1	7	(5' flanking region -465)	aattaaattccaggttggg G/A ccaacttttttagtgtgac	2872
GSTM1	8	(5' flanking region -383)	gcgagagaaggctgaggga C/T accgaggcaggagagagaa	2873
GSTM1	9	(5' flanking region -382)	cggagagaaggctgaggga A/T ccgaggcaggagagagaa	2874
GSTM1	10	(5' flanking region -378)	gagaaggctgaggacacgc C/T gggcaggagagagagagag	2875
GSTM1	11	(5' flanking region -343)	agggagaaggcttgcctc G/A ttaggatctggctgtgtct	2876
GSTM1	12	(intron 2 118)	tgcgtgagctgaggtgtgc I/C ctctccctgagccccgttag	2877
GSTM1	13	(intron 3 233)	agtggatggccgtctctc I/C ctgctcttcttaagggaag	2878
GSTM1	14	(intron 4 26)	tgtgggtggctgcaatgtgt G/A gggggaagggtggcctctcc	2879

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
GSTM1	15	(intron 5 140)	actatcagcaggttatttca C/I gactcaatgtcatgcaac	2880
GSTM1	16	(intron 5 577)	ctgccaccattagaagga A/G cttttactttccctgagct	2881
GSTM1	17	(intron 5 645)	gttggtctgatatccagaggc I/A gccaggtgcttggcgctcc	2882
GSTM1	18	(coding region 519 (Asn 173 Lys))	caocgtatatttagcccaa G/C tgcitggagccttcccaaa	2883
GSTM1	19	(coding region 528 (Asp 176 Asp))	tttagcccaagtgccttggg C/I gcttcccaaatctgaagga	2884
GSTM1	20	(intron 7 2421)	cagcacgtatagatcttc A/G taagtgttagctgttactgt	2885
GSTM1	21	(3' flanking region 42)	atttgcctcggccatctac C/I cagactgtctgtctgtctgt	2886
GSTM2	1	(intron 1 7)	ggacatcccggggtgagc C/G agggctcgtggcggtggg	2887
GSTM2	2	(intron 1 45)	ggcacgggggtgcgtgggg C/I ggggaagtgtggagcagctg	2888
GSTM2	3	(intron 3 70)	gactgcattcctctcccca G/C cttagagggttaagatcag	2889
GSTM2	4	(intron 3 224)	agcaggccctggctcctct I/C tgccttgcataatgggaagg	2890
GSTM2	5	(intron 5 100)	ttgattcctcttggtgagtt C/A ttggtcttgcactctaag	2891
GSTM2	6	(intron 5 341)	tcctcttgggtggttcattg I/C ctggctggcttcaggagtga	2892
GSTM2	7	(intron 5 696)	accttiagctagacacagag C/I gctgatttgcatttaca	2893
GSTM2	8	(intron 5 723)	ttatgcatttacaatcctt A/G gctaggcagaaaagtctcc	2894
GSTM2	9	(3' untranslated region 1006)	ctcagcccgagctgtcccc G/A tgttgcataaggaagcaga	2895
GSTM2	10	(3' flanking region 139)	ttctgtggcatagtaagg C/I gcttgagaattcttgcctcc	2896
GSTZ1	1	(5' flanking region -546)	agcaggccacacagccgac C/A gctcgaagccgcgtgagcc	2897
GSTZ1	2	(5' flanking region -321)	tgtctgaccagccgccgc I/C aaggagtcaagagagggcag	2898
GSTZ1	3	(intron 1 2890)	aaatactgcatacaaa G/A gccacgtctgttgggggga	2899
GSTZ1	4	(intron 1 2896)	ctgcatacaaacagccac G/A ctctgttggggggacaccaa	2900
GSTZ1	5	(intron 2 255)	ttcccaacactgcctcca A/G agcccttggcaaccatgtt	2901
GSTZ1	6	(intron 2 1560)	cacactgttaaggccctg G/C gggggcagagttaaacaca	2902
GSTZ1	7	(coding region 94 (Lys 32 Glu))	ccttgaaggcatcgactac G/A agacggtgccatcaatctc	2903
GSTZ1	8	(intron 4 297)	agaaggaggagttgtctggc C/I ctgtccctctgtgtccaggg	2904
GSTZ1	9	(intron 6 94)	tatctgaaccagccctccag G/A ctgcttggccctgacagtt	2905
GSTP1	1	(intron 1 269)	ctcccgggctccagcaaa C/G tttcttggctgcgcagtt	2906
GSTP1	2	(intron 2 134)	cccgggcctctctctgtt C/I ccgcctctcccgccatgcc	2907
GSTP1	3	(intron 5 438)	gtgtgtgcgtgcgtgtgc G/A tgtgtgtgcgtgtgtgtgtg	2908
GSTP1	4	(intron 6 162)	cccgctggctgagtccttag C/I cccctgcccctgcagatctc	2909
GSTT1	1	(5' flanking region -103)	taagagtgctccagggtc C/I gtgcccacaaatgggcaca	2910
MGST1	1	(promoter region -1879)	ttataaattgtttattcaat I/G aaaccaactgctaattct	2911
MGST1	2	(promoter region -508)	ttctggaccctgaacaggagg G/C gacatcgtgacaaagcaat	2912
MGST1	3	(promoter region -314)	ctcggagattttaattctt G/A cgaagtttttaaaacaact	2913
MGST1	4	(promoter region -131)	atcagcaggagtggttact G/C tgggggggtaaatcaggtga	2914
MGST1	5	(intron 1b 36)	ggagaaaggaccccatgca A/G aggggtggcaggcaggagg	2915
MGST1	6	(intron 1c 456)	cccttgggacggttctcac C/I tgtgcccacattcccgctg	2916
MGST1	7	(intron 1c 719)	ggcgcgaagcatttgcgtat A/G gcaccagggcctccagtgag	2917
MGST1	8	(intron 1c 985)	cgagtaaaattttctaccg C/G ttgttttttagagtggtgtct	2918
MGST1	9	(intron 1c 1428)	gtaaagggaaggcgcttcc I/A caactgagaagtgaagattc	2919

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
MGST1	10	(intron 1c 2914)	ctcctcaggtgtgtgtcaga I/G gotttggtgtgcccagttctc	2920
MGST1	11	(intron 1c 4274)	attgtaataagattacaaga G/I tgaataaagtagtgtacata	2921
MGST1	12	(intron 1c 4276)	tgtaatagattacaagaagt G/I atgaagaagtagtgtacataat	2922
MGST1	13	(intron 1c 4767)	gccttctctcagcacatt C/I ccaattatacttccaattcc	2923
MGST1	14	(intron 2 2379)	ttctcaatttccattata G/C tattttccaacccaagttt	2924
MGST1	15	(intron 2 2767)	tttaactatagatgccttct I/G ctctctctgtgtttgattta	2925
MGST1	16	(intron 2 2974)	tcactcagctcaacctct C/I gggctcagtgatctcccaa	2926
MGST1	17	(intron 2 3083)	aaaaatttgtagatagg I/G actcctatgttgccaggc	2927
MGST1	18	(intron 2 3106)	tcctatgttgccaggctg A/G tottgaattcttgggtcaa	2928
MGST1	19	(intron 3 1495)	gtcagacaatggcttcagc G/A tctctcttgcagaatatg	2929
MGST1	20	(intron 3 1703)	ttctcttaagaagaagtc I/C gtgcagatacttagcacaaa	2930
MGST1	21	(intron 3 2528)	ttttggagacacttticaga G/C agagcgtttccagcatcttc	2931
MGST1	22	(intron 3 2557)	tcagcatcttcccttcca I/C ttttaagttagactttttt	2932
MGST1	23	(intron 3 2731)	atacacaatggacaatta A/C ctataaaccttaaggtaatat	2933
MGST1	24	(intron 3 3032)	agagacaatttagaataatt C/A cctttaaaggtagagaataa	2934
MGST1	25	(intron 3 3045)	atatactccctttaaggta G/C agaataaaccttcacatgaga	2935
MGST1	26	(intron 3 3289)	ggttatagtttccccccc I/A cccgcccccaaaagaccca	2936
MGST1	27	(intron 3 3976)	ggaagctagggaactgtt G/I cotggaacagagtctcaaaa	2937
MGST1	28	(intron 3 4288)	coatttattgtcaactgc G/A taacacagcgctagaagtgg	2938
MGST1	29	(intron 3 4298)	tgcaactcgtaacacagg C/I gtagaagtggaactgtttt	2939
MGST1	30	(intron 3 4429)	attggaggtagacatatctc I/C gtgaigctgggggagaaatc	2940
MGST1	31	(intron 3 4519)	tttaatagaaaatggtaic C/I tgccttttcttcccatc	2941
MGST1	32	(intron 3 4817)	attgctatagaagagagtaa C/I gtaaagcagaataagtttctc	2942
MGST1	33	(intron 3 6077)	tttgaattagtgtctttaa I/C agttatctttttccacagag	2943
MGST1	34	(3' untranslated region 603)	ggtaaacccattttgaata I/C tagcatggccaatatctgt	2944
MGST1	35	(3' flanking region 147)	tattgctttctctctct C/I tgtttcttttctctgaaa	2945
MGST1	36	(3' flanking region 237)	cagcaagttttctctatgaa C/I aagacattctccaataaact	2946
MGST1	37	(intron 1C 904*923)	tgcgattatotttggttaatt (A)16-19 ggcaaatcagtcacaatttg	2947
MGST1	38	(intron 1C 3433*3434)	cccttcaatactagaaacaa (AA) gcagacacattaaatgttac	2948
MGST1	38	(intron 1C 3433*3434)	cccttcaatactagaaacaa gcagacacattaaatgttac	2949
MGST1	39	(intron 1C 5146)	actatttcaattttttttt I/ Δ ggagggggagacagagcttc	2950
MGST1	40	(intron 2 552*563)	ccagcattataagaatgac (I)10-12 aagtgcagatgtggggagg	2951
MGST1	41	(exon 3 172*173)	tagcaattggcaagagagaa AA/ Δ tgcaagaagtattottgaa	2952
MGST1	42	(intron 3 152*158)	agaaactggagtcctgaaa TIGACA/ Δ (GTCCAAAT) cactgcaattgtatgtgttg	2953
MGST1	43	(intron 3 2198*2200)	ggattttagattctctccta CTA/ Δ ttcttccgaccttcaccc	2954
MGST1	44	(intron 3 2567*2568)	cccttccatttttaagtta (A) gacttttttttttcaactct	2955
MGST1	44	(intron 3 2567*2568)	cccttccatttttaagtta gacttttttttttcaactct	2956
MGST1	45	(intron 3 2571*2580)	tttccatttttaagtttagac (I)9-11 caactctctctgttacttcag	2957
MGST1	46	(intron 3 3288*3289)	ggtttatagtttccccccc (C) tccccgcccccaaaagaccc	2958
MGST1	46	(intron 3 3288 3289)	ggtttatagtttccccccc tccccgcccccaaaagaccc	2959

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
MGST1	47	(intron 3 4682~4683)	tctcttcattgtctctatgt (GAGAGTGGTGGCAGACAT) agtcattctctttgtgagac	2960
MGST1	47	(intron 3 4682~4683)	tctcttcattgtctctatgt	2961
MGST1	48	(3' flanking region 1359~1360)	acacacacacacacacac CC/Δ tgcctcaggagttgggcaact	2962
MGST1	49	(3' flanking region 1889~1891)	ttagaatagtttaactat ACT/Δ tttaactccaagagaagcctt	2963
MGST1L1	1	(5' flanking region -105)	tgtgcgcgtgcogtggggc G/A gggcgtggcggtgctgggt	2964
MGST1L1	2	(intron 1 277)	agtgtoigtgagagaagcag G/A ttctggagggtggagtggtg	2965
MGST1L1	3	(intron 2 8030)	gggtttatacagagccctc C/G gccccacacacacatgca	2966
MGST1L1	4	(intron 2 8499)	gtatggcagagtgaggctc C/I ggcgaagccatagaggatg	2967
MGST1L1	5	(3' untranslated region 468)	cgccacctgtgaccagcagc I/G gatcctccttggccaccag	2968
MGST2	1	(5' flanking region -46)	ggtcagcattcaagtcgaag A/I aggcacatttattctccgt	2969
MGST2	2	(intron 1 176)	ggtcacccatgcgcctgct A/C cctctctccaggggcgaag	2970
MGST2	3	(intron 1 204)	tccaggggcagcagagac I/C gagaacattccagagattag	2971
MGST2	4	(intron 1 373)	ttacaaggttccaaaggaa A/I cgtgcctgcttctaaacctg	2972
MGST2	5	(intron 2 -3245)	ctctgtgatttgcaccctc G/A gctcccaagtgctggat	2973
MGST2	6	(intron 2 -1998)	agcccgagtgggcgatca I/C gaggcagagatcgagacc	2974
MGST2	7	(intron 2 -1640)	tgttattctctgtagacc A/G taatataagatgaatttt	2975
MGST2	8	(intron 3 41)	actgtgttctaagtgaact A/G tgatgottaaacgattaaagg	2976
MGST2	9	(intron 3 453)	atcagagtgctatgttgcaag A/G tatatgaactttggcttcat	2977
MGST3	1	(5' flanking region -520)	acaaaaaggccctaacagcg A/C taaatccattcaacttcggga	2978
MGST3	2	(5' flanking region -355)	cgctaaaaacgctacggig G/A ctctgtggggacaaattat	2979
MGST3	3	(5' flanking region -234)	ctggggagtagatatatgt T/A tttagaatgagaggagtaa	2980
MGST3	4	(intron 1 74)	agcctttgcgcagcactcc C/I atatttcagcctatgagagc	2981
MGST3	5	(intron 1 682)	agaaaatgcccctcttttat G/C tggggcggcagcagcgagcc	2982
MGST3	6	(intron 1 832)	cgagtttacaagctacataa I/C agcgtcggggcgaagtaagt	2983
MGST3	7	(intron 1 1919)	aataaaattctcigagtttct G/C tcactcgtcttaccagtaac	2984
MGST3	8	(intron 1 1991)	tgtaattaggcaacaggaaa A/G ttgtactatcttcaaatgc	2985
MGST3	9	(intron 1 4458)	tcttcacatcctcctaataa I/C agttagcttccactctccaa	2986
MGST3	10	(intron 1 4676)	tgaataigcaatgaattgt C/G gggggatagttacttttcat	2987
MGST3	11	(intron 3 278)	cagcatgaccatctaaacc G/C atgttactctccagccct	2988
MGST3	12	(intron 4 423)	cttgcctttttgttgagg I/G gtegggtggctcacagagaag	2989
MGST3	13	(intron 4 506)	gtcagagagaagaacaaaag I/C ggggaaggtggaaggggat	2990
MGST3	14	(intron 4 -162)	tccagatattttattttcc C/I gactgaactaaacttaattc	2991
MGST3	15	(intron 4 -130)	acttaattctacciaatttg C/G gteggagtagtggccaaa	2992
MGST3	16	(intron 4 -105)	ggagtagtggccaaatcat C/G aaatgttaacttttcta	2993
MGST3	17	(intron 4 -65)	aacatatgtgtataatcaacc C/I taggtgttaaaaaaggttg	2994
MGST3	18	(intron 5 105)	atccagcactttggaggc G/C aaggcaggcagattgcttga	2995
MGST3	19	(intron 5 197)	aaaaaatacaaaaattagcc G/A gatgtgtgtgacacactg	2996
MGST3	20	(intron 5 222)	tgggtgtgcacacctgtagt C/I ccagctacttggaggactga	2997
MGST3	21	(intron 5 374)	tcttatgctactatatttt I/C tcttgggaatttgaaaaa	2998
MGST3	22	(3' untranslated region 517)	atgacttaccattatttoca G/I ttacatttttttttaataa	2999

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
IMS13	23	(3' flanking region 166)	agctgatttggtgtagta G/I gtatagtcattgcacagtga	3000
SULT1A1/STP1	1	(5' flanking region -1597)	gcagagtaaggagactcaact C/G aagaagagaaactgggggt	3001
SULT1A1/STP1	2	(5' flanking region -1491)	gaggggtatattcaaga G/I tcaggaagaaagtaaagatt	3002
SULT1A1/STP1	3	(5' flanking region -1376)	cgtttcatatgttactgat C/I a/g taca a/g tgagatcctaggtg	3003
SULT1A1/STP1	4	(5' flanking region -1375)	ggtttcataatgttactgat c/t A/G taca a/g tgagatcctaggtga	3004
SULT1A1/STP1	5	(5' flanking region -1370)	ataatgttactgat c/t a/g taca A/G tgagatcctaggtgaacct	3005
SULT1A1/STP1	6	(exon 1B -65)	caactgtcattccacaca G/A caaccacaatcagccactgc	3006
SULT1A1/STP1	7	(intron 1B 442)	gagccacctgtcctaggcct G/A tgcctttgtgagtcacag	3007
SULT1A1/STP1	8	(exon 1A -197)	gctgggggtccacagcaggaa A/G tegttagacaaaggcgctg	3008
SULT1A1/STP1	9	(exon 1A -159)	ctgctggcaggagagacagc A/C caggaaaggtcctagagcttc	3009
SULT1A1/STP1	10	(exon 1A -95)	gagaccttcacacacctga I/C atcggcccttgcccgacga	3010
SULT1A1/STP1	11	(intron 1A 60)	ctggttttcagcccccagccc C/I gccaciga c/g tggctttgga	3011
SULT1A1/STP1	12	(intron 1A 69)	agccccagccc c/t gccactga C/G tggctttgtgagtcgagga	3012
SULT1A1/STP1	13	(intron 1A 174)	ttgatagtgtagtaagggaac G/A ggcctggctctggccctga	3013
SULT1A1/STP1	14	(intron 6 11)	catgaagaggagtagaacac C/G tgtga a/t gcttccctccatgt	3014
SULT1A1/STP1	15	(intron 6 17)	ggaggtgagaccac c/g tgtga A/I gcttccctccatgtgacacc	3015
SULT1A1/STP1	16	(intron 6 35)	gaagcttccctccatgtgac A/I cctggggccggccacatcac	3016
SULT1A1/STP1	17	(intron 6 71)	ctcacaggaccaccacagg I/C caaccagccccctcccttgg	3017
SULT1A1/STP1	18	(intron 6 108)	ttggcagccccacagcagg C/A cc g/a gattccccctcctcct	3018
SULT1A1/STP1	19	(intron 6 111)	gcacccccacagcagg c/a cc G/A gattccccctcctcctct	3019
SULT1A1/STP1	20	(intron 6 270)	ciccctgccaaagggtgtgc C/I acccagggccacagtcattg	3020
SULT1A1/STP1	21	(intron 6 488)	ttttacttttctgaatcag C/I aatccgagcctccactgagg	3021
SULT1A1/STP1	22	(intron 6 509)	aatccgagcctccactgagg A/G gccctctgtcgtcgaacac	3022
SULT1A1/STP1	23	(coding region 600 (Pro 201 Pro))	ccctctgtcgtcagaaacc C/G aagaaggagattcaaaagat	3023
SULT1A1/STP1	24	(coding region 638 (His 213 Arg))	gattcctgagtttgggggc A/G ctccctgccagaggagaccg	3024
SULT1A1/STP1	25	(coding region 645 (Leu 215 Leu))	gagtttgggggcactccct G/A ccagaggagaccgtggactt	3025
SULT1A1/STP1	26	(coding region 902 (Gly 301 Ser))	gctgtgagagggtctcctgg G/A gtcactgcagaggaggtgtg	3026
SULT1A1/STP1	27	(coding region 973 (Trp 325 Arg))	taaaatatgaattgaggccc I/C gggacgtagtgcattgtctg	3027
SULT1A2/STP2	1	(5' flanking region -547)	tgtctcttcttggttctatg G/C atccatgctctgtccaccc	3028
SULT1A2/STP2	2	(5' flanking region -425)	tgtgggttgactggccag G/A accctggcacttcaagac	3029
SULT1A2/STP2	3	(5' flanking region -358)	ctttccaggcctcctatc C/I ca g/t ctttctcctcaatccc	3030
SULT1A2/STP2	4	(5' flanking region -355)	tcagggcctcctatc c/t ca G/I ctttctcctcaatccc	3031
SULT1A2/STP2	5	(5' untranslated region -28)	actcggcgcaggaggacac A/G aggcacagtttcccaagact	3032
SULT1A2/STP2	6	(intron 1A 85)	ctgacgtgcttggtagtgc G/A ggcaagtcactcagccctccc	3033
SULT1A2/STP2	7	(coding region 20 (Ile 7 Thr))	catagagctgacaggaca I/C ctc t/c cgcccgccactggagt	3034
SULT1A2/STP2	8	(coding region 24 (Ser 8 Ser))	gagctgatccaggaca t/c ctc I/C cgcccgccactggagt	3035
SULT1A2/STP2	9	(intron 2 34)	ggcaccacacctctcccagg I/C ggcagtcaccaacttggcca	3036
SULT1A2/STP2	10	(intron 5 77)	cagcaacctgtgtggcac I/C ccttgcgcgtttctccagtg	3037
SULT1A2/STP2	11	(intron 6 684)	actggggtcccagggtcga G/C gagctgctctatgggtttt	3038
SULT1A2/STP2	12	(coding region 704 (Asn 235 Thr))	gttcaaggagatgaagaaga A/C ccttatgaccaactacacca	3039

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
SULT1A2/STP2	13	(3' untranslated region 895)	gctctgagctgtgagagggg /C tcttgagtcactgagaggg	3040
SULT1A2/STP2	14	(3' flanking region 98)	ctccocgcctccagctctc A/I actgcccgttttggagagg	3041
SULT1A2/STP2	15	(3' flanking region 817)	ccactgactggggcttgcc A/C aggcgcccagggcgtggcaaa	3042
SULT1A2/STP2	16	(3' flanking region 1006)	ctctccctctggagctgct /C taccogctgtggggcggcat	3043
SULT1A2/STP2	17	(3' flanking region 1464)	tcocgtagccagcagatt C/I ggtgaccagagacagcccc	3044
(SULT1A2/STP2)	18	(intron 4 1728)	tcagcttcctcccttggcaa A/ Δ ccaagatgagctggcctg	3045
SULT1A3/STM/ HAST	1	(coding region 843 (Ala 281 Ala))	cgcttcacgcgactatgc G/A gagaagatggcaggctgcag	3046
SULT1C1	1	(intron 3 2280)	gcaatttttgggtatttta G/I tacagtcagggttttaccat	3047
SULT1C1	2	(intron 3 3742)	gcagatcactttctggca G/A attccotgaatttgcctccc	3048
SULT1C1	3	(intron 3 4453)	ttcatagggctttccctca C/I ttgttttgaattttgtata	3049
SULT1C1	4	(intron 3 5234)	gaaaagagactagagcagg A/G gacttttgagttcttctaa	3050
SULT1C1	5	(intron 3 6175)	tggctggcaggaaggtagg G/C agtcctctctctctgctcc	3051
SULT1C1	6	(intron 4 205)	acatgaagcaggatccaga /C tgaatgtttggagggaacta	3052
SULT1C1	7	(intron 4 408)	ggctcaocgctgtaatccca G/C caotttggaggccgagggcg	3053
SULT1C1	8	(intron 4 429)	caatttggaggccgagggcg G/C gtggatcacaaaagtcaggag	3054
SULT1C1	9	(intron 3 2106~2115)	tgcagtgctcttggttgg (I)8-11 gagacaaagtcgtgctgt	3055
SULT1C1	10	(intron 3 4199~4210)	atgccagctaatttggta (I)10-13 agagacaggtttccaccatg	3056
SULT1C2	1	(5' flanking region -110)	tcctgttaactcacagagaa C/I ggaaggctggaaaggagcc	3057
SULT1C2	2	(coding region 15 (Asp 5 Glu))	acactaatggccttacaaga C/G atggagattttacatttga	3058
SULT1C2	3	(intron 1 297)	gtacactgtttattatc A/C ttcccaatctaggcccttat	3059
SULT1C2	4	(intron 1 363)	gagtggtgagctagaaagg /G gatccgagctgctgattggg	3060
SULT1C2	5	(intron 1 2300)	gggtactatcagcagccac C/I acctcaggaaggatgacttc	3061
SULT1C2	6	(intron 2 455)	aagacttggagaaataaga /G aaaaaaaaatcgtagaat	3062
SULT1C2	7	(intron 4 55)	caaaatcccaaacacctta G/A aagaaagaatcttttctt	3063
SULT1C2	8	(intron 4 111)	ctgcctttttaatggaaaca /C tctcacttccttcaggaaat	3064
SULT1C2	9	(intron 5 1657)	ctttgtgttactttgttt /C acttggtaaaaaagtgtgt	3065
SULT1C2	10	(intron 5 2082)	tctgctcctagatggagg C/A gtccacagccacagtgatg	3066
SULT1C2	11	(intron 6 933)	agctactgaacctctccac A/G taactgtatttcaggggcag	3067
SULT2A1	1	(intron 2 478)	ggactggcctcgtgtacacac /C tgccttactgtgtgtaaat	3068
SULT2A1	2	(intron 3 382)	caaaacctttaatatct G/A ttctatctgtctcagaact	3069
SULT2A1	3	(intron 3 409)	tctgtctcagaactatgac A/G tgactctaggatgcctatat	3070
SULT2A1	4	(intron 5 249)	agctgggaattacagggaca C/I gccacacacccagctaat	3071
SULT2A1	5	(intron 5 395)	aggcaatgagccagcgccc G/A gccaatattacgcttaaat	3072
SULT2A1	6	(3' flanking region 33)	ttccttgtaaagaattacca G/C ggttggccagc a/g cgggtgtt	3073
SULT2A1	7	(3' flanking region 46)	gttaacca g/c ggttggccagc A/G cgggtgttcatgctgttaaat	3074
SULT2A1	8	(3' flanking region 199)	tttagccagcgcatttggctc A/G tgtgttaatcccgacact	3075
SULT2B1	1	(intron 2 4162)	ttctccctctctctccact C/I ogcacacaggtgatctaat	3076
SULT2B1	2	(intron 3 879)	gaggscatccagctctgagg G/A ctggacctgggggttgg	3077
SULT2B1	3	(intron 4 3882)	ttccacgctccttcttggc C/I gagtgcctctccctccgtga	3078
SULT2B1	4	(intron 5 1780)	cttcgagaagggggtccctt C/I catgtccaagcagtaatggc	3079

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
SULT2B1	5	(intron 5 1814)	taatggctcagcatggagc G/A ttgtggggcattgagacag	3080
SULT2B1	6	(coding region 789 (Cys 263 Cys))	cactcttcacagggtcttg C/T ggcagactggaagaacactt	3081
SULTX3	1	(intron 1 332)	catgcttcctcctttaccctg G/T ctggctgtgaccttggac	3082
SULTX3	2	(intron 1 1167)	taggaatggctaagcgtgc G/A ttggctttgtggccactca	3083
SULTX3	3	(intron 1 2872)	catttcactgatgcagac G/A aagcttcctgggctaggcgt	3084
SULTX3	4	(intron 1 6242)	caccttgctctttaccagc A/G tggaaacattttacctgaat	3085
SULTX3	5	(intron 1 6601)	gggtggcttcaggaggag C/T gagaggagagtggaggccc	3086
SULTX3	6	(intron 1 6768)	agcttgaatgagccagact C/T tcttgggacctgttaccoc	3087
SULTX3	7	(intron 1 6905)	agtactttttttatctcc C/T catctcacaactttggccat	3088
SULTX3	8	(intron 1 7464)	ggcaggatcccttgagagc G/A acatgaacacagccaggagc	3089
SULTX3	9	(intron 1 7833)	tgtctoggctgggcttggc G/A ggggcagctgtgtccaggc	3090
SULTX3	10	(intron 1 8189)	caaatlgggcccttaatgc C/T gcacaccagagcctcttctt	3091
SULTX3	11	(intron 1 8316)	ctctcacaaaggcggagc C/G tcttcccttgaggcagagc	3092
SULTX3	12	(intron 1 8617)	agacagaggctggggccaag C/T cagggttgcgggagcttcc	3093
SULTX3	13	(intron 1 8631)	ggcaagccagggttgcggga G/T ctctctgactggctcaggcc	3094
SULTX3	14	(intron 1 9493)	ttttcctcttagagcttcc G/A togtctctgtgtcgagggc	3095
SULTX3	15	(intron 1 10306)	caggcggggagctgaatgc C/T gcagtcgtgagggtggccag	3096
SULTX3	16	(intron 1 11987)	tcataaataatgatatcag I/G acacttttggaaatttag	3097
SULTX3	17	(intron 1 13085)	ctctgtgcgcgtgtgtgaga C/A aggcctatgcccttagagtcct	3098
SULTX3	18	(intron 1 13108)	ggcatcccttagagctctgg G/A gagttccacccacagacagc	3099
SULTX3	19	(intron 2 700)	gaaccatcgggagctgttc C/T gtacigccgtgocgaggcc	3100
SULTX3	20	(intron 2 818)	agccatagtagctagccagc G/A atcagcgtggaggaggagc	3101
SULTX3	21	(intron 2 1677)	actccacttcccctgaacc C/T acccttctctctctctctg	3102
SULTX3	22	(intron 4 4954)	gggtgccgaaggcggagggg C/T tgggatggctcaagacgtga	3103
SULTX3	23	(intron 5 3632)	ccagctgactccacacaccag C/T ggtcagagaacattgtcttt	3104
SULTX3	24	(intron 5 3662)	acattgtctttaaggcttc C/T gaagtcgtcaataaagaaa	3105
SULTX3	25	(intron 6 1874)	tctgatctcagagagctgac A/G atggaaagaattctaaacga	3106
SULTX3	26	(intron 6 2133)	agaccggtgctgcagtta T/G cccacagctcagccctccct	3107
SULTX3	27	(intron 6 2524)	ggaaaggccaggctgcctg T/G gatccacagagcagtgcaact	3108
SULTX3	28	(intron 6 2573)	agatcatactcgtctcctggg A/G tgtttattaaacacctgccaa	3109
SULTX3	29	(3' flanking region 12)	gttcccggttctcgtcag C/G gtttctgttgggggtag	3110
SULTX3	30	(3' flanking region 445)	tcaaaagctgtctctctga T/G ttccctgtggaagagagctcc	3111
SULTX3	31	(intron 1 6418)	ctctccctgttagtgggg G/ Δ cagctctttccagtgctctg	3112
SULTX3	32	(intron 5 2458)	cccttaagaggagttcatc C/ Δ ttctctgcttccaggctcc	3113
TPST1	1	(5' flanking region -298)	accgcacacatcccagct A/G atttttttattttttt	3114
TPST1	2	(intron 1 3520)	agaaaagcagattaatgtaa C/G agtgacgttagacaacaag	3115
TPST1	3	(intron 1 3610)	ggcagaagagagaatatagca A/G ctatttaaacacaaataaatt	3116
TPST1	4	(intron 1 20828)	tattgtgtccacctggtoa A/G tgtgtcctgtgtataagtgc	3117
TPST1	5	(intron 1 -6761)	aatacaataattttctgta T/G aattctagaggggccagaga	3118
TPST1	6	(intron 1 -544)	tagaacaagtgaaatttta C/I gtcttagtggtttatggtt	3119

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
TPS11	7	(intron 1 -526)	tacgttcttagtgggtttatg G/I ttggcagttttccccaaca	3120
TPS11	8	(intron 1 -234)	taagacatttaataatga C/I atgtttcagctaacccctttt	3121
TPS11	9	(intron 1 -48)	ttatagtggttttaagcatg A/G ttcttaaaaaatttaataa	3122
TPS11	10	(intron 2 -18944)	aaaacattagaaciggaag G/A ttaaaaaatcttttagcttt	3123
TPS11	11	(intron 2 -18687)	taigtgacccctaataacat A/G ttctttaaaactagtacta	3124
TPS11	12	(intron 2 -18501)	ttggaaggtaacttaatgta A/G gtgcotgaaaaaacaggata	3125
TPS11	13	(intron 2 -159)	gaatggggatttccctcagt C/G ctgcocactggctgtcttg	3126
TPS11	14	(intron 2 -19)	acctgtgctttaaactcac G/A cctgtttgtttttocaggt	3127
TPS11	15	(intron 3 158)	tectggggaagaagaatcag C/G gtctgggactgttgatttt	3128
TPS11	16	(intron 3 3779)	agcaggcgactcacocctc C/I ggacacacacatgtgtcaoc	3129
TPS11	17	(intron 4 292)	ttgtatttttcattatgaac C/I atgaatatattcaegtga	3130
TPS11	18	(3' untranslated region 1518)	gtgtctgtacatgttctaa I/G gttttgtagaacacgtgtgc	3131
TPS11	19	(3' flanking region 264)	acgggtcttgccctgcattta C/I cattttgtagtgaatttct	3132
TPS12	1	(intron 2 578)	tcacctatcatctcactgc G/A aggatgcaggagataoctc	3133
TPS12	2	(intron 2 789)	cctaagccatcgtgcaggtc A/G ttgtctgtcttctgtcactt	3134
TPS12	3	(intron 3 2009)	ccagagctggagtgtagtgg I/C gtgatct c/t ggcactatgcaa	3135
TPS12	4	(intron 3 2017)	ggagtgtagtgg t/c gtagct C/I ggcactatgcaacctcggcc	3136
TPS12	5	(intron 3 2035)	ctcggctcactgaacctcc G/A cctccgggttcaagcagtt	3137
TPS12	6	(intron 4 104)	aatgttcagtctctcaatc C/I tggtoactgtattgttct	3138
TPS12	7	(intron 4 379)	taataataaactatttgt C/I cctttctgtcttataaggt	3139
TPS12	8	(intron 4 588)	tactgcagcctataacttct C/I ggcttaagccatccctcacc	3140
TPS12	9	(intron 4 626)	caccocaggctcctgagtag C/I taggactgcagggtgcagcc	3141
TPS12	10	(intron 4 718)	ccagagctgcttagaactc C/G tggcctgaaggatgccct	3142
TPS12	11	(intron 4 873)	gttgatggccttatttatac G/A ttccattacagctcttagt	3143
TPS12	12	(intron 4 949)	caaatatttgaatatgggac C/G caggcctgagggaagagcttt	3144
TPS12	13	(intron 4 1033)	taagctcagcatttctgagc G/A tgtgtgatttttagaaaata	3145
TPS12	14	(intron 4 1051)	gggtgtgtgatttttaggaa A/G taaacagttatcgtatigaa	3146
TPS12	15	(intron 4 1356)	gattcaacgtacataccagc C/I gacattgacaggtgaatggc	3147
TPS12	16	(intron 4 1707)	gtctccttaaaaggtggctc G/I ctgccccgtggcttgccccag	3148
TPS12	17	(intron 5 215)	aagacagcctgacccaaaac G/A gtgaacccccgtctctacta	3149
TPS12	18	(intron 5 341)	tgggaggcagaggctgcagt G/A agctgagatcacgcgttgc	3150
TPS12	19	(intron 6 31)	ggacttcactgggggttccc G/A ctgtctctgggtggccccgg	3151
TPS12	20	(intron 6 273)	gtttgtcgacactggggac A/G gggcagggaagccaccactatg	3152
TPS12	21	(intron 6 693)	aaaggatttttttgaactt G/C gtaattcaagaatttaagat	3153
TPS12	22	(intron 6 1635)	tcctgggtacagagttggcc I/G tgaacaaacatgagtccttc	3154
TPS12	23	(3' untranslated region 1147)	cttccocactttcagatctc C/I gcaaatgacttcattggccaa	3155
CST	1	(intron 1b 6302)	agagctcccccagagagact A/G tgaggctgcgatgcacatga	3156
CST	2	(intron 2a 1004)	gagtgaagcccccatctcta C/I aaaaatttttttaaaaaagta	3157
CST	3	(intron 2a 1395)	atgcctaaattttacagtagc I/C aggcaggaaaaggcacaacca	3158
CST	4	(intron 1d 473)	ccagagcctgaggttggtgc I/A gggggccctcccatggcigcc	3159

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
CST	5	(intron 2b 726)	ctatctctcagtgctctctc t/c gtcctgtctggacctgct	3160
CST	6	(intron 2b 745)	ctgtccctgtctggacctg c/a tggggggccacagacagcgc	3161
CST	7	(coding region 85 (Val 29 Met))	taactagtttctctgctg g/a tgaactctatgocgtgccc	3162
CST	8	(intron 3 308)	tgtctgagctcaggagttc g/a agaccagcctggccacaatg	3163
CST	9	(intron 3 853)	ttttgctctataaaatggca g/a tticattgtggcccaagctga	3164
CST	10	(coding region 198 (Asn 66 Asn))	gagcagatgcctggccca c/t ggcctggcggggagtgcca	3165
ST1B2	1	(intron 1 80)	actgtccataaatcattta c/t cattctaaataaagttaata	3166
ST1B2	2	(intron 2 -352)	aacatttaaatagctatta t/c agcaatgcacaggtataata	3167
ST1B2	3	(intron 2 -85)	attacataatgcataaaat g/a tottgaanaaacigtgggca	3168
ST1B2	4	(intron 4 460)	gtacttgacattaaaaata t/c ctgattgtt a/g tataccata	3169
ST1B2	5	(intron 4 470)	ttaaaaata t/c ctgattgtt A/G tatatccataaataagctaat	3170
ST1B2	6	(intron 4 518)	tttaagatgtctctcattt c/g ttacttccctttgtttactaa	3171
ST1B2	7	(intron 4 616)	aatgtttatgaaatagact t/c ttatctggttttagtgccct	3172
ST1B2	8	(intron 5 58)	cgcacatcgtctgtaaaag g/a ttgatatgtttgtttccaact	3173
ST1B2	9	(coding region 612 (Glu 204 Asp))	taatagaattccaaaggagg a/c atcaagaagatcattagatt	3174
ST1B2	10	(intron 6 582)	aatacattacttccatttaa g/a tagtgtttttattgtggctt	3175
ST1B2	11	(intron 6 3130)	agatgtaaaaaattattcaa A/t ttttaaaagccigaaaaatt	3176
ST1B2	12	(3' untranslated region 907)	tttaagtgcttaaatcaca c/a atctgaagaataaagagatt	3177
ST1B2	13	(3' flanking region 50)	tcagatccagttttgttcc t/g ttgattctgagtttccaat	3178
ST1B2	14	(3' flanking region 328)	tttgaccaggaacactgtgt t/g coactgtctgtaccagatt	3179
ST1B2	15	(3' flanking region 446)	gtagttcagattttgaaat c/a tttttctatatactaccta	3180
CHST1	1	(intron 1 3900)	gcctgcccccactccaga c/g ttggccctccagccctt	3181
CHST1	2	(intron 1 6520)	ctctcccccagagagctgg c/t acactggggcctgtgtgt	3182
CHST1	3	(intron 1 7963)	aaacattcatggggatta g/c tctgtgctacgtcagagtca	3183
CHST1	4	(intron 1 9173)	ggctgccacagatcaggcc g/a aggtggggacagaaatgoc	3184
CHST1	5	(intron 1 9701)	ccagaattctgaatacagc A/g ggaatgacgggactacgagg	3185
CHST1	6	(intron 1 12132)	aacagatccacaggaccaga c/a agcaaaagggaggaaacatgc	3186
CHST1	7	(intron 1 12465)	atgcagggaaggcgctggc g/a caaaactgtcaactagata	3187
CHST1	8	(intron 1 12561)	atgctccctgttccacttc g/a ctttgagtttcaggtagctg	3188
CHST1	9	(intron 3 529)	ccatggctgcagggtcct t/g catgtcagggtattggggt	3189
CHST1	10	(intron 3 617)	agaggacagaggaagagg a/c aacciggagaactggcgcc	3190
CHST1	11	(intron 3 796)	aagagcttccgcagctgtc c/t gcaggttaaatctcgggtg	3191
CHST1	12	(intron 3 818)	caggttaaatctctgggtgc A/g aggaatgtttgttcagctcc	3192
CHST1	13	(3' flanking region 762)	ataactgtacagtttact g/c gtgtctacactggcagagaa	3193
CHST1	14	(intron 1 7874)	gttttcccttgcttgcct t/Δ cattttcatcactcatitt	3194
CHST1	15	(3' flanking region 335-349)	cacactggcacactggcta (T)12-15 ggatttttagtagacagggg	3195
CHST2	1	(5' flanking region -260)	agccggacagctcccgggc g/a gtgatccggggcgccgtccc	3196
CHST2	2	(5' flanking region -56)	ggcctggggaccagcgccg c/t gcccgctcggagtcggcg	3197
CHST2	3	(3' flanking region 218)	aggagtgaacacatctttg t/a attctaaaggcagaaaccaa	3198
CHST2	4	(3' flanking region 383)	gcagagaccaatgttttgt g/c ctgaggtgtgttcagaaaa	3199

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
CHST2	5	(3' flanking region 952)	tactgaacattctcgaaa /C gttatactatgagaagaat	3200
CHST3	1	(5' untranslated region -294)	tcagcgtccagaccggccc C/G gaagcgcctccatccctcog	3201
CHST3	2	(intron 1 96)	gggtccaggcgcgcgcgcca G/A actttggaggagaaggggg	3202
CHST3	3	(intron 1 4467)	agagaagaatggggcagagc C/G ggagcagccaggggagggtga	3203
CHST3	4	(intron 1 4853)	ggatgagcactgccacgctg A/G tccctgccacotccacag	3204
CHST3	5	(intron 1 4965)	tcacgtcagaggggacaca G/C tgaccaggacggaagtgggg	3205
CHST3	6	(intron 1 5046)	ggcgtgccatctttttacc C/T cigggtccatccagtgct	3206
CHST3	7	(intron 1 5300)	ccctttctctotaaggcct A/G aagagatgacagaatgctgc	3207
CHST3	8	(intron 1 5354)	agcgcgtgactccacagcg G/A ggtgtggggtggccctggc	3208
CHST3	9	(intron 1 5428)	gacacgttcagccctctgt C/G tctattgccccaaatctggc	3209
CHST3	10	(intron 1 6555)	gggtgggcacgtctggaag G/C tctgtttctcgtttgttc	3210
CHST3	11	(intron 1 6990)	aaacacactgggccacccc G/A tccccgcactgtgactaac	3211
CHST3	12	(intron 1 7133)	ctgaggccctgtcctcgagg /G ttgatgtgtctgaaggcc	3212
CHST3	13	(intron 1 7161)	gtctgaaggagcccgagaa /C agaaatctagaacctggccag	3213
CHST3	14	(intron 1 7199)	cagtcacgaagcagtgctaac C/T caccagaggatgaagaactg	3214
CHST3	15	(intron 1 7316)	cttgcatctgggtagggtgc C/T tgggggtagcgtgccagga	3215
CHST3	16	(intron 1 7967)	gacaggaaacccaccccgag /G gatgtctggccctgtgacot	3216
CHST3	17	(intron 1 11412)	gcctgcactctgattcatt C/T tgcagtcactggcctctttgt	3217
CHST3	18	(intron 1 11591)	ccctggaaggccctcactgc G/A gtgaactattaccagcatg	3218
CHST3	19	(intron 1 12541)	accacacagcatgaatggg G/C ccagcccagcctgcccgt	3219
CHST3	20	(intron 1 12672)	gtagccacagctggggcgtg G/C gggtcaggccatggcaagg	3220
CHST3	21	(intron 1 14809)	ggatgttaggggtttgggct C/T agccttaagggaatgggtga	3221
CHST3	22	(intron 1 16161)	gatgtctgtagcagcattgtc G/A ttgggatctttaaccaccc	3222
CHST3	23	(intron 1 16385)	tatttagcatgtgggtttca A/C ctttctgttttttcaagg	3223
CHST3	24	(intron 1 33638)	gacttggccacgtccttgg G/C catgaatcttgtctatgtc	3224
CHST3	25	(intron 1 35145)	agggaaagccgaagccctcact /C gcitggggttgctggcctc	3225
CHST3	26	(intron 1 35340)	tgtgaagtittgcccacagt /C gctggccatgggttcgcacog	3226
CHST3	27	(intron 1 35436)	gcacatcatgtatggagcaa /C tgccttttttttctctctt	3227
CHST3	28	(intron 1 36150)	ccatagaaggctgggct G/T aggaagccagggaagcagga	3228
CHST3	29	(intron 1 36194)	gggtggggaggccagcagg G/A gtgtggccctcagcggggag	3229
CHST3	30	(intron 1 37602)	ctgggaacagcaacttaaaa A/T agaaatagtccttggaagg	3230
CHST3	31	(intron 1 37725)	gggtagccaggcagctccc C/T gaccogca c/g ctgccttttca	3231
CHST3	32	(intron 1 37734)	gggacctccc c/t gaccgca C/G ctgccttttaccctctcc	3232
CHST3	33	(intron 1 38208)	gcattctagatcgagatcc C/T gactttggg t/c gcttgcatt	3233
CHST3	34	(intron 2 255)	ctacagctgtgaaggttag A/G caagatacttaacatttctg	3234
CHST3	35	(3' untranslated region 2202)	acacctcaggagagcctgtg C/A ttaacattttaggattatt	3235
CHST3	36	(3' untranslated region 2569)	aggcctcatctgggttaggg C/G caagaggaaagtacagagt	3236
CHST3	37	(3' untranslated region 2717)	ctggaattcctcttagggc C/T ctgggaagagatttgottaa	3237
CHST3	38	(3' untranslated region 2753)	cttaacgcagagtgctcgg G/A tgtttgttcgggctttta	3238
CHST3	39	(3' untranslated region 2800)	gccttgatgtcttctctgttt C/T atggcgtgtgttttctgttt	3239

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
CHST3	40	(3' untranslated region 3283)	ccgagggtgccagcctc C/I tctggtttctggacaatt	3240
CHST3	41	(3' untranslated region 3327)	ctgtacagatagcccatc C/I aaacccagaggctgcattt	3241
CHST3	42	(3' untranslated region 3387)	gttcccatctggagtcgg A/G gggctggagactggggagg	3242
CHST3	43	(3' untranslated region 3860)	ggccctgtcaatggagac C/I agactttatccctctctt	3243
CHST3	44	(3' untranslated region 4915)	ccagatgtcattagagcca G/A tctctgcacatacacccga	3244
CHST3	45	(3' untranslated region 4993)	taagcaaatcttagcttt G/A tctcttgcacatacacccga	3245
CHST3	46	(3' untranslated region 6208)	attcatgtctgatgtac G/A agacaccccttcac g/a gcata	3246
CHST3	47	(3' flanking region 281)	agacagaggtgtggccag C/I ggtcaggggcctggggatg	3247
CHST3	48	(3' flanking region 997)	acctctaaagtattgagc C/I ggtcctgtcatcccaacct	3248
CHST3	49	(intron 1 22595)	cgggagcaggaataaaaa A/ Δ gaataagagaaagaggct	3249
CHST3	50	(intron 1 35423 35424)	gctcatgctcacagccactc A/ Δ gtatggagcaa t/c tgcctttt	3250
CHST4	1	(5' flanking region -1092)	atgaagctgtgcccattc G/A ctgtctgtgcccagcacctg	3251
CHST4	2	(5' flanking region -941)	ctgccagagagaacaggaa G/A ggaggaagagccacacaatt	3252
CHST4	3	(intron 1 -150)	caggaaatgatttggagaag G/I actgtgcatctgtggcac	3253
CHST5	1	(intron 1 -144)	ggcctcttaggtttcagcca A/C gacagtgactcttagcaac	3254
CHST5	2	(intron 2 17)	caacgtaagagagcttctca I/A tgtccagctcttctttct	3255
CHST5	3	(intron 2 139)	aatccagcaccttggagg C/A gtagatgtcggatgata	3256
CHST5	4	(intron 3 1829)	gactgtatgtctgtattca I/C ataggacaataatattcatg	3257
CHST5	5	(intron 3 2037)	aaatgaacacacaccca C/G tgcagagagcaacacaaag	3258
CHST5	6	(intron 3 2134)	aagcagctaatgtgttcc G/A tacagtgcaattaggcagg	3259
CHST5	7	(intron 3 2528)	atgtaaaagtgcctgggt G/A cagatgtcagcatctcgtct	3260
CHST5	8	(intron 3 2674)	gcattatcctagaagacc A/G tttctgaagactcagcagga	3261
CHST5	9	(intron 3 7039)	ctggctcccgccggccacc I/C gggacgcagccacgtctga	3262
CHST5	10	(intron 3 7211)	gtagcccccagacaccccca I/G cctcaacatcccattctggg	3263
CHST5	11	(intron 3 7294)	ggagcttcagtggttgg I/C accccagactcttctgacct	3264
CHST5	12	(intron 4 108)	gcagggtcctgcactcigca G/A gggcaatcacagggtggag	3265
CHST5	13	(intron 4 402)	agcactggaaaaagtacagt I/C gcactgtagcggaggtggg	3266
CHST5	14	(intron 4 547)	ctctgtcccgcatcagg C/G gaaggagcagaggtgagatc	3267
CHST5	15	(intron 4 1142)	gcccaggtctcatagctcc C/G catggcagtcgctgggattt	3268
CHST5	16	(intron 5 1187)	caatggcagtaattggggc A/G tggatgggcatgaggccc	3269
CHST5	17	(intron 5 139)	gtgttttggcactgaaga C/I ctccctagttcggggagta	3270
HNK-1ST	1	(intron 1 139)	acctgagcagaaaattctct I/C ctctcgtgaatgaaattg	3271
HNK-1ST	2	(intron 1 1020)	aagaattgttaaacatcaca G/A gcaacttgcagttatatcg	3272
HNK-1ST	3	(intron 1 1091)	ctataactatttcaacata C/I gaaacaggcataattgatt	3273
HNK-1ST	4	(intron 1 1971)	atttagaattatttacc A/C agaatacacaataaacctg	3274
HNK-1ST	5	(intron 1 2096)	ctatccagtgacagaggaa C/A caagaacctcagttcaggg	3275
HNK-1ST	6	(5' untranslated region -91)	agtgggcggagcagagagc G/A tcaagtgttcattccttctct	3276
HNK-1ST	7	(intron 2 -530)	gctacatcttgcagccagt C/I agaattttaaacacacagcag	3277
HNK-1ST	8	(intron 2 -466)	acgaaatatttctgtgat A/I cttaactgactgaatacact	3278
HNK-1ST	9	(intron 2 -92)	catgcccctcgttcttcat G/A ttacagagggttgaggagag	3279

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
HNK-1ST	11	(intron 3 312)	cacaggcgccttcaggct	3280
HNK-1ST	12	(intron 3 1948)	tcctttgatgtatcaagttt	3281
HNK-1ST	13	(intron 3 2140)	ttacacctggaggagacac	3282
HNK-1ST	14	(coding region 187 (Leu 63 Leu))	agaagacatttcctgaggaa	3283
HNK-1ST	15	(intron 4 581)	ccatgatttccttcagctgg	3284
HNK-1ST	16	(intron 4 615)	tcaggaggcccttcctac	3285
HNK-1ST	17	(intron 5 7)	gattgttctaaatgggtgt	3286
HNK-1ST	18	(intron 5 123)	acctgaagggaactggggcc	3287
HNK-1ST	19	(intron 5 721)	ataattatgggtctctt	3288
HNK-1ST	20	(intron 5 867)	tgctgccacagatcgtgg	3289
HNK-1ST	21	(coding region 444 (Ile 148 Ile))	ccaggagcattttctccat	3290
HNK-1ST	22	(intron 6 94)	ctgagttctgtactggcag	3291
HNK-1ST	23	(intron 6 247)	catgaagggtgaatcatttt	3292
HNK-1ST	24	(coding region 696 (Thr 232 Thr))	aggaggaacccggacagac	3293
HNK-1ST	25	(coding region 870 (Ala 290 Ala))	gagacactggagcagatgc	3294
HNK-1ST	26	(3' untranslated region 1110)	tcaaatattcttattagacc	3295
HNK-1ST	27	(3' untranslated region 1178)	ccacacccctcttttgagg	3296
HNK-1ST	28	(3' untranslated region 1393)	ggaagcatcacacaggtta	3297
HNK-1ST	29	(3' untranslated region 1452)	tgaggttctcctggctagtc	3298
HNK-1ST	30	(3' untranslated region 1540)	gcaagggtctgtgtaaatc	3299
HNK-1ST	31	(3' untranslated region 1696)	gggtgtgtgtgtccagg	3300
HNK-1ST	32	(3' untranslated region 1829)	agggaggctttttctacct	3301
HNK-1ST	33	(3' untranslated region 2211)	tcacgagtcggcttctctg	3302
HNK-1ST	34	(3' untranslated region 2212)	ccagcagtcggcttctctg	3303
HNK-1ST	35	(3' flanking region 1016)	ccacgaagggtgtgcactca	3304
HNK-1ST	36	(3' flanking region 1152)	gaatggtttgctcatctgga	3305
HNK-1ST	37	(3' flanking region 1291)	gcgagacactcagcaggat	3306
STE	1	(5' flanking region -605)	caggtttctaaataataat	3307
STE	2	(5' flanking region -536)	taaaatttcaggctctgctt	3308
STE	3	(5' flanking region -231)	cccttcccccaccctga	3309
STE	4	(5' untranslated region -64)	tcagattgaatctgcctt	3310
STE	5	(intron 1 69)	aaatatagaatgaaaattat	3311
STE	6	(intron 1 311)	caatgagaaaataaagcaag	3312
STE	7	(intron 1 655)	tctaagaagtaggactat	3313
STE	8	(intron 1 671)	ctatgagaacctatgatat	3314
STE	9	(intron 1 772)	aaagcagattggaaagatg	3315
STE	10	(intron 1 1715)	taaccatttgttaacctt	3316
STE	11	(intron 1 1928)	aaatgatacatattcaggaa	3317
STE	12	(intron 1 1953)	aaatctctgacttagatacc	3318
STE	13	(intron 1 2087)	aaatttgaagaagaatigaag	3319

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
STE	14	(intron 1 2323)	taggtatgtaggagggtcc G/C ttatacatagttgttaat	3320
STE	15	(intron 2 165)	tctattccatgaccacaatt I/G ttacotgttaacttgaatagt	3321
STE	16	(intron 2 1707)	cttaggacccaacatgagac A/G taataaccatcagtaaaat	3322
STE	17	(intron 3 850)	gggtccattccccaagaa I/G ttatactttgtgttacacac	3323
STE	18	(intron 4 1653)	agtaacaggctagtataaa I/C ataaataactgaggccaacg	3324
STE	19	(intron 4 1899)	tacatgaacttagagaatca A/G gtagatcacacacacaaca	3325
STE	20	(intron 4 1930)	cacacacaataaaattac A/G cagaatgataaaagaatttg	3326
STE	21	(intron 5 666)	ttcgtatcatgtagtaacaa I/G tataagaataataatagt	3327
STE	22	(intron 5 982)	aggcaagcagaacacittg A/C ctcacacacattatattat	3328
STE	23	(intron 7 369)	agattttattctctctctt I/C ttgagttgaagaataaagtt	3329
STE	24	(intron 7 447)	caacttcaaggtaagtgg C/A aaaaaatagaataatcaaat	3330
STE	25	(intron 7 672)	aattctgtcitttgaacct A/I cgtcagtgagagtcaggga	3331
STE	26	(intron 7 856)	gttiacagaggacattaaac A/G gtgtctgtcttgcaaacgg	3332
STE	27	(3' flanking region 218)	cagctcccaagttagctagg A/G ctacagacatgtgcaacct	3333
N001	1	(intron 1 80)	aggaggtttaggggttgg C/A ctgaattttgttccctgaact	3334
N002	1	(5' flanking region -434)	tttctttgcacacacgacc C/G toattctgtaacocgggatac	3335
N002	2	(5' flanking region -406)	gtaacgggataaccacccag A/G gatgggagcgggagcgca	3336
N002	3	(5' untranslated region -102)	tcctgggctctacttggg A/C gtgcctgtgtcgggaaggtga	3337
N002	4	(intron 1 1919)	tcactcaatatagactgagt I/C agtcactcagctcttggacc	3338
N002	5	(intron 1 2004)	aaacatcacatgccaccag C/G cataigtatgaacatgttaa	3339
N002	6	(intron 1 3391)	aaagcagagggtgtgcagg C/I gccctgccccctaggctagg	3340
N002	7	(intron 1 3456)	caaaagccctacactcaggg C/A ggccaactcttctgttttag	3341
N002	8	(intron 1 3595)	actgcacagcttttaggttca I/C tottgaagtgttgcgtgtg	3342
N002	9	(intron 1 3596)	ctgccagcttttaggttcat I/C cttgtgaagtgttgcgtgtgt	3343
N002	10	(intron 1 3598)	gccacgttttagttcattc I/G tgaagtgttgcgtgtgtca	3344
N002	11	(intron 1 3651)	ccctggcctttgaaggatg A/G atgtgacctctccacattc	3345
N002	12	(intron 1 6036)	tagtgtggcgttcactgat C/I cccagccttctgtctgatac	3346
N002	13	(intron 2 14)	atggcaggtaatgattcaat A/G ttgtggagtaagacttttt	3347
N002	14	(intron 2 192)	gccactggaagtgtataaa C/I tatctgggaattatcttgttt	3348
N002	15	(intron 2 635)	cacctgttttagcacctagc A/G ccattccctggcctctgccca	3349
N002	16	(intron 2 685)	agtagacccctcccccacc G/A gcgtgacaaacccaaaatgt	3350
N002	17	(coding region 139 (Phe 47 Leu))	ctgatttgtatgcatgaac I/C ttgagccggggccacagac	3351
N002	18	(intron 3 36)	aatgctctattataaaaac I/C atctttatgttttttacttt	3352
N002	19	(intron 3 728)	aacgtgggataaacaccca I/G ctatggccaaaagaaggttg	3353
N002	20	(intron 4 1577)	tgcctctgcacaccccttc C/I gacaccagcccttctttac	3354
N002	21	(intron 4 1832)	tgggcggcgcacgtggagcc C/I gctttcctcctgcacccac	3355
N002	22	(intron 4 2583)	tgtgttaagcacagctcct C/I gtccctcctcctgcctgccca	3356
N002	23	(coding region 330 (Pro 110 Pro))	cigtactgtttagctgacc A/G gccatccctgaaggctggat	3357
N002	24	(coding region 405 (Ser 135 Ser))	atcccaggattctacattc C/I ggtttgctccaggtatgtgc	3358
N002	25	(intron 5 21)	gtaigtgcctctggataagg A/I tcaatgatgtagtggagg	3359

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ND02	26	(intron 5 253)	atggcaacaaggagtgagg /C cagggtgcaggtgacggggg	3360
ND02	27	(intron 6 2435)	cccccttaaatcatitaa /C gaattgtaaacaggtgt	3361
PIG3	1	(5' flanking region -47)	gggaaggaggaagaaga G/A gggagggtggttctgcta	3362
PIG3	2	(intron 2 243)	taacacgggagccagcag A/C agtccagcttcttagaatc	3363
PIG3	3	(3' flanking region 282)	agcagggccagccagctccc G/A ctactcaactggggccccc	3364
PIG3	4	(5' untranslated region -93)	tcgcgaggagataacggccc (CG/GY)16 cagacaataagttagccgtg	3365
PIG3	5	(3' flanking region 625~626)	ctctcagggcccccctt (T) ccattactcaacttgggtccc	3366
PIG3	5	(3' flanking region 625~626)	ctctcagggcccccctt ccattactcaacttgggtccc	3367
PIG3	6	(3' flanking region 770)	tcacctgggtcccccctac C/Δ tgtcataaccctgtccaagc	3368
NDUFA1	1	(5' flanking region -1437)	aggctaaaaatcctgatta T/A acctacttgaagcttttaa	3369
NDUFA1	2	(intron 2 3071)	aataaagtcacatggcatat C/A tttagtggaacagacttgt	3370
NDUFA1	3	(3' flanking region 1218)	aactcaatgtataaagca A/G caccacagatgacacttcca	3371
NDUFA1	4	(3' flanking region 1411)	ggattgtccatcccttgat C/T ggcaatgaccttttactttt	3372
NDUFA1	5	(3' flanking region 1411)	ggattgtccatcccttgat C/G ggcaatgaccttttactttt	3373
NDUFA2	1	(intron 2 1087)	aacatacaaaaattagccgg A/G t a/g tggtaggggacactgta	3374
NDUFA2	2	(intron 2 1089)	catacaaaaattagccgg a/g t A/G tggtaggggacactgta	3375
NDUFA2	3	(intron 2 1356)	ttccctgaacaacccattg T/C ggccatccagaatcagccaa	3376
NDUFA2	4	(3' flanking region 467)	cacagcctcatggttcagcc C/T actccagagggtgcattccc	3377
NDUFA2	5	(3' flanking region 744)	gggaagcaggccctggccca C/T agccgtggcagtaagcagg	3378
NDUFA2	6	(3' flanking region 838~839)	tatagtcaaaaagaatgaa (AAC) aaagatcataacaatagcta	3379
NDUFA2	6	(3' flanking region 838~839)	tatagtcaaaaagaatgaa aaagatcataacaatagcta	3380
NDUFA3	1	(intron 2 2656)	tcctcgtccctccctcgc G/A caatttatcttcccttggc	3381
NDUFA3	2	(coding region 241 (Leu 81 Val))	agggcccccagctggagtg C/G tgaagaaactgtgagcaact	3382
NDUFA3	3	(3' flanking region 1019)	tccttaactcactggccacc A/G gctctggagcccccagctccct	3383
NDUFA5	1	(intron 3 2155)	agacttagcatgtaacg G/C aacataagggttccttagaaa	3384
NDUFA5	2	(intron 3 2493)	ggcataatgtctgtttctc G/T gctcaatttcatcatctat	3385
NDUFA5	3	(intron 3 2712)	acaaatttgaactgttcc C/T taacacagggctttttctgaa	3386
NDUFA5	4	(3' flanking region 1296)	aggtatcaaaaggatattg C/C atttgctattggtttcttc	3387
NDUFA5	5	(intron 3 30~31)	aagtcagttttgtgtcttg (GATTTGGTATCCAG) igtaacatttaacccaaaaa	3388
NDUFA5	5	(intron 3 30~31)	aagtcagttttgtgtcttg igtaacatttaacccaaaaa	3389
NDUFA5	6	(intron 3 427~428)	attaagtagcagtttaataaa AG/Δ tctagactgtctgattcatac	3390
NDUFA5	7	(intron 3 4733~4734)	tataggaaatttaaaatata TA/Δ ggtatigaacattcagtt	3391
NDUFA6	1	(5' flanking region -1148)	ttataatttatatattta C/T ggttttcttttttatagct	3392
NDUFA6	2	(5' flanking region -363)	actaccaaggagcgcgcgg G/A cagccggtatagcaggagct	3393
NDUFA6	3	(coding region 26 (Ala 9 Val))	gggagcggctccgcaag C/T tacttcaocgcagcacct	3394
NDUFA6	4	(intron 1 1318)	attcagcagtttgaatacat A/G atgtttgcttggcagaatac	3395
NDUFA6	5	(intron 2 562)	agttaaagaatcgaagaagt G/C tcagaaatgatttaccctga	3396
NDUFA6	6	(5' flanking region -861)	ctgtaaaatgggggtgtga (T) ggtacotacgtgacctatga	3397
NDUFA6	6	(5' flanking region -861)	ctgtaaaatgggggtgtga ggtacotacgtgacctatga	3398
NDUFA6	7	(intron 1 1251~1278)	tgtgggagtgactgtagca (GT)12-14 ttgggggtgtgtcattcaaa	3399

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
NDUFA7	1	(5' flanking region -31)	accacacaaaggtctatcaa A/G ggggtgtctctctttgcaccc	3400
NDUFA7	2	(5' flanking region -434)	aaagggaacacatcagaaccc C/I gtgatgaaatgagaatcgcc	3401
NDUFA7	3	(5' flanking region -395)	gtcccggtattccggctggc A/G ggggttagggcaggtagag	3402
NDUFA7	4	(5' flanking region -100)	agaggagtcacgtgtctcgg G/A gagagcctttataggacgtt	3403
NDUFA7	5	(intron 1 92)	tcacctccctcttaagccag G/A acccttgcctctcccgaaat	3404
NDUFA7	6	(intron 1 133)	ctctctgggaaccccagct A/C gt c/g acccttcagcccgga	3405
NDUFA7	7	(intron 1 136)	cttgggaaccccagct a/c gt C/G acccttcagcccggaaccc	3406
NDUFA7	8	(intron 2 89)	tccttttagacccctgaagc G/C agggctgacatctctgccaac	3407
NDUFA7	9	(coding region 196 (Pro 66 Ala))	ggcgcgggaattctgtgcc C/G ctccatcatcatgtctgtctg	3408
NDUFA7	10	(intron 3 4203)	gctccacccctggggcgcc I/G cctccatcaccccccactcc	3409
NDUFA7	11	(intron 3 4604)	ggccctgtgtacgtcggag A/G ccaaaagggaaggaggaga	3410
NDUFA7	12	(5' flanking region (-1353)~(-1360))	agggtccagggtccctcgt CAGAGGCT/Δ aacactggccgaagagaag	3411
NDUFA7	13	(5' flanking region (-1233)~(-1234))	agccctgaccacccactct CT/Δ gaaactctttgtctaataa	3412
NDUFA7	14	(intron 2 4142~4143)	catttgtactgaggtgac AG/Δ gggccacacggggggccatg	3413
NDUFA8	1	(intron 1 -75)	tttgtttctctattctgac C/I cgaatgaggtaaagctgaga	3414
NDUFA8	2	(intron 2 790)	caaacctagacaaagtgct C/I cttatccagaagtgagcag	3415
NDUFA8	3	(intron 2 900)	ttcaggagataaaaagctct G/A attgtcagggcctgagatag	3416
NDUFA8	4	(intron 2 3837)	gaagtgtctgttaagtgag A/G taagaatatgtactcacata	3417
NDUFA8	5	(intron 2 3942)	tcattgtttgcaaaagat G/I cccctaacccagctttcttt	3418
NDUFA8	6	(intron 3 -66)	gaggagacacccaggagcgc A/G tttgaaggttacagattcttc	3419
NDUFA8	7	(3' untranslated region 520)	tttatcttggaaccaagtaa A/G gatggctcgtggccacac	3420
NDUFA8	8	(3' flanking region 367)	gtcatacaaggagctctc A/G ggtatagaagtgcagaaactt	3421
NDUFA8	9	(3' flanking region 777)	attcttttttcaactagg C/I tgtttctccacatcigtact	3422
NDUFA8	10	(3' flanking region 1053)	aaagaaaaacacgtgtga I/A ctgccatggcggctttgtca	3423
NDUFA8	11	(3' flanking region 1190)	gattctcaatgaaaaataa G/I actttttttgtcatttttt	3424
NDUFA8	12	(intron 2 449~453)	tcattgtgcatactacttaa GTAAA/Δ aaaaaactaagctgtgtaat	3425
NDUFA8	13	(intron 2 455~459)	tgcatactacttaagtaaaa AAAAA/Δ ctatgctgtgtaattgttagg	3426
NDUFA8	14	(intron 2 707~708)	tcattttggaaaactctca (A) ccttgtgtaccacaaaatgg	3427
NDUFA8	14	(intron 2 707~708)	tcattttggaaaactctca ccttgtgtaccacaaaatgg	3428
NDUFA9	1	(5' flanking region -807)	gatggctctttgttagaacaa I/G gcagattctcaaaaggtagcc	3429
NDUFA9	2	(5' flanking region -769)	accacagttaagaaaaaat I/C acaagccattgcgttagaga	3430
NDUFA9	3	(5' flanking region -353)	caacacctattttgtttct C/G ttctccacttttccctcgt	3431
NDUFA9	4	(5' flanking region -322)	ttccctcgtcttcttccc C/I cttttctctcctggggccc	3432
NDUFA9	5	(intron 1 447)	attcataatgagcacaaatga A/G atgataatattacaatcca	3433
NDUFA9	6	(intron 1 1039)	ggcttgaatttcagccctgag G/A caagaattaggagtggttag	3434
NDUFA9	7	(intron 1 4010)	aatgtatccaaaaagagattc I/G cattctgcctatagaagaa	3435
NDUFA9	8	(intron 3 49)	gacaaataaattactaag G/A tcatttttaggagtagtagg	3436
NDUFA9	9	(intron 3 107)	aatcttccacagaatggac C/I aaaggcatcctctgttccca	3437
NDUFA9	10	(intron 3 1183)	atctctgagtaattatcatc A/G gattattgttaatcccttta	3438
NDUFA9	11	(intron 3 1395)	attcctagtttcttctcct C/I aagttttgttgtaaccttgt	3439

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
NDUFA9	12	(intron 3 2363)	agaaaatgcatgaatggc C/I ccaactaacactagctcttta	3440
NDUFA9	13	(intron 3 2608)	gtcatttgattaccctgagta A/C agtgactgttaccctgttg	3441
NDUFA9	14	(intron 4 561)	atttataaatcttttgaig A/C ctgggggtctttatcaact	3442
NDUFA9	15	(intron 4 860)	atigtagagtaatgacag C/I agagctgcaacttttttaa	3443
NDUFA9	16	(intron 4 879)	gcagagctgtcaacttttt A/I aaaaaataatatttagcttaa	3444
NDUFA9	17	(intron 4 893)	tttttttaaaaaataattt A/G gcttaaaaaataaaaaatt	3445
NDUFA9	18	(intron 4 1090)	atcattgcgttttaaaagt I/C aagtagtgaatttcagta	3446
NDUFA9	19	(intron 4 1188)	aaccaatcttttttttt A/I tcttcagaaaactttgatit	3447
NDUFA9	20	(intron 5 161)	gggtgtgtgtatgttttga C/I gttttgattgattgctctct	3448
NDUFA9	21	(intron 5 373)	cttttcacaccttgcaactg C/I agtggtttggccacictt	3449
NDUFA9	22	(intron 5 457)	gcagggaagatgcctattc A/C cacagtgcttattgctctt	3450
NDUFA9	23	(intron 5 3113)	gattttctctcttccaat G/A taagcttcccttaaaaaaa	3451
NDUFA9	24	(intron 5 3339)	tctaaactcaaaaacaggtt G/A tttgtttattgtttaggctg	3452
NDUFA9	25	(intron 6 414)	tatagtttggcctttccag G/C atattacatatatgggttga	3453
NDUFA9	26	(intron 6 518)	ctttcatttcttttcacag I/C tgatagctcatttctttata	3454
NDUFA9	27	(intron 7 974)	ggattatgcgtacttggaaa A/G tacttggatagcgggtgatt	3455
NDUFA9	28	(intron 8 368)	acattaattttgatggagta I/G cacaatgcctccagaggctg	3456
NDUFA9	29	(intron 8 954)	gcatacatcagttatatag I/C ctagataagaattacaattc	3457
NDUFA9	30	(intron 8 1253)	tctcttgaatttagata G/I gtactacacatttctc	3458
NDUFA9	31	(intron 8 11608)	gaaaagatagatgataaat G/A accaaaaattcgtgaagaaa	3459
NDUFA9	32	(intron 8 11930)	ctacaaatatcttcaaat G/I gtaatcatgataaagtacaa	3460
NDUFA9	33	(intron 9 1998)	tgtttttaagcctttaaac G/A gctgtggaacctgtgctca	3461
NDUFA9	34	(intron 9 2238)	ccagctattggaggctga A/G gggaggagatcaactttagcc	3462
NDUFA9	35	(intron 9 2885)	acagcgctctgtcttctc A/G gtctcattaggttagcttacc	3463
NDUFA9	36	(intron 10 801)	tacactaaagtgtctcttac G/A tttatacttgagaaagtgtt	3464
NDUFA9	37	(intron 10 910)	tgcagactttcaggtggagta G/C gatggagattgtgtctgt	3465
NDUFA9	38	(intron 10 1180)	aaaactgagtcagacacccc G/A tgcacagaaaacaggggcgt	3466
NDUFA9	39	(3' flanking region 554)	gtgccagcacttaggaatta I/G gaacttctaagtgacttctt	3467
NDUFA9	40	(5' flanking region (-1129)~(-1128))	taaacagtaggggcaagata (TC) gagtggaaaacagccaagatt	3468
NDUFA9	40	(5' flanking region (-1129)~(-1128))	taaacagtaggggcaagata gagtggaaaacagccaagatt	3469
NDUFA9	41	(5' flanking region -341)	tggtttot c/g tttctcaactt I/Δ cccctcgttctgttcccc c/t c	3470
NDUFA9	42	(intron 4 594)	attcaaatttttttcccccc I/Δ aatgatttaacatagtatt	3471
NDUFA9	43	(intron 10 356~375)	taacttctcttaactgctct GAAGAACTGTGACAGTII/Δ ctctctcttcttcttaacct	3472
NDUFA9	44	(intron 10 379~381)	gaaactgttgcagtttctt CCT/Δ tcttctttaaactactcca	3473
NDUFA9	45	(intron 10 384~387)	tggtgacagtttcttctctc IITC/Δ tttaactactaccagtcagg	3474
NDUFA9	46	(intron 10 436~437)	ccatttctcccttaaaattg (TTCITIIIAAAITG) ctctttcaagggttatccac	3475
NDUFA9	46	(intron 10 436~437)	ccatttctcccttaaaattg ctctttcaagggttatccac	3476
NDUFA9	47	(intron 10 495~496)	gccacatccaatgtgcagtt (TTGAGGCCITTT) ctccagacctcatgtcatgtg	3477
NDUFA9	47	(intron 10 495~496)	gccacatccaatgtgcagtt ctccagacctcatgtcatgtg	3478
NDUFA9	48	(intron 10 519~520)	gaactcatgtcatgtgcctg (GGCCIG) tgcatttgccttagggagg	3479

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
NDUFA9	48	(intron 10 519'520)	gaactcatgtcatgtgctg tgcatttgccttagggagg	3480
NDUFA9	49	(intron 10 558'559)	gatcaaaaataaaaaa (A) tactataccaataaccacatc	3481
NDUFA9	49	(intron 10 558'559)	gatcaaaaataaaaaa tactataccaataaccacatc	3482
NDUFA10	1	(5' flanking region -1734)	tgcacttgaactgtttact T/C tctgttaaccatttaccctt	3483
NDUFA10	2	(5' flanking region -1492)	aaacatccacgcaaacagg T/C ttgagaagttaactgtcgcg	3484
NDUFA10	3	(intron 3 370)	agactgtgcattgtccatg C/A agacagagatgtggatgcca	3485
NDUFA10	4	(intron 3 2485)	ttgtattttctttctctg G/A aatgcagtatcagtigaca	3486
NDUFA10	5	(intron 4 236)	ctgtgaagcagattggagc C/T cgggaacctcaaacacagca	3487
NDUFA10	6	(intron 4 1742)	tgtcggcatctgtcgtggt C/T tgcgaagctcaggagcctgg	3488
NDUFA10	7	(intron 4 2090)	ggctggggggaagcagatca T/C gttgctaaaggacaggtgg	3489
NDUFA10	8	(intron 4 3054)	cagctgattatactactgaa A/C cgggataaatg c/t agcttgat	3490
NDUFA10	9	(intron 4 3066)	ctactgaa a/c cgggataaatg C/T agcttgatgattttcagctg	3491
NDUFA10	10	(intron 4 3377)	gtcacagttaataatgctgt G/A ttttaactcigtgtaagtagc	3492
NDUFA10	11	(intron 5 46)	aagcatctctattttgaatg T/C agatcagcactaaaagccct	3493
NDUFA10	12	(intron 8 1465)	gcacgcccagtttctggtta C/T aggcctcatatccaogctgc	3494
NDUFA10	13	(intron 8 1809)	cttggaggcacaaggatggc C/A ggggaactcaacttccctct	3495
NDUFA10	14	(intron 8 11226)	gttgtgtaactgtgtggggc A/G tctcaactctcgggcgcag	3496
NDUFA10	15	(intron 8 11319)	atcttgcttccctcctgcgc G/A tctgttcaggcttgaatcct	3497
NDUFA10	16	(intron 8 11386)	ccataatcctagcttgaac C/T tcttttccctgctgaccc	3498
NDUFA10	17	(intron 8 13361)	ccaggccactgattgcttcc G/A cattttctagcattttctta	3499
NDUFA10	18	(intron 9 183)	tttctgttggaagctgat G/A aagtcctcagatcacagccc	3500
NDUFA10	19	(intron 9 8028)	gaggacattccacagaacct G/A tgactattagcagaaggt	3501
NDUFA10	20	(intron 9 10742)	ctggagagagggtggagc C/G agttcagccagcactgggt	3502
NDUFA10	21	(intron 9 13908)	cacattgttatgtaaccaag C/T ct g/t gaattgcagtgtaaga	3503
NDUFA10	22	(intron 9 13911)	atgttatgtaaccaag c/t ct G/T gaattgcagtgtaagaact	3504
NDUFA10	23	(intron 9 14064)	tcttgactattagaacct A/G tcagataaatittiaaacag	3505
NDUFA10	24	(intron 9 14184)	tggctttggttgggaacagc G/A agagatacagaaccgagct	3506
NDUFA10	25	(intron 9 16487)	cttgaagctgatcttccct C/A cttgaagctgatcttccct	3507
NDUFA10	26	(intron 9 16779)	gcagaagtgactgcttttag G/A ttctcatgacattcagaac	3508
NDUFA10	27	(intron 9 17663)	ttccaaatcaccocagaact T/G tgcagtatttgaagctcct	3509
NDUFA10	28	(5' flanking region (-1668) ~ (-1659))	gtaaaattgttttaactaga (C)9-11 ttccataaaccaaggtataaa	3510
NDUFA10	29	(5' flanking region (-1355) ~ (-1334))	ctgtatccattggaagcac (A)15-21 tgcagaagaaacaaggcaaa	3511
NDUFA10	30	(intron 1 46-61)	tggcggggtggcagggtggc GGGGTGGCGGGTGGG/Δ gagcagttccacatctcccc	3512
NDUFA10	31	(intron 4 2486)	ctcactggaactttttttt T/Δ aatttaatttttaaaatttt	3513
NDUFA10	32	(intron 7 1600'1601)	cacttccattctgactgtta (A) cgggtgattcttcccgcca	3514
NDUFA10	32	(intron 7 1600'1601)	cacttccattctgactgtta cgggtgattcttcccgcca	3515
NDUFA10	33	(intron 9 1054)	gogcgtcgtgtttctcctt A/Δ tctgtccttgtacacgtgtg	3516
NDUFA10	34	(intron 9 8161'8172)	tttctcgtttctggagagc (T)10-12 aatgttgaaaatatgtgttt	3517
NDUFA10	35	(intron 9 8646'8647)	aattccccattgtctctct (TT) ctgtagacatttttaaaccta	3518
NDUFA10	35	(intron 9 8646'8647)	aattccccattgtctctct cgttagacatttttaaaccta	3519

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
NDUF-A10	36	(intron 9 16503-16523)	ccct c/a ctgaagcgtatcgt tcccctcccttgaagcctgaacg/Δ gtccaagatagttgctaggga	3520
NDUF-A10	37	(intron 9 17905-17936)	caaatatagtatacatgta (GA)12-18 tcoitcatgaataaactctttc	3521
NDUF-B1	1	(intron 1 8451)	cagcacccctgtagagccctc G/A ggaatgctgaagatgccatga	3522
NDUF-B1	2	(intron 1 8495)	ggcacagggaattctgcagac G/A ctgacacaatttttagtggcag	3523
NDUF-B3	1	(5' flanking region -1439)	ttaaaagttagcttttttt G/A cc g/a ggcacggtaggcacagc	3524
NDUF-B3	2	(5' flanking region -1436)	aaagttagcttttttt g/a cc G/A ggcacggtaggcacagcctg	3525
NDUF-B5	1	(5' flanking region -213)	ggcggatgaacctctctact A/C aagaaggggcacaacccggcgg	3526
NDUF-B5	2	(intron 1 6288)	ggggatgttgattacctagg I/C caagtaagtaagaagagcat	3527
NDUF-B5	3	(intron 1 -1581)	cttcggccacgtatcct A/G ttcttccctgtttaccct	3528
NDUF-B5	4	(intron 1 -1487)	ccctcttagaccgtatag I/G tctagcataggatcgcaca	3529
NDUF-B5	5	(intron 2 556)	ttgtctggaccatctgccac G/A gtagataaagctcgaatca	3530
NDUF-B5	6	(intron 3 467)	ggcgcaatgcactccagcc C/T gggcaacagagtgagactct	3531
NDUF-B5	7	(intron 3 497)	agtgagactctgtccccc C/G caaaaaaaactataatcct	3532
NDUF-B5	8	(coding region 397 (Tyr 133 His))	atgatagctctgaagagata I/G atgaagaacaatggccgctc	3533
NDUF-B5	9	(intron 1 213-215)	attagcatttctaaaacgtt G/T/Δ attcaaccatcccaattaatg	3534
NDUF-B7	1	(intron 1 68)	ctgtaaacctggcaccoca G/A ggcctggcaccocaggcctgg	3535
NDUF-B7	2	(intron 2 266)	gggctcttagggccctgtt I/C gatgggacagggcaggtgg	3536
NDUF-B7	3	(intron 1 4480-4481)	agctctgagggctgagagaga (GA) ggccacgcccggccagtg	3537
NDUF-B7	3	(intron 1 4480-4481)	agctctgagggctgagagaga ggccacgcccggccagtg	3538
NDUF-S1	1	(5' flanking region -3)	tcctaggggctgtctgtgt C/G cagacagtttagcagaacag	3539
NDUF-S1	2	(intron 1 445)	gtgttagcaatggctcagc I/C totgtttgttctctgttt	3540
NDUF-S1	3	(intron 1 470)	tttgtgtctctgtttgttt G/T gtccattgaccacgttggac	3541
NDUF-S1	4	(intron 1 502)	aggttggacagcatttttt A/G ttccitttaactaacgggaaa	3542
NDUF-S1	5	(intron 1 557)	ttttgaaaagttagccagg A/G ttgcattgcaataaacaata	3543
NDUF-S1	6	(intron 1 5218)	tatctcaagaatatctcaggga A/G catttagtagacagctatgc	3544
NDUF-S1	7	(intron 3 1371)	aagccctaaatatagatagtg I/G caatgggaatgaatacaaga	3545
NDUF-S1	8	(intron 5 414)	ttttgaaacagaggtctcact A/G tgtttccaggctgggcttg	3546
NDUF-S1	9	(intron 10 812)	gagtgagggtggcggatctc G/A atctggggtcactgcagcct	3547
NDUF-S1	10	(intron 11 233)	ggagggcaagggcaggcagat C/T gactaagtgacaggagttaga	3548
NDUF-S1	11	(intron 11 283)	ggccaacatggcgaaacccc G/A totctactaaaaatacaaaa	3549
NDUF-S1	12	(intron 11 585)	cigtatgtcttaatttttaa G/T taaatttgcatitttatat	3550
NDUF-S1	13	(coding region 1251 (Arg 417 Arg))	ggcaccacttttaattctag A/G attcgaagagggttgtaat	3551
NDUF-S1	14	(intron 13 5159)	attacttttagaaaaacgtt I/C ttatgtgatactcaggcata	3552
NDUF-S1	15	(intron 14 250)	aaaaattgttatattagtta C/T accttggttcaaaaattgca	3553
NDUF-S1	16	(intron 14 550)	gataagctctcactatgttg C/T ccaggttgatctcaactcc	3554
NDUF-S1	17	(intron 14 2429)	cigaaaatacaaaaattagc C/T ggggtgggtggcagtgcct	3555
NDUF-S1	18	(intron 14 2530)	ttacagtgagccgagatcac G/T ccactgctccagcctggg	3556
NDUF-S1	19	(intron 14 2659)	acacatttaattttttacat I/C gaaaatactgcagttatggt	3557
NDUF-S1	20	(intron 16 150)	agaaaaacatgtattcagaaa C/T aggaattcaaggttaacagt	3558
NDUF-S1	21	(intron 18 279)	cacttgtagcaattttatgg I/C gaattttccaaagtgacaaa	3559

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
NDUF-S1	22	(3' flanking region 182)	tctaggataattataataa I/A aataatcatagtaacaatgg	3560
NDUF-S1	23	(intron 12 3226)	aaatgtattgtctgtcttt I/ Δ aacattttgttaataataat	3561
NDUF-S3	1	(5' flanking region -194)	tctgccacaaggagctagga C/I cagctcacctcacgatttc	3562
NDUF-S3	2	(intron 1 46)	cgggttcaggcgcagggcg I/G gccagtcgagagagctcct	3563
NDUF-S3	3	(intron 6 -439)	aaagctgttcaaatgtact G/A ctttagatctggagctgtgaa	3564
NDUF-S3	4	(intron 6 -280)	ggtaggtgagcagtcagttc G/A gagctctgtatgtggagtg	3565
NDUF-S4	1	(5' flanking region -439)	actgaatacagccctgtcc I/A gaggcttgcagaagtgaaic	3566
NDUF-S4	2	(intron 1 1829)	gaaaataatcttaataagca G/I ggaagacgttttttaaatac	3567
NDUF-S4	3	(intron 1 2057)	attaatgggaataatctacat C/G taataatcattttttattgtaa	3568
NDUF-S4	4	(intron 1 -521)	ttcattttaactaaattttat I/G totccatttttgtgaatggg	3569
NDUF-S4	5	(intron 3 -1259)	ataaaattatgatatattta G/A tactaatatagccagccata	3570
NDUF-S4	6	(intron 3 -1174)	aataataataattataggaa I/G ctacagtagcaaccaatgtt	3571
NDUF-S4	7	(intron 4 10682)	cacaatataggcacaactt A/C ctaccaaaagcactaaacaagt	3572
NDUF-S4	8	(intron 4 12299)	tttactatatagatatatgg A/I atagactatagagatatctct	3573
NDUF-S4	9	(intron 4 12560)	acaaataagggtattatgca G/A gctcatctttttatataaga	3574
NDUF-S4	10	(intron 4 18801)	gaaaagactgtcttgccag I/C gtaacgaaacotcgtttat	3575
NDUF-S4	11	(intron 4 19888)	tgcacagctgagaagaca A/G ggggtgttttcagtaacc	3576
NDUF-S4	12	(intron 4 20178)	agaaaagatgagtataatc G/A totaacttaccattotttaa	3577
NDUF-S4	13	(intron 4 23016)	ctactcttgaaagtaaggt I/A atgtigaacaagtaataataa	3578
NDUF-S4	14	(intron 4 23124)	actttotttggagatggagt I/A ccagcagttgggaatgaat	3579
NDUF-S4	15	(intron 1 766)	tgtgatgtatttttttttt I/ Δ ggcgtatttaaccttccatt	3580
NDUF-S4	16	(intron 1 1261)	ttctttctcttttttttt I/ Δ gagatacattctcaccttga	3581
NDUF-S4	17	(intron 4 19744~19745)	ctcatcatttagtgtctgtt (I) agttgggtttgtggcaaatc	3582
NDUF-S4	17	(intron 4 19744~19745)	ctcatcatttagtgtctgtt agttgggtttgtggcaaatc	3583
NDUF-S5	1	(intron 1 388)	ccaaaatagccagcacttc C/I ggcgttaactcgggtgttt	3584
NDUF-S5	2	(intron 1 -13082)	agtgagccgagattgcacca G/A tgcattccagcctgggcaac	3585
NDUF-S5	3	(intron 1 -12905)	gttttcaacaagaagactcca G/I agtagtagagaagtittctgt	3586
NDUF-S5	4	(intron 1 -12564)	atttcatcacactcaact I/G aaggtaataacagccttaaga	3587
NDUF-S5	5	(intron 1 -12561)	ttcatcacactcaacttaa G/A gtataacagccttaagaalg	3588
NDUF-S5	6	(intron 1 -10561)	aacaatgtgtatagtgagg C/G ggtgtgagcaggtgtcat	3589
NDUF-S5	7	(intron 1 -9065)	ctgtatgctctggtccag G/A gtacaccttttccctttaga	3590
NDUF-S5	8	(intron 1 -8871)	tcaccagctgtcttagata I/C aggaacgcagaccttgcctt	3591
NDUF-S5	9	(intron 1 -7312)	aaatccttgctcttagaat G/I ggtcaactgatggtatataat	3592
NDUF-S5	10	(intron 1 -6827)	aaacttgcctcccccattc A/G gccattctcccgccicagc	3593
NDUF-S5	11	(intron 1 -6725)	agtagaacgggttttcacc G/A tgttagccagctggtctcog	3594
NDUF-S5	12	(intron 1 -6631)	agcgtgagccactgccc G/A gctagaccttcttcttata	3595
NDUF-S5	13	(intron 1 -6531)	ccaaacagctcccaatgtaa A/G acagatctattaataatctg	3596
NDUF-S5	14	(intron 1 -6346)	gcaacagatottgacctata I/C cccataggttagacgtgagg	3597
NDUF-S5	15	(intron 1 -6327)	atcccataggttagacgtga G/C gactttaatcagaaaaggag	3598
NDUF-S5	16	(intron 1 -6122)	tagccttgttttactctac I/C gttcttcccaaatcacacc	3599

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
NDUF55	17	(intron 1 -2512)	acaacacttaagtgaatt I/C tgcagatcaaaagtggctta	3600
NDUF55	18	(intron 1 -1945)	tttaatctctttaaatttc G/A caatttcacaacctagggtta	3601
NDUF55	19	(intron 2 75)	tttttttttttttttttttt G/A aagtctcactcttgcctct	3602
NDUF55	20	(intron 2 148)	ctgtagcctctgcctccag G/A ttcaggcgattcgcgtacct	3603
NDUF55	21	(3' flanking region 150)	cagattcaagtgtctct G/C cctcagcctccaagttagt	3604
NDUF55	22	(intron 1 (-10682) ~ (-10681))	attataacactaaacaaac A/ Δ gtgtgtctcttttagagggg	3605
NDUF55	23	(intron 1 -10267)	caagtgactaccocigaaaa A/ Δ gaagagatgaacaaatcac	3606
NDUF55	24	(intron 1 -2069)	accagacagattcccttta C/ Δ ttgtttcctgtggcaaga	3607
NDUF56	1	(intron 1 26)	ggccgtgggtacaggatgc A/C cctctccagccgcacctc	3608
NDUF56	2	(intron 2 1076)	ggatcatgtgtgtggagagg G/A gcttgtgtctgtgtgggttg	3609
NDUF56	3	(intron 2 1260)	cagttgtcagtaagtggig I/C ataggtaagtctctttct	3610
NDUF56	4	(intron 2 1413)	caaggagctcatggcatig C/I gaatgggacatttcttcgt	3611
NDUF56	5	(intron 2 1568)	tggagaaggagggtttctc I/C tagtggtggtgcgttatgt	3612
NDUF56	6	(intron 2 1692)	ggcgtgtgtgcaggagttt C/I ctgggcatcgatgggtgtt	3613
NDUF56	7	(intron 2 6488)	tagcttaataattattggc A/G ttcatgttcaagaatcctga	3614
NDUF56	8	(intron 2 6563)	tttaaacctttattttaa G/A tccatgaatgggtcggtat	3615
NDUF56	9	(intron 2 6740)	aaagatttaaacctacat C/I ttatgcccaatcatttgat	3616
NDUF56	10	(intron 2 6832)	ggagaggactatttacag A/I ggttgacacttcactgtgt	3617
NDUF56	11	(intron 2 7054)	ttcactgcaggagcttggcc G/A tgtgaacccggagccggct	3618
NDUF56	12	(intron 2 7186)	ggtcagggtcaccttggagc I/C ggcacactaaatgacggga	3619
NDUF56	13	(intron 2 7225)	gggggcatcccgctcagtc G/A ccagtgctgagggcgcagca	3620
NDUF56	14	(intron 2 7810)	cttccactctggggcgggga C/I gctgtagaaggagacacaaag	3621
NDUF56	15	(intron 2 11080)	gtaactgttcagtgctttct C/I ctttggatttcatgtaaatc	3622
NDUF56	16	(intron 2 11657)	ggagacaagcagtggtgtg G/A gagaagaggcgctggcagag	3623
NDUF56	17	(intron 3 208)	cgaaaaccccttticaactg I/C gaagtggtggggcgcatgtt	3624
NDUF56	18	(intron 3 1031)	ctagagtggagactgggcacc C/I ggcatgtccctctctgggt	3625
NDUF56	19	(3' flanking region 270)	gcttcagagagcaaggtgg G/C tottgaggtgcatagtgaag	3626
NDUF58	1	(5' untranslated region -45)	agtgtagctcagctcccg A/C ttgaatggcctgttggcaa	3627
NDUF58	2	(intron 1 163)	aggtgcagcggggagccggc I/C ctccaggcgcatgcgcggc	3628
NDUF58	3	(intron 3 123)	tctctgagcctgtttccact I/C ttaaaatgattatgtgtatg	3629
NDUF58	4	(intron 5 -505)	aggcaaggcagccggcgacc G/A gtggctcagcttctaacc	3630
NDUF58	5	(3' flanking region 491)	ggccctagctggcctgcgt C/A cagccacatcctctttcttg	3631
NDUF58	6	(3' flanking region 693)	ttcacttcatttgcagttag G/A aaacagctccagagagtgta	3632
NDUF58	7	(3' flanking region 1267)	ttttccagacgtaaacgcc G/A tccagagcgtggcattggagcc	3633
NDUF58	8	(3' flanking region 1362)	cgctgggtcttttcccttac C/I gtggctccacaggcacttac	3634
NDUF58	9	(3' flanking region 1449)	tgtcagaacaggcctatggc G/A cccaacacaaagtccccaa	3635
NDUF58	10	(3' flanking region 1572)	cagcccccagggcctgtgt C/A gctgtgtgggttagggat	3636
NDUF58	11	(3' flanking region 783~784)	cagagaccttgaaccccccc (C) atctaccatcatttccaaaa	3637
NDUF58	11	(3' flanking region 783~784)	cagagaccttgaaccccccc atctaccatcatttccaaaa	3638
NDUFV1	1	(intron 3 670)	ctgggttggagtggtggca I/C ggagttgaagaccagctct	3639

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
NDUFV1	2	(intron 6 160)	tgtgcggcccgagccctga C/G catgcatccctttggggacc	3640
NDUFV1	3	(intron 9 27)	accaccccttcgctagcac G/A gagggtaggtgcatcaagg	3641
NDUFV1	4	(3' flanking region 1111)	tgtaggctgaggtcagccccc A/C atccagtcacaagccacccc	3642
NDUFV1	5	(3' flanking region 1658)	gaatcggaagtgctctgtg G/A gcacccacatgctccgggc	3643
NDUFV1	6	(3' flanking region 1713)	gaticggggcggagggtaca C/T ggggctggcgtgggtgagg	3644
NDUFV1	7	(intron 4 214)	tgggtaaaattttttttt I/ Δ gcttcaaaaatatagatttt	3645
NDUFV1	8	(3' flanking region 772~774)	tgaactcggggttcaggctc T/C ctgtgaacacttggtttttaa	3646
NDUFV2	1	(intron 1 526)	ggaatgcctggctaaataaa C/T ggatcaaacactaaccttgaa	3647
NDUFV2	2	(intron 1 6689)	tctgttgatggtagtatgt I/G tgaacaacagagaagaattca	3648
NDUFV2	3	(intron 1 14767)	ccaaatgcagtcagcagag C/T gtggcagggaaggtacacaag	3649
NDUFV2	4	(coding region (Ala29Val))	aaggaaatttgcaataagacag T/Ctatgcaaaatggagctggag	3650
NDUFV2	5	(intron 2 ~289)	cagaagatottactctctaa I/G gaagctggataaacacttttt	3651
NDUFV2	6	(intron 2 ~168)	tttactttggtaatacact I/C atcaaatgtgttttagaca	3652
NDUFV2	7	(intron 4 677)	aaacacatactatttgatt C/A tgaatgagaatcacataacca	3653
NDUFV2	8	(intron 4 2295)	tatgattcaactttcaaaag A/T gtattgtgatatgaaataga	3654
NDUFV2	9	(intron 5 102)	caacttcgcactcttatig G/A atctgtacttaactagtaaat	3655
NDUFV2	10	(intron 7 5466)	tgttaagagccttaagata A/C caaatgctcagcttticagga	3656
NDUFV2	11	(intron 1 13562~13563)	tactcttaaaattaaacctt (G11) ttattataagtatacagctct	3657
NDUFV2	11	(intron 1 13562~13563)	tactcttaaaattaaacctt ttattataagtatacagctct	3658
NDUFV3	1	(5' flanking region ~222)	gcgcgcgcgcgcgcgcgc G/A cccaggcgcgcgcgcgcgc	3659
NDUFV3	2	(5' flanking region ~111)	tggccccaaggaggacactt A/G gccctacttggggatgocgc	3660
NDUFV3	3	(intron 1 137)	tiggccgcctgaccccgctc C/T ctggcccccaggactgaccgc	3661
NDUFV3	4	(intron 2 152)	tataaagacacaaagatcta I/C aacagatttttagaccaaca	3662
NDUFV3	5	(intron 2 6304)	ttcacagatgaagggttcc G/A aaatttttgtcaagaaagac	3663
NDUFV3	6	(intron 2 6433)	tgccttctcttctcctc I/G tccagctcctctgtattctga	3664
NDUFV3	7	(intron 2 6563)	cccttgaacacagagccccc C/T gagttacagatcagcaaaa	3665
NDUFV3	8	(intron 2 9619)	actatctctgtgctgcatgc G/A cagagccacaccttgacagc	3666
NDUFV3	9	(intron 2 9858)	aggatgccagcttttaaat G/A agacatgctttttgtctaac	3667
NDUFV3	10	(intron 2 11673)	cttggtaggtgaagcgcctgt A/G tgtgagcacaagtcaattcata	3668
GGT1	1	intron 1 + 85	ttatccagtaagtggtctcc G/A tcacctcttttctgtgtgg	3669
GGT1	2	exon 3 + 68	gacggccaggttcoggatgt G/T gtggagctgtctggggcac	3670
TGM1	1	exon 2 + 179	tgcgaatatgcagcatga C/T gactgggaacctgaaaccttc	3671
TGM1	2	intron 9 + 1594	acttaacctctgtctctc C/T tggcaggctcttctgttoa	3672
TGM1	3	intron 9 + 1933	cgcacacatgtacctgcc C/G ccactctccagcagcagcagc	3673
TGM1	4	intron 10 + 54	tcagtcattgggttctctgt G/T ccaacttcaccgctgactga	3674
TGM1	5	intron 10 + 420	aggagccgggagtcaggcc A/G ccctcagacctcttggtctca	3675
TGM1	6	intron 12 + 101	ggaggtcccttgggggaagcc I/G catgtagggaagcagccctc	3676
TGM1	7	intron 13 + 72	ggataaggacatcagagggtg G/A gogctaagccacagcagcagc	3677
TGM1	8	intron 14 + 1671	atctcttaaccacaccccca C/G catgtggggagggttctctca	3678
TGM1	9	intron 14 + 1691	ccaatgtggggagggttctctc G/A tccctaaggagatccgcagagc	3679

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
TGM1	10	intron 14 + 2983	tcctgctccctccttcaag G/A gagtcagaacacaccttcaa	3680
TGM1	11	intron 14 + 3158	ggaacccctcagaaccagg T/C tccaagcaaatgctttgco	3681
TGM1	12	intron 14 + 3816	cagaatacaaaagtggatg G/C gagcaaggagtcocgtag	3682
TGM1	13	exon 15 + 233	ctcgaggtgagcttagccc T/C gtccagaggaatgggaact	3683
TGM1	14	exon 15 + 369	ggagtcagcttcacttga C/A tgggggaacagatgctaata	3684
CYP1A1	1	5' flanking - 1061	cgcgcgcactccctccccc C/G tcgcgtgactgcgagccccc	3685
CYP1A1	2	5' flanking - 1035	tgactgcgagcccccgcgc G/A ggcgggggaatgggtcggct	3686
CYP1A1	3	5' flanking - 1020	ggccggggccgggggaatggg T/G cggctgggtggtgcggcgg	3687
CYP1A1	4	5' flanking - 947	cgcgcctcggggccaggtgg G/A gcggggacgggcgcctgac	3688
CYP1A1	5	intron 1 + (1326-1334)	cattcaattgagaattgagcc (A) 8-9 cctggcctggattctctg	3689
CYP1A1	6	intron 1 + 1357	ctggcctggattctctgac T/C aaagagctcaatctagctgg	3690
CYP1A1	7	intron 1 + 1590	ccactttcaaaaggaggta C/T atgtgacagcagctggaat	3691
CYP1A1	8	exon 2 + 160	gaatccaccaggcccatggg G/A cggcctctgattggcaca	3692
CYP1A1	9	3' flanking + (710-720)	caccgcgagattccaggic (T) 10-12 gagacggagtcicactgtgt	3693
CYP1A1	10	3' flanking + 834	gctcagctcccaagtagc C/T gggactacaggcgcctgcca	3694
CYP1A2	1	intron 1 + 103	ggctgggtaggtagtaggg T/G cctgagttccgggctttgct	3695
CYP1A2	2	intron 2 + 371	cttccctgtttcacactaa C/T cttttcctttttgaaattg	3696
CYP1A2	3	intron 4 + 44	atagccaggagaagccttga G/A acccaggtttgtttgtcagt	3697
CYP1A2	4	intron 4 + 206	aagagtacatgggggtataa G/C aggggataattcattggggca	3698
CYP1A2	5	intron 5 + (623-648)	tgcccaggctgctgctgc (T) 22-25 catagaaaatagaaaaaat	3699
CYP1A2	6	intron 6 + 81	tcctctgtaggaactttta T/C ataataaaggaggggacot	3700
CYP1A2	7	exon 7 + 181	ctggccatctctgacagca A/T ctggagttcagcgtgcgcgc	3701
CYP1A2	8	exon 7 + 295	cggctgcgtcttccatcaa C/T tgaagaagacaccacattc	3702
CYP1B1	1	5' flanking - 3669	tgtatctgtgaagcatcac G/A gttatctctctctgcacatg	3703
CYP1B1	2	5' flanking - 3149	tgacagcaattaccaccccta G/C ttctctgatttttagtca	3704
CYP1B1	3	5' flanking - 1222	gggggaagccaccccgcgc G/A agcgcctcgggttccctta	3705
CYP1B1	4	5' flanking - 376	ttccgggaagcaagctcaag T/C cgcggagagggaaggaggt	3706
CYP1B1	5	5' flanking - 265	ctgggacacgtgcggcct C/T gattggaggtggctgtgatg	3707
CYP1B1	6	intron 1 + 129	tgccgcagcgtttgtcccca G/A attgcaggaacogttacgg	3708
CYP1B1	7	intron 1 + 379	tgagttcacgccttctct C/T tctgtcccccagcatggcac	3709
CYP1B1	8	exon 3 + (799-800)	agctctcgggagatttttt (T) gagtcaaaagacttaaaaggc	3710
CYP1B1	9	exon 3 + (799-800)	agctctcgggagatttttt gagtcaaaagacttaaaaggc	3711
CYP1B1	10	exon 3 + 1284	agatatgtgggttccatga G/T ttatcatgaatttttaagta	3712
CYP1B1	11	exon 3 + 1398	tcagcaaaagaaaaaaa A/Δ gccagcaagctttaaatta	3713
CYP1B1	12	exon 3 + 1468	ttctcatagttaaaaaaa A/Δ gtccaccaatagttgaaat	3714
CYP1B1	13	exon 3 + 1564	ttgaataataatgcttgg G/A taataattgaaaattgaaaag	3715
CYP1B1	14	exon 3 + 1762	ttgaattctattataata C/Δ agaactttgttttgaataa	3716
CYP1B1	15	3' flanking + (2216-2226)	agccagcctctttcttttc (T) 10-12 aaatttattctatttct	3717
CYP1B1	16	3' flanking + 2230	ttttcttttttttttttaa A/Δ ttattctatttctttaca	3718
CYP3A4	1	intron 2 + (754-763)	cacaaaatgattttgtgggg (T) 9-11 acacaaaggcggaatcacat	3719

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
CYP3A4	2	intron 7 + 258	acacctaataaactttctgc C/I totatggatttgcctattct	3720
CYP3A4	3	intron 7 + 894	tgtgatctcactgctgtag C/I ggtgctcctatgcatagac	3721
CYP3A4	4	exon 9 + (32-33)	ttcttcagctgctgattga (A) cctcagaattcaaaaagaaa	3722
CYP3A4	4	exon 9 + (32-33)	ttcttcagctgctgattga cctcagaattcaaaaagaaa	3723
CYP3A4	5	intron 10 + 12	ccaataaagtgagtgatg G/A tacatggagaaggagagagg	3724
CYP3A4	6	intron 10 + 459	agcattgactttttttttt I/Δ gaaaggtacaatcaacttctc	3725
CYP3A4	7	intron 10 + 608	agcgtctcgaatgctctcc C/I acttcaaacctctccacac	3726
CYP3A4	8	intron 12 + 2467	tttttggccattactctcat A/G gagatcagaatatacactctg	3727
CYP3A5	1	exon 1 + 69	ggagacatcacagaacacag I/C tgaagaaggaagtggcgat	3728
CYP3A5	2	intron 1 + (955-956)	tgtgggtagtgagggtccca (A) cctgtccattaaactctctac	3729
CYP3A5	2	intron 1 + (955-956)	tgtgggtagtgagggtccca cctgtccattaaactctctac	3730
CYP3A5	3	intron 1 + 1126	acatttttaaatgaattgat A/G tggtttaaatcattcatttt	3731
CYP3A5	4	intron 1 + 1145	tatggtttaaatcattcatt I/G tttaaacagaaatttttgg	3732
CYP3A5	5	intron 1 + 1543	ttcatgggtcctggccccc C/A gtggaggctcactcaaaagggc	3733
CYP3A5	6	intron 1 + 2366	cttatcttatgacctact G/A caccatttgcctatcaacagg	3734
CYP3A5	7	intron 4 + 1813	tggttctaatttactcttc G/A tgttcttcccttggaaaat	3735
CYP3A5	8	intron 4 + 1887	aatgacaigacaagggttg A/I tigtgaagcaagggtatatt	3736
CYP3A5	9	intron 4 + 3384	gagtgtctctatttgcct C/I aacaagaanaagtcatttgt	3737
CYP3A5	10	intron 4 + 3415	agtcatttgcacttttca I/C tgaacaattctctctcatcc	3738
CYP3A5	11	intron 4 + 3760	aagataacacactggagtc G/A cacaccacataaaaactgaa	3739
CYP3A5	12	intron 4 + 3885	acaattcacttcacgtggca C/I tgaataggctctctcgct	3740
CYP3A5	13	intron 4 + 5061	tacctacttttcaaaaaaa A/Δ tcaccacatcgtggcatccc	3741
CYP3A5	14	intron 4 + 5316	ccagatggctgggtctcccc A/I ctcccaccccccccacat	3742
CYP3A5	15	intron 9 + 77	gtctgaaatgtgaggaa G/I tattccaggagaatgagaat	3743
CYP3A5	16	intron 9 + 1791	aaatttttattgggaaaaag C/I ctaccocataatttacttaca	3744
CYP3A5	17	intron 12 + 1408	atttaataaaaaaa A/Δ caccagtcacacaagaatttg	3745
CYP3A5	18	3' flanking + 542	tggagaaaattatcatagtt I/C cattctgctcttttgaaga	3746
CYP3A5	19	3' flanking + 737	atgaacactgaataaaaaat I/G gtoaatctgctagttgattg	3747
CYP3A5	20	3' flanking + 804	ttttccttttttattcttc A/C ttttccctcttttctgaaat	3748
CYP3A7	1	5' flanking - 1680	cccaaggaacatgtggctcc C/A ggacacatacctggcacaaca	3749
CYP3A7	2	5' flanking - 1191	tagaaaatctctcactgtc A/C aaaaagaagccatttgcctt	3750
CYP3A7	3	intron 1 + 1173	ccccatttcaaatcacact G/A cttagcaggttatctctaaac	3751
CYP3A7	4	intron 1 + 1597	tttttctgttagctcttca I/C tgaacacaaagcagcatta	3752
CYP3A7	5	intron 3 + 762	tcagtgctgctctatccc I/C tctcttttttttctccctt	3753
CYP3A7	6	intron 7 + (1060 - 1069)	atggtttcttttttctgttg (1)9-10 ctacagaagcttttccattc	3754
CYP3A7	7	intron 11 + (592 - 594)	taagacaaggtaggagag AAG/Δ gagagaattagaaaaaca	3755
CYP3A7	8	intron 12 + 911	ccccctcattaaacaatc C/I tctcatttttattccatttaa	3756
CYP3A7	9	intron 12 + 1137	gtctgtctgcagggaataa I/Δ attcagcttttggaaaatt	3757
CYP3A7	10	intron 12 + 2147	tattgtcagtaattttttt I/Δ acttggatgctatacttct	3758
CYP3A7	11	exon 13 + 218	ttcatccaatgtctgcata A/C ataacagggttctgtacg	3759

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
CYP3A43	1	intron 1 + 35/9	tcatgtcaactttttttttt I/ Δ ctcaaaatgatoatcacac	3760
CYP3A43	2	intron 2 + 2427	tagaggaaatctttttttt I/ Δ ccttttttcgtgccag	3761
CYP3A43	3	intron 3 + 3034	ttttatatagtcaggaga I/C tgaataaacaagtcttct	3762
CYP3A43	4	intron 3 + 3433	agfcaagataactttttt I/ Δ cataaaggaccacagtatgt	3763
CYP3A43	5	intron 3 + 3504	catgaactagtttccaaaca I/C aactttcattttggcatag	3764
CYP3A43	6	intron 4 + 2767	tagtgacttttgaaaaaaa A/ Δ tttagtaataagcaaaagact	3765
CYP3A43	7	exon 5 + 22	aaacttaaggcacttttca G/A aaatccattggacctaaag	3766
CYP3A43	8	intron 12 + (1585-1584)	tactttgagccctattctc (A) ccaagtcacttcaagtgtcag	3767
CYP3A43	8	intron 12 + (1585-1584)	tactttgagccctattctc ccaagtcacttcaagtgtcag	3768
CYP4B1	1	5' flanking - 333	gaacattccacgtcttgt A/I tgaagaacagtgtttatta	3769
CYP4B1	2	5' flanking - 18	gagcagctgaagcaggtca G/I atgaagctagggtggctgga	3770
CYP4B1	3	intron 1 + 341	tccaaaacctcttgatagta C/I atagaagtagggcaatccatt	3771
CYP4B1	4	intron 1 + 542	ccatagggtgctcaggagc C/I gtgacaccttcccaggttca	3772
CYP4B1	5	intron 1 + 2856	gaggaacttccacatagtag G/A tgcacagctatattgttggc	3773
CYP4B1	6	intron 1 + (2923-2938)	cacaaattgtgtgttgg (G1) 7-8 agaattgccagctcccagatc	3774
CYP4B1	7	intron 1 + 6086	tttggaaactaaagactggg G/I cacgatgttagttgtgtgac	3775
CYP4B1	8	intron 1 + 6598	ttttggggtgtgggagagg G/A cccatagtagggagacagct	3776
CYP4B1	9	intron 1 + 6660	acctaaagggtctcoactctg A/G agggagacagctctaggggg	3777
CYP4B1	10	intron 1 + 7242	ccctggctcccttaactca I/C gctggactgttccctttggt	3778
CYP4B1	11	intron 2 + 107	gcctgttaactaagtctgcg C/G agctgaggttcccaccctac	3779
CYP4B1	12	intron 3 + 361	atggtgtgtgttaggacca C/I ggcgtgtcaaccagaggtgt	3780
CYP4B1	13	intron 4 - 492	aaaggctttcacatctaaaa C/A ggtgtcctctatcttctgtc	3781
CYP4B1	14	intron 4 - 315	ggattacttcaatatacacc A/G tgcggggagctcaccacct	3782
CYP4B1	15	intron 4 - 157	ctacccacctatctgtata I/C tccagcaggtatggagggcag	3783
CYP4B1	16	exon 5 + 22	acaagttgggaagagaaagt C/I gggagggtaagtctttgac	3784
CYP4B1	17	intron 5 + 125	cccaggagagccttagcttgc G/A gggagacagagacctgtcat	3785
CYP4B1	18	intron 5 + (287-289)	tgtctaagccaatccctct CCI/ Δ acctctgttagcaggagac	3786
CYP4B1	19	intron 6 + 54	gcctgggttctctctctgg C/I cctctatgccccctcccat	3787
CYP4B1	20	intron 7 + (99-100)	agctcttaagcatttccccc (1C) ttctcagcaataataacc	3788
CYP4B1	20	intron 7 + (99-100)	agctcttaagcatttccccc ttctcagcaataataacc	3789
CYP4B1	21	exon 8 + 114	tcctgggtttctctactgcat G/A gcctgtacctgagcaccac	3790
CYP4B1	22	exon 8 + 139	tgtaccttgagcaccagcat C/I gtttagagagaggagtcocgc	3791
CYP4B1	23	intron 8 + 247	agaagttgtcaacaagagg C/I tgaattttgtgtctaact	3792
CYP4B1	24	intron 8 + 366	tgtgggggtgaacagagctg A/G gacagctgggagagccaggt	3793
CYP4B1	25	intron 8 + 650	cccttgccttgggtcagaca C/A ccgtcccttctctctgtgct	3794
CYP4B1	26	intron 8 + 844	tcataatgtagaatccccc C/A ccacgggggtatccagabaca	3795
CYP4B1	27	intron 8 + 1767	ttccattccaagaattgtct G/I gttgtgttctgtggcaggat	3796
CYP4B1	28	exon 9 + 53	tgtgcatacaggagagcttc C/I gcctctaccacccgtggccc	3797
CYP4B1	29	intron 9 + 652	agtcggatgtgtgtatgaac G/I cctgtcacctggcagtagtc	3798
CYP4B1	30	intron 9 + 774	ccctggctaccacacctctgtt C/I tgcacacaggaagcctgcat	3799

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
CYP4B1	31	intron 10 + 33	tggcctggagatcacacag G/I ggggggacaggagggtca	3800
CYP4B1	32	exon 12 + 224	ccagatggctcaggctgga C/A ctccctggcaccacccctcc	3801
CYP4B1	33	exon 12 + 270	ctgggtgtgagaggttgg G/A cccctgccttcaggaggct	3802
CYP4B1	34	3' flanking + 129	ttgtgtctcaagtcacgt G/A gtgtccaggcattcagggt	3803
CYP4F2	1	intron 1 + (145-146)	ccaagccctggcaacctca CA/Δ gtatcaggctggcccttt	3804
CYP4F2	2	intron 1 + 193	tttaacagctctctctct C/I ttcccatcttaagtgctta	3805
CYP4F2	3	intron 1 + 324	ccctgcttacctccggac I/C gccctgcctgcctctccac	3806
CYP4F2	4	intron 1 + 367	tcctggaggtccctggcc G/C ttctctggccctcaggatct	3807
CYP4F2	5	intron 1 + 402	ggaatcacagtcacatccg I/C ctgccctgcaggatgtccca	3808
CYP4F2	6	exon 2 + 35	gcctgtccctggctggccctc I/G ggcagtgccagcatccct	3809
CYP4F2	7	exon 2 + 166	cagtggttccacacacccc A/G agacggaactgattttgggg	3810
CYP4F2	8	intron 2 + 125	ggcagagaagcagaggaggc A/G tottactatctctctgtt	3811
CYP4F2	9	intron 2 + 440	ggccgctctccacttccac I/C acacccgaggcacccttct	3812
CYP4F2	10	exon 3 + 48	gttctgactcagctgtggc C/I acctaccocaggcctttaa	3813
CYP4F2	11	intron 3 + 701	aaactcaccccagcttggg I/A cctttccttgacccctgtg	3814
CYP4F2	12	intron 3 + 742	cttcccatogttggacgggc G/A agcctgagcaggggggaatgg	3815
CYP4F2	13	intron 3 + 1020	gctttagctttctcatgtc G/A cttttctatcaaggtggcc	3816
CYP4F2	14	intron 3 + 1039	cgcttttctatcaagggtg C/A cttttctatcaatgctcaac	3817
CYP4F2	15	intron 3 + 1040	gcttttctatcaagggtg C/G ttttctatcatgtgtcaacg	3818
CYP4F2	16	intron 3 + 1920	ccaccgtctaacctctgtt G/C ctgtttgtcatgtcttgggg	3819
CYP4F2	17	intron 3 + 1945	ttgtctcatgtctggggcgtg I/A ctctacaatggctgttatat	3820
CYP4F2	18	intron 3 + 2621	agcattctgtagaaatctga G/A cigtgtcagggggttgcgga	3821
CYP4F2	19	intron 3 + 2665	tgttgatctgttagagggc A/G tgtcaaggcagtgtggaacc	3822
CYP4F2	20	intron 6 + 194	gggtttgaactgtatggatgt G/I gtcagagctctgttagggac	3823
CYP4F2	21	intron 7 + 67	tgtgaaatgtcagatgaag G/A atttgaactgtattaagagg	3824
CYP4F2	22	intron 7 + 2811	ttccaagggaattgccatt I/G aattctcigttaactcaggt	3825
CYP4F2	23	intron 7 + (3096-3097)	gggttgggggttgggggggg (G) ttactgccttctctccagg	3826
CYP4F2	23	intron 7 + (3096-3097)	gggttgggggttgggggggg ttactgccttctctccagg	3827
CYP4F2	24	intron 8 + 145	gggtgtctctaccttgggt G/A ctgaagcagcccagagacc	3828
CYP4F2	25	exon 9 + 44	ctctcttgggtctctgtacca C/I ctgtcaaaagcaccagaata	3829
CYP4F2	26	exon 11 + 48	gaaccacacacacccagct G/A tggcccgagccctgagggt	3830
CYP4F2	27	intron 12 + 108	tgttcaagttccagctctc C/I ttccctcacctctctggag	3831
CYP4F2	28	intron 12 + 285	gcattgggattccaggcacgg A/I taccctctctctctctc	3832
CYP4F2	29	exon 13 + 238	aagtgaagcctagaattacc C/A taagaccctgttccacagt	3833
CYP4F2	30	exon 13 + 342	tgtgcgtgaatgtttcagtc G/A gccctattcacatagccaa	3834
CYP4F2	31	exon 13 + 563	tagtgtactgtcttttata I/C gaaatttccagaacagccca	3835
CYP4F2	32	exon 13 + 707	aaatgttccgagacctagata G/C tgaacaggttagcacacac	3836
CYP4F3	1	intron 2 + 258	cattaatgcacctctgtggg G/I ctcttggcaggggttggg	3837
CYP4F3	2	intron 2 + 916	ttaggacatgtctctagtc C/I aaactgtccccacaaacct	3838
CYP4F3	3	intron 2 + 3417	atccaggtctcacacagtgt C/I acttctctcttggcttag	3839

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
CYP4F3	4	intron 2 + 4090	gagagcatgaattgggtcct G/A tgcctttctctccagattca	3840
CYP4F3	5	intron 3 + 89	tgctgcctccaggggtc G/A ogtgccatgtgcagacagg	3841
CYP4F3	6	intron 3 + 243	taagctctgttacggcta C/I gctctgcacctgtatatt	3842
CYP4F3	7	intron 3 + 502	aggctcggaccacagggtcc G/C taagtgaactgtctgagaca	3843
CYP4F3	8	intron 3 + 755	tittgtggccatgtcaggac A/I tgtgacacatgtcagtgtc	3844
CYP4F3	9	intron 3 + 855	gggacagacagggttctcta G/A gtcccttgaaggcattctg	3845
CYP4F3	10	intron 3 + 970	ctgacatagctctacgtg C/I catgttaggcagtgtcatg	3846
CYP4F3	11	intron 6 + 122	gaggagtgttatacctgat C/I gttaggactggtatgaat	3847
CYP4F3	12	exon 7 + 159	ggtgcacgacttcacagatg C/A cgtcatccaggagcggcgc	3848
CYP4F3	13	intron 7 + 2107	caggttgcagtgattttt I/ Δ ctcaagaattttcatcaag	3849
CYP4F3	14	intron 7 + 2255	gaccaagaagggtctaggag I/A gcaagatgggcttgggttc	3850
CYP4F3	15	intron 8 + 132	ctcgaatgaaggttgcgt A/G caccctcgggtgctgaagca	3851
CYP4F3	16	exon 9 + 59	taccaccttgcaagcacc G/A gaataccaggagcgtgtcg	3852
CYP4F3	17	intron 9 + 13	attgaatggtgagtgagg G/A ctgggtgcccgttctctgagc	3853
CYP4F3	18	intron 9 + 36	ggtgcccgttctctgagcct G/C tctcattggtctctgtcccc	3854
CYP4F3	19	intron 9 + 167	accatctcagctgtctgg G/G aaagttataggcccttagg	3855
CYP4F3	20	intron 9 + 369	tccctaattcctacccttc G/A tccagtcagggaattataa	3856
CYP4F3	21	intron 9 + 458	tcattcatcctccagtcct I/C gttcagcaatactctcata	3857
CYP4F3	22	intron 10 + 46	ctctgggtagggaaggagg A/C cctccaggcaggagcattg	3858
CYP4F3	23	intron 10 + 63	ggcccccctcaggcaggagg C/A ttgtctcagctgccccttc	3859
CYP4F3	24	intron 11 + 14	ccctgagggtcgggccccc C/G tctctgtttttgtccattcc	3860
CYP4F3	25	intron 11 + 84	gatacaggagaatccaatc G/A cctccctcaagacacacac	3861
CYP4F3	26	intron 11 + 113	caagacacacacactgtct I/C tccaaggctggcggactggg	3862
CYP4F3	27	intron 11 + 164	cgcacaccttcttggctc I/G cctccaggctctatgacctct	3863
CYP4F3	28	intron 11 + 165	ggcaaccttcttggctc I/G ctcagggtatgacctct	3864
CYP4F3	29	intron 12 + 156	gaaaaggccacacagatagg G/A ttgggttggtctctagaggga	3865
CYP4F3	30	intron 12 + 253	gagctcggctaggctccag I/G atatgaagcccacatgggg	3866
CYP4F3	31	intron 12 + 346	ttgggttcccaaggccaggtt A/C cgggttgatggggccaggga	3867
CYP4F8	1	5' flanking - 61	accatgtttaccatcattg G/I tcttgagotccccacccc	3868
CYP4F8	2	exon 1 + 67	gtggcagcatcccggtggct G/I ctctcgtgggtggcggggc	3869
CYP4F8	3	intron 1 + 707	tacgcagcaggtatcacca I/G tattccacattatccactg	3870
CYP4F8	4	intron 1 + 857	acacccctaccctcacatc G/A tgacacagotggggccagaag	3871
CYP4F8	5	intron 1 + 907	tgccatctccacctcccc G/A tgcaggggcatcttctttat	3872
CYP4F8	6	intron 2 + 668	tgtagcaacttccaccatag I/C tcatigccccttctgtccag	3873
CYP4F8	7	intron 2 + 818	ggcacagagaccatggctca G/A gcccacaaatgctgagtgc	3874
CYP4F8	8	intron 2 + 1079	tatgcttggtgttgagaa C/I atgttggaccatgtaggagc	3875
CYP4F8	9	intron 2 + 1194	cgggtccctttatgcccc C/A accctcttcttctctctgc	3876
CYP4F8	10	intron 5 + 45	aaatggatggagtggggg G/I ggggtgtggggagagcaaa	3877
CYP4F8	11	exon 8 + (19-20)	ggccatgacaccaggccag (GCCAG) tggcctctcctgggtcttgt	3878
CYP4F8	11	exon 8 + (19-20)	ggccatgacaccaggccag tggcctctcctgggtcttgt	3879

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
CYP4F8	12	Intron 8 + 222	tttatttcccaactaacttg C/G tatgaagcttagtaaaatc	3880
CYP4F8	13	Intron 8 + 334	cttgagaattaaaggcaaa A/T accgaatgaactttggacc	3881
CYP4F8	14	Intron 8 + 1999	ttctaaagtacatttattctc I/C tgcctttagctatgatctag	3882
CYP4F8	15	Intron 8 + 4184	caggaggccggtgatgctc C/T ctggataatgttggggtt	3883
CYP4F8	16	exon 9 + 119	acgtgctgtccagacagc C/T gagtcatccccaagggtgoc	3884
CYP4F8	17	Intron 11 + 282	gggttggggttccgggct G/C gtctctggcagtgaggcc	3885
CYP4F8	18	Intron 11 + 340	tgcagtcagaccttccacct C/T ggccccaggaaactgcacgt	3886
CYP4F8	19	3' flanking + 35	atcacctactttgcaccaa I/C taccctttcagatttccggt	3887
CYP4F8	20	3' flanking + 83	ctgtgtggccctgtgct G/C agtcocgggatggocagta	3888
CYP4F8	21	3' flanking + 90	ggccctgtgctcagtcoc A/G cggatggccagtagggggcg	3889
CYP27A1	1	Intron 1 + 295	aggaggagctgtcttggga A/G gagatggcagagggcaaatg	3890
CYP27A1	2	Intron 1 + 17503	cagtgataaagcctctgat C/T ctccttagagaaggaggac	3891
CYP27B1	1	Intron 6 + 173	cagccctagcctcctcttg C/T tgcctccattttgtccttg	3892
CYP27B1	2	Intron 8 + 113	atataagacctgtagaatg A/C atctctgaaatatgataag	3893
CYP27B1	3	3' flanking + 1081	taccttggaatcagtgatga G/C aatttgcocctccgtactc	3894
AADAC	1	exon 1 + 29	attaaagctacatttcagg C/T atatoatgtagtttacttt	3895
AADAC	2	Intron 1 + 138	gctgtggccttggacaatgt G/A ttacttagaaaatgtgtttg	3896
AADAC	3	Intron 1 + 142	tggccttgacaaatgtgtta C/T ttagaatgtgtgtgtttt	3897
AADAC	4	Intron 1 + 1033	ttccagcagagacacacaa A/G gtaaaacacccacagatcaa	3898
AADAC	5	Intron 1 + 1253	ttttttccctcatalttgc I/C gctctgtctacaatatgtga	3899
AADAC	6	Intron 1 + 1366	ctctgtagccttttaatta A/G ttaattcatttacttactta	3900
AADAC	7	Intron 1 + 1369	tgttagccttttaattaatt A/C attcattcatttacttactat	3901
AADAC	8	Intron 1 + 2501	ggttacagaagaatggttg C/A ttggccaaaaaatgatattgg	3902
AADAC	9	Intron 2 + 46	tgtcactgaggttagttogca A/G acatttttaactaagtcttcag	3903
AADAC	10	Intron 2 + 1971	aaatgagagttaaagtaggag A/C attttcttttattttgtgc	3904
AADAC	11	Intron 2 + 1988	gagaattttcttttattttt A/G tgcaggagaaatataaaca	3905
AADAC	12	Intron 2 + 2341	aggtgcttttctattgtcc C/T atgcagacttaggtgatcct	3906
AADAC	13	Intron 2 + 2546	gtctgacacagaaggatcaa I/A ggcaaatgtgcaagacaaa	3907
AADAC	14	Intron 2 + 2609	taggaggttccactgggaac I/C tgaattccactagtcactga	3908
AADAC	15	Intron 2 + 2663	tataaatacagtttaaat I/C gctctctgtattttaaggta	3909
AADAC	16	Intron 4 + 605	tgtgtcagtaaaaattata I/C taagttaggtgaatgagatca	3910
AADAC	17	Intron 4 + 621	tattattagtagtgaaatga G/T atcatgtaattgtgagacta	3911
AADAC	18	Intron 4 + 679	ttagagattcagacgaattc A/G tataatcttcctgattgtgtat	3912
AADAC	19	Intron 4 + 1680	gttaaatgtggataaatac C/T acaatttgcaaaatatttgg	3913
AADAC	20	Intron 4 + 1748	atttgaagttctatcacatc I/C ttatagtatatttacacact	3914
AADAC	21	Intron 4 + 1771	tatagtattatcacacttc G/A aaaacacaaaattttttt	3915
AADAC	22	exon 5 + 238	caagtoatcttccaattt A/G ttaattggagttccctgcctc	3916
AADAC	23	exon 5 + 678	ttagaatgtgttcttctta A/G aatggtctagtttaagttcca	3917
AADAC	24	3' flanking + 208	aatgcttaaaaaaaataa A/ Δ tcaotgttggtactttggsga	3918
CE1	1	5' flanking - 983	tatttctcttagccagggta I/C cacagtgtgttagtgaatt	3919

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
CE1	2	5' flanking - 814	tcacattgcttgacatcac A/C cctactgtctctccacccta	3920
CE1	3	5' flanking - 248	agtcttcaagggtgacacc G/ Δ ttaigccacaagcagttggg	3921
CE1	4	intron 1 + 22	tgaatctctcgaagtcacaa I/ Δ atgoggcgacatttttgaaa	3922
CE1	5	intron 1 + 30	tctgaagtcacaaatagcggg G/I cacttttgaataatccttgtt	3923
CE1	6	intron 1 + 1662	aagggaatcctctgagctgag C/A atgaccagccagtggttgc	3924
CE1	7	intron 1 + 1726	cctccotgaagtctcagca A/C tottagctggttctctogccc	3925
CE1	8	intron 1 + 2716	tgtttccaggaaggttcatc I/G cagtattatttgaattagc	3926
CE1	9	intron 1 + (2747-2749)	tgaattagcaacaacaaca AAA/ Δ gaaaagaagctaaattga	3927
CE1	10	intron 1 + 3288	ttattgttcattaaagaaa A/ Δ ctcaagcgttagcctggca	3928
CE1	11	intron 1 + 3691	gagaatattggacacccctt I/G ttcatctctctcatccagcat	3929
CE1	12	intron 1 + 3819	tccttttgattttttttt A/G gctggatgttttttatgcctc	3930
CE1	13	intron 1 + 3880	aaccagctcaatgggttagg G/A aggaatgatcgtcatccc	3931
CE1	14	intron 2 + 74	gagtcaggcagtcctcciga I/C gggctgactcttctgtctgg	3932
CE1	15	intron 2 + 552	atggaaggtgtgtccattca C/A cotggccaagctgggaagaa	3933
CE1	16	intron 2 + 885	cagatttttagatggtaaaag I/C attatgatgaatatattgt	3934
CE1	17	intron 2 + 2001	tiggcatgtcaggcgtgcaa G/A actcatgtagaatactactcc	3935
CE1	18	intron 3 + 2119	cgttgatgtcatgaatagtc I/C agccttgagggtgatggag	3936
CE1	19	intron 4 + 127	taaggcatccaagcccttc G/A taattggacactacactacc	3937
CE1	20	intron 4 + 347	tctgtcatgacacttagcag I/G cagccagcaggtgaaggtt	3938
CE1	21	intron 4 + (1984-1985)	gtggtctgaagtcctgca (C) tgacatctctgtctccacc	3939
CE1	21	intron 4 + (1984-1985)	gtggtctgaagtcctgca tgacatctctgtctccacc	3940
CE1	22	intron 5 + 766	gggtggcagaggggcagc I/C cactacgttgattctcagtc	3941
CE1	23	intron 5 + 825	ggagtagatctagcctggaa I/G agcagtagtgcactgaccc	3942
CE1	24	intron 5 + 828	gtagatctagcctggaaatag C/I gagttagtgcactgaacccac	3943
CE1	25	intron 5 + 868	ctcctgagcagtaactctcc I/A cccctccactcgtctcag	3944
CE1	26	intron 7 + 68	actcttcatttcagctgc C/G tcttgccagggacagtttc	3945
CE1	27	intron 7 + 681	cttccaaaatcaacaatcca A/G ttatgcctgtctgttagtt	3946
CE1	28	intron 7 + 885	aggaactatccaaagagaaa I/C acattcatatacttcgagg	3947
CE1	29	intron 7 + 2151	gtcgtgtaactgaaaatct C/G aggagttgatggcttcaggc	3948
CE1	30	intron 7 + 2470	atataatatacaaatccac G/A gagtatcggggaagaacct	3949
CE1	31	intron 8 + 128	cgtgtttgttctcaggccc A/C gagagggttagtgactcacc	3950
CE1	32	intron 8 + 2618	cctgatggcaacacatgagt I/C gggctctctctaatctgtga	3951
CE1	33	intron 8 + 2665	aaaaattattcatcaaggt G/A aaacctaaaattaaagacatg	3952
CE1	34	intron 8 + 3785	ccatggcgcagtgccctgcc G/A gctctatggctacgtctcac	3953
CE1	35	intron 8 + 3791	cgcattgcccattgocgtcta I/C ggtactggctcaccctcag	3954
CE1	36	intron 10 + 222	gtgggctggagaagctgcat C/I gctcaccggggctgtgtgtt	3955
CE1	37	intron 10 + 230	gagaagctgcatcgtctcacc A/C ggggctgtgtgttcactttt	3956
CE1	38	intron 11 + 1177	ctagcaggtgccctgacaca C/G ctttgcaaggaaggggcag	3957
CE1	39	intron 11 + 1311	gcctatgctctcgtctga A/G ctatataataggtccatc	3958
CE1	40	intron 11 + 2025	ttctcatitgggatgctaaag A/G ttaaaaattagcataaact	3959

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
GES1	41	intron 11 + 2029	cattgggatgctaaagatta A/C aaattagcataacacttcca	3960
GES1	42	intron 11 + 2317	cattcacaaaagcctttct I/C ctatgttggtcctgagttt	3961
GES1	43	intron 11 + 3887	caaatatttggcttaattc C/I goitccacotcagacagcta	3962
GES1	44	intron 12 + 2311	ggcctctaggcctcact G/A tgcctgttaggcgccttgc	3963
GES1	45	intron 12 + 2331	gtgcctgttaggcgccttg C/G ggcctgtgttttttcaagaa	3964
GES1	46	3' flanking + 71	aacgggtgatgaagaggcga I/C gtgagaaggaaggtgcttt	3965
GES1	47	3' flanking + 362	tigcatggcacttaccgacc G/A ttgcacaggccttgcacaccc	3966
GES1	48	3' flanking + 581	attcttggtattctgttagta C/I gtgaaagctttaaagcatg	3967
GES1	49	3' flanking + 1348	aaatctgctctggagaga G/C agcaagcatgcagatcaac	3968
GES2	1	intron 1 + (1303-1321)	caacaagactgtctctaac (A) 17-19 gtaagcatgttgccagaca	3969
GES2	2	exon 5 + 60	ggaccaagtggctgcactac G/A ctgggtccagcagaatatcg	3970
GES2	3	exon 12 + 256	agcctgctgtgccacacac A/G cocactaaggagaaagaagt	3971
GES2	4	3' flanking + (155-172)	acacagtgcagcccttctc (A) 16-18 gagagagtgtgattagaa	3972
GES2	5	3' flanking + (173-178)	tcaaaaaaaataaaaaaa (GA) 4-6 gtgtgtgattagaactaaa	3973
GES2	6	3' flanking + 377	ggtaagggtgagcagaacac C/G tgaggacaggagtttagac	3974
GZMA	1	5' flanking -424	cttcagcttgcaattggcct A/G ctatctttatataaoccaa	3975
GZMA	2	5' flanking -134	agcctgctctgctggcagiga G/C ccatcatcaccattctcac	3976
GZMA	3	intron 1 + 1947	gacataaggttctctctatc A/I gcatgtatggtttgtccttgt	3977
GZMA	4	intron 2 + 958	gaotgctgaccaggtagaa C/I tagcctcagcatggaaagggt	3978
GZMA	5	intron 2 + 1525	gttggtagttttatactag G/A ttatgaatgatagccttaat	3979
GZMA	6	exon 4 + 105	tgccaagtgcagggtgggg C/G aggactcacaatagtcac	3980
GZMA	7	intron 4 + 696	atagacctttacotgaagaa A/G ggtgtcagatgcattggtt	3981
GZMA	8	intron 4 + 1141	ctgttcaggaggatccccc G/A ttccaacatggttctttatt	3982
GZMB	1	5' flanking - 961	gttttagcaaatgtttactg I/C gagcctgttatgtcgtgagc	3983
GZMB	2	5' flanking - 263	ggctgatcacacatcctaca A/G ttacattcatagcttgggt	3984
GZMB	3	exon 2 + 109	gtcgggtggtctctgatac A/G agacgacttctgctgacag	3985
GZMB	4	intron 2 + (242-243)	tggggcctactttggcata (A) gaatacaactgaagcaatt	3986
GZMB	4	intron 2 + (242-243)	tggggcctactttggcata gaatacaactgaagcaatt	3987
GZMB	5	intron 4 + 131	atttctcttggaagagaa G/A aggggactagactgagctgg	3988
GZMB	6	intron 4 + 182	ggcctctgcaaacattacca G/A gaggcttatggtagtggtg	3989
GZMB	7	3' flanking + 54	attctcaggcaccacatctg C/I gctatcaggccaatgacac	3990
GZMB	8	3' flanking + 184	tcacacaccatttctccagg G/I cctgcccctctgccaaggct	3991
GZMB	9	3' flanking + 256	ccactttgcttggggctt I/A ggtaaaccttcttacctct	3992
GZMB	10	3' flanking + 406	ctgagctcaggctcagctc G/A tctccagcctctctggctgc	3993
ESD	1	5' flanking - 333	gtcttgggacagaggattg G/A gggagtgaatttagccct	3994
ESD	2	intron 1 + 603	gtcaatttctgatgggtcat C/I agggaaatgggattgagcgc	3995
ESD	3	intron 1 + 698	tgtgtgtagaagcagcatt C/I taagcactaogtgaattaac	3996
ESD	4	intron 1 + 1864	gcttcacagcaggtatc G/C tagtggagtattaggaag	3997
ESD	5	intron 1 + 2389	ttttgggaacacctgtctag G/A tigttaagagccagtggaat	3998
ESD	6	intron 2 + 22	taaacctgtttttattgitta I/C atgttactctgaacattgaa	3999

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ESD	7	intron 2 + 589	taaaattagatctctct G/A taagttcattatttaagata	4000
ESD	8	intron 2 + 1499	tagaaaaatgtatcacac C/I gtaagtgtaoagtaagtta	4001
ESD	9	intron 3 + 92	ctttatctagattattagt C/A cctcattttacttttaact	4002
ESD	10	intron 3 + 422	gtaagagattaaacacaca C/I gcacacatacatataociat	4003
ESD	11	intron 3 + 581	agaaacctgagaaatgaca C/I aattttattaaagccatagt	4004
ESD	12	intron 3 + 2270	gccagtaattacatgtagcc G/A ttatcatcaaattagetaat	4005
ESD	13	intron 3 + 2951	taatgaagtaaatgtttca A/G ctccotatacaaaaagttaa	4006
ESD	14	intron 3 + 3003	aaatgcagaaatttttgt G/A cegtcagtcatacaagaagaa	4007
ESD	15	intron 3 + 3097	aaggagcatacagaanaact G/C ccatgatggggcctttgttg	4008
ESD	16	intron 4 + 2616	tctaattgtccocagtatta A/G tgggtgcacatcttcaigtcc	4009
ESD	17	intron 5 + 392	tcctttttcatctcgtgtta C/I atcaaccatacagtttaaca	4010
ESD	18	intron 7 + 107	ttagtattggaactaaactt I/C tctagtttgagaaacttgg	4011
ESD	19	intron 8 + 1091	aaattctaactaattaaagg G/I ttcattccttttagtaactaga	4012
ESD	20	intron 8 + 1652	tataaagttgtgttaatga A/G tatatatgaataagaatatt	4013
ESD	21	intron 8 + 2048	agaaggaaaagccatttt G/C ttaagaatccctgagatatg	4014
ESD	22	intron 9 + (1523-1526)	ctgccacaagtcigaaaa (IC) 2-3 aagttgtttataaaaaacagg	4015
ESD	23	intron 9 + 2468	atagaaggagggtataact A/G cctccttaagtcicaggacc	4016
ESD	24	intron 9 + 3362	actaaggataaaaataatggc A/G tactcagtcacattggaact	4017
ESD	25	intron 9 + 5292	aggccttaatgacataattt I/C cctcacataaagatacaaca	4018
ESD	26	intron 9 + 5298	taatgacatatttccctca A/C ataaagatacaacatgcttt	4019
ESD	27	3' flanking + 798	tatggtaactgaagaaaaig A/G cattaaagttcctaaagttat	4020
CEL	1	5' flanking - (611-617)	tggatcaaggcaaaaattt (A) 6-7 ggaattattttgaagaaaa	4021
CEL	2	intron 1 + 20098	atctctaccaagggtacaaat I/G ccttaaggaaagtgttaatt	4022
CEL	3	intron 1 + (20911-20924)	taatgacatttaactttagc (A) 13-15 ctgaatatgactaaaaactga	4023
CEL	4	intron 1 + 22374	ttaagtttaaatgtaaacagc A/G cctttgcacactattcagtg	4024
CEL	5	intron 1 + (22460-22469)	ttaaatttttagtttagttg (I) 9-10 ctcittttattttatcacatg	4025
CEL	6	intron 1 + 24205	agaatttgatctattctgtg I/G gtgccttctgactacatcct	4026
CEL	7	intron 1 + (24404-24417)	gcaagtttttaactgaattac (A) 11-14 gcagatgataatcattctat	4027
CEL	8	intron 1 + 26983	tagattttgatgagtttgag I/G tttttttttttttttttttccaa	4028
CEL	9	intron 1 + (26983-26999)	tagattttgatgagtttgag (I) 14-17 ccaaaagggtggggtgtt	4029
CEL	10	intron 1 + (32166-32174)	tcactttgtctgtaaccag (A) 8-9 gaaaagccactattatatac	4030
CEL	11	intron 1 + 37217	aaatttgtaagtgaatgta I/G ataaaaatctgtaacaatta	4031
CEL	12	intron 1 + 37685	taattcaaatggaattatca I/A tgataattctatttttttaa	4032
CEL	13	intron 1 + 38032	caggccataaatgaatg I/C tcactactgttgccaacacc	4033
CEL	14	intron 1 + 38133	attcgggagtcctctctgoc A/C ttgttagaaccatccagct	4034
CEL	15	intron 1 + 38169	cagctcatctctctactctt A/I ggtgtgggattttttgcccc	4035
CEL	16	intron 1 + 38544	gtttctgtaactctcaaga I/C ataaaatcaaatgtctcttcc	4036
CEL	17	intron 1 + (38642-38643)	caatttcttacaataactg (G) attgctgccaggcagcaata	4037
CEL	17	intron 1 + (38642-38643)	caatttcttacaataactg attgctgccaggcagcaata	4038
CEL	18	intron 1 + 48429	gaaagagaactgtgtgtcc A/C gaaactgtgtgaagtgtcc	4039

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
CCL	19	intron 1 + 49038	ttgaacatgcacgacacta A/G tttaaattttacaagtaatt	4040
CCL	20	intron 1 + 49040	gaacatgcacgacactaat I/G taaattttacaagtaatttt	4041
CCL	21	intron 1 + 49256	acaaggagaaagaatggag C/A taagttaaaaaacagaatga	4042
CCL	22	intron 1 + 49386	aatagttctcagtagatatt C/A tttaacctatatttagtata	4043
CCL	23	intron 1 + 50786	taottttgctccaccaatgc G/A tattttcccttaaacagat	4044
CCL	24	intron 1 + 50977	ctccacccagagaggacaga I/C agctgagtttcigtgttgct	4045
CCL	25	intron 1 + 51150	agcaccatgacagctttttg C/G agtctctcttttattatgc	4046
CCL	26	intron 1 + 52333	tcagtcaaaccttaaggctc A/C gagatctattaatgtttatg	4047
CCL	27	intron 1 + 52589	gtgtcagcatctgttagtga C/A gggagggtgtgaaagaaaa	4048
CCL	28	intron 1 + 55838	tctcgaggttaaatgaggat G/A gaatactttaaatatacaaatc	4049
CCL	29	intron 1 + 56028	ataagtttgaaaattttgtg G/C taaatacacataaatatttc	4050
CCL	30	intron 1 + 58738	tgttgagaaataggttata G/A tctgtgcaaacctgtcccat	4051
CCL	31	intron 1 + 59358	cagaaattgtactttaaat A/G cgaactgcaagcactgcagt	4052
CCL	32	intron 1 + 59359	agaaattgtactttaaata C/I gaactgcaagcactgcagtc	4053
CCL	33	intron 1 + 59464	accagaaaaggagcatgcc C/G ttgtcoattttggtgaaac	4054
CCL	34	intron 1 + 61340	aaaaaaacttcaaaataact C/G caatatccaaagtgtgtaca	4055
CCL	35	intron 1 + 62739	cagcttttaggcacaagag A/G caaagagtctctcatctct	4056
CCL	36	intron 1 + (64764-64779)	ctgggtgttttcataaag (T)14-17 aatgtggatagtgataaa	4057
CCL	37	intron 1 + 65243	tttcaggctctggacagaa I/C agtattatgataaaagctat	4058
CCL	38	intron 1 + 65269	tatgataaaagctatata I/A ttagaagattctctcigact	4059
CCL	39	intron 1 + 65325	aattagaaaagcaagttttg G/C ggggggggtgcacaaacaaa	4060
CCL	40	intron 1 + (65326-65334)	attagaaaagcaagttttgg (G)7-9 tgcaaaacaaaaaagaaaa	4061
CCL	41	intron 1 + 65524	caacccataaacaccagtt A/C gtgtcctctctcigagccatg	4062
CCL	42	intron 1 + 65869	cagagtaaacattogggtcc A/I actgtcctttctttatagaga	4063
CCL	43	intron 1 + 65910	aaggctgtctcgtgctttt G/C tggatccaaagccgtgtgaa	4064
CCL	44	intron 1 + 66000	gctgtgttgcatgcctcac C/A gacatatttcaactgtctat	4065
CCL	45	intron 1 + (66226-66235)	tctgtttttgaaaaaacaag (A)9-10 tctctcctgcttttgaaa	4066
CCL	46	intron 1 + 81816	aatgttgcttactttccac A/G tatttccagaagccctgac	4067
CCL	47	intron 1 + 83480	tatgactgtcagaagaaaa I/C tagaattatctttgtcct	4068
CCL	48	intron 1 + 83732	gggtttgaaatctatggag I/C catttctcttttttaaaaa	4069
CCL	49	intron 1 + 85507	ctggaagaagaattttgtgc A/I ctgcattatttaaatgttag	4070
CCL	50	intron 1 + 87299	caatgtcatatatacttcc G/A tgtgtgaagacagatcaagaa	4071
CCL	51	intron 1 + 87426	caacagataatcccaaat G/C ctctgtctcccttggctct	4072
CCL	52	intron 1 + 87670	tatttggctctcatatca I/C gacatgacacacacacataa	4073
CCL	53	intron 1 - (77494-77503)	ttgttctctgttttttttt (A)9-10 caactctgtcaacaggggc	4074
CCL	54	intron 1 - 77368	agctcagggggagagaacact G/C gggggaggcaagaacggg	4075
CCL	55	intron 1 - (75135-75129)	tggcggctgcccagaaggggt (G)6-7 tgggaactctctgacgctc	4076
CCL	56	intron 1 - 74785	gctgcacaggaagctgggg G/C cgttgcgtctcttctctgt	4077
CCL	57	intron 1 - 74755	tcttctctgtgtccatgaa A/G cctcagggctccagggtcag	4078
CCL	58	intron 1 - 73099	ccccggggtctctctctggc C/I tcttcttgcgcgcgtctgt	4079

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
CEL	59	intron 1 - 72559	agcagcagctggcccgctcc G/A tgcaggagtgaggtagggca	4080
CEL	60	intron 1 - 70098	acaggaggaacacagcaaaa I/C ctcaacactgttgatctcat	4081
CEL	61	intron 1 - 69440	gttggccatgagagaaaaa C/I aggaaggtattggaaaaatga	4082
CEL	62	intron 1 - 65270	atttcgactggcgggaag G/ Δ ctggcttggcttcctggc	4083
CEL	63	intron 1 - 64434	ccacattaggagtggaatg C/I aacatctgaattaatttca	4084
CEL	64	intron 1 - 63966	agatcagatccccccacc C/I atgcctagagaaacigagcc	4085
CEL	65	intron 1 - 63916	tcgtctacatgacctagc C/I ttacgggtgaccccagtc	4086
CEL	66	intron 1 - 60392	tctggggtccaggatgca C/I gggaaatcccggagcag	4087
CEL	67	intron 1 - 60321	aattactgaacccattcc A/I tcccaccacaacccctttcc	4088
CEL	68	intron 1 - 60318	tactgaacccattccatc C/I caccocaacccctttctctcc	4089
CEL	69	intron 1 - 56852	tgtccaaagccctccccctg C/A gccacagacgaccccatctc	4090
CEL	70	intron 1 - 56133	gtggctctgggatgtcta C/I ggggttgctggcaccctccc	4091
CEL	71	intron 1 - 55964	ccccagccctcagcccg G/A cctgagactttacatgcgc	4092
CEL	72	intron 1 - 52016	tcttgaactagggtgggg G/A ggcactggcagtgcccgagg	4093
CEL	73	intron 1 - 51998	ggggcactgcagtgccca G/A gggaggggactgggggac	4094
CEL	74	intron 1 - 51578	gtggatcacttgcatctt G/C ggggagagaagcatccctggt	4095
CEL	75	intron 1 - 39557	ggcccagcatggcttcca I/C gaggctctaagctccccaag	4096
CEL	76	intron 1 - 39490	ggcctttctcagggtgtc A/C tgggcactgatggcaccag	4097
CEL	77	intron 1 - (31332-31340)	tccgacttctcattggctc (A) 8-9 ctgcctcgccctcgattc	4098
CEL	78	intron 1 - 19634	ttattcagggctggccatc C/I tagctgctgcaggagctgt	4099
CEL	79	intron 1 - 6589	gacgggtgatgcaggagact I/C gctgtcccccagtgctgtgg	4100
CEL	80	intron 1 - (3340-3345)	gctggcagtgctggcctgtg (C) 4-6 tcacatgtgtgggtggg	4101
CEL	81	intron 3 + 35	tgcggacttggccctcgcc G/A gggcgggtgaggcgccctgc	4102
CEL	82	intron 6 + 157	gtgggagcggccttggtga C/I gggattctgggtcccgtag	4103
CEL	83	exon 9 + 137	aacatggagggccacatctt C/I gccagcatcgacatgcctgc	4104
CEL	84	intron 9 + 41	tcaggggcgaccctgcggg A/G gggccgcgggaaagcacctg	4105
CEL	85	intron 9 + 151	gggtgagtatgcacacac I/C tctgttggcacaggctgag	4106
CEL	86	exon 10 + 82	agacatttgatgtctacac C/I gagtctggggccaggaccc	4107
CEL	87	exon 12 + 583	ccacagggtgactccggggc C/A cccccgtgacccccacggg	4108
CEL	88	exon 12 + 759	gttttagctcccatgagcc I/C tggatcaagaggccacaag	4109
IL17	1	5' flanking + 832	cctgagaaggaaactattctc A/G aggaactgagtccaagtcca	4110
IL17	2	5' flanking + 692	tgcctccctttctccatct C/I catcaactttgtccagctctc	4111
IL17	3	5' flanking + 76	ccctgaaccactgcgacac C/A ccacgttaagtgcacacagaa	4112
IL17	4	intron 1 + 18	tggtgagtcctgcactaac G/A tgcgatcctcttgctgatt	4113
IL17	5	intron 1 + 126	cgtatattgagtagtagaa A/G tgaagcttggtaggtatt	4114
IL17	6	intron 1 + 762	ctgagaacaatgagcagga G/A gatatttctacctagaaaat	4115
IL17	7	intron 2 + 594	tatttgcatoatttgacttc A/I tacaataagctctctgttct	4116
IL17	8	exon 3 + 1487	agctgtagggcagacgaa C/I ttttaagtagagaaaaagttc	4117
IL17	9	3' flanking + 657	ccctgaatctttttctctct G/I cctctccctcattcttaaca	4118
UCHL3	1	5' flanking - 1034	ataatgtgaagaagaaaaa A/G agacactgtctactggcctcc	4119

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
UHL3	2	5' flanking - 490	caatctgcaccgccgacaaa G/C gaacacagcaccgctgctgc	4120
UHL3	3	5' flanking - 480	ccccgacaacgaacacag I/C accgctgcacggcgctcct	4121
UHL3	4	5' flanking - 295	atcgctaggaacggcgct I/C ggaagctcgctcgctggaag	4122
UHL3	5	5' flanking - (25-11)	tggcggaaagcggcgccg GGGGAAAGGGGGG/Δ tgcagagctgagaggccggg	4123
UHL3	6	intron 2 + 28	aggctctgctgcgcggac I/C toggagctttctctgctgc	4124
UHL3	7	intron 2 + (5639-5640)	aattttattataataa (ATA) tataagtagaagaattatat	4125
UHL3	7	intron 2 + (5639-5640)	aattttattataataa tataagtagaagaattatat	4126
UHL3	8	intron 2 + 7862	agtggaattcacaccacca G/A gctaacgtctaacattttag	4127
UHL3	9	intron 2 + (7936-7947)	tgaatcatttcaaacacagg (I) 11-12 aattgtaaaagtaggacatt	4128
UHL3	10	intron 2 + (7975-7988)	aaagtaggaacatttaata (I) 12-14 gaagacgtgagtggtaaaag	4129
UHL3	11	intron 2 + 8117	ccgtactatggcaatctgg A/C gicaggaatcaacaatat	4130
UHL3	12	intron 2 + 8361	ttgttagcttggcgacat G/A gtagatcttgagtggaact	4131
UHL3	13	intron 2 + 9800	taagataatgtagcattt C/I taatatgattttgtttcct	4132
UHL3	14	intron 2 + (10738-10747)	taaccaactatgttccattg (I) 9-10 cttctttttttaccagtt	4133
UHL3	15	intron 3 + 11	taagaaaaagtaatttta A/I gtaaaatagaaaagttctgg	4134
UHL3	16	intron 3 + (662-675)	cttaaatcacagttttttcaa (TA) 6-7 aggaatcttctgtgtatt	4135
UHL3	17	intron 3 + 866	tcaagtctacatatatttagt I/C tttttttctagaatgata	4136
UHL3	18	intron 3 + (944-945)	tacatacgtatacgtatata (TGTATACGTATACATACGTATACATATATACATACGTATATA) cgtaoagtatacgtatacgt	4137
UHL3	18	intron 3 + (944-945)	tacatacgtatacgtatata cgtaoagtatacgtatacgt	4138
UHL3	19	intron 3 + 5052	aggcagtcagatagagcc I/C acattttgagcttattat	4139
UHL3	20	intron 3 + 5282	acctctattagtttttga I/C acctttcagactttccaat	4140
UHL3	21	intron 6 + 2191	tttttaggggtttcttagtg C/I gtagacagtgattctcaag	4141
UHL3	22	intron 6 + 8264	ctgcacagtcacaaatggaag G/C caagaaagaaaaatccaaaa	4142
UHL3	23	intron 6 + (8741-8744)	atgtgagtaaacacaaattt A/TI/Δ tcatcttcttaacttttga	4143
UHL3	24	intron 6 + 9411	tcctctgttttagaatctact I/G ggcctttttggccagccag	4144
UHL3	25	intron 6 + 9459	tgtcagtgccagtaaatagt I/A taaagtttcatcttcattag	4145
UHL3	26	intron 6 + 9772	gaacacatacatgtatcatg I/C ggttcagagtagagtcga	4146
UHL3	27	intron 6 + 10158	ttattttaaaggaaaattct C/I agaccgaacttaccagttca	4147
UHL3	28	intron 6 + 10839	tttactaaaaaatctacaga A/C atccatttagaataattta	4148
UHL3	29	intron 6 + 12493	agtcacaaattagttgacagtt A/G atggcgagtgacotttgcaa	4149
UHL3	30	intron 6 + (20435-20437)	tttttttaattagtagtctt CCI/Δ cgccatctctcatcacagct	4150
UHL3	31	intron 6 + 21202	ttgactgactctttctgccc C/I attcagtttctaaagattctt	4151
UHL3	32	intron 6 + 21295	caaatittagattttctt I/C ataggctaataatctgca	4152
UHL3	33	intron 6 + 21639	taagaacaattaaaaagtcga C/I ggaagcaattttcttctcc	4153
UHL3	34	intron 6 + 21778	tccattttctgtagtatac A/G caaatcacaatctcttctta	4154
UHL3	35	intron 6 + 23299	cttttagatttaaaagtgcaa I/C gatgcacaaattttgagtcac	4155
UHL3	36	intron 6 + 23498	tattcagttctctgactcga A/G ttgtactactttttacctota	4156
UHL3	37	intron 6 + 23790	ttagccttaaaaaattggac A/I ctcttcgattattgataaa	4157

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
UCHL3	38	intron 6 + 23894	actcattatcactgtcttca A/C atatttaagaataatgtttc	4158
UCHL3	39	intron 6 + (24729-24732)	agtccttaattcaaatgtt TGI//Δ aagcatcaagaagagaaa	4159
UCHL3	40	intron 6 + (25083-25084)	catgtattcatttattcag (A) taagtatgaatgtgcata	4160
UCHL3	40	intron 6 + (25083-25084)	caigtattcatttattcag taagtatgaatgtgcata	4161
UCHL3	41	intron 6 + 25084	catgtattcatttattcag C/T aagtaatgaatgtgcata	4162
UCHL3	42	intron 7 + 1342	gaagaagtcattattttgtt G/A gtatataatggacctccagg	4163
UCHL3	43	intron 7 + 1387	ttttgaagaatgtccittgt G/A attgagtctacaaaatctgc	4164
UCHL3	44	intron 7 + 1760	actcggttttactagttaga T/G agctgtcttggtcagagcg	4165
UCHL3	45	intron 7 + 2096	taggtacattacaagaatgg G/A cagttgtcgtattcattgcaa	4166
UCHL3	46	intron 7 + 2873	ttaattatattatccctac T/G ctaataaattgtaaggtaa	4167
UCHL3	47	intron 7 + 7554	tctctgagcctcatggattc T/A totgcagcgtatgcatttac	4168
UCHL3	48	intron 8 + 207	cctatagaacaaatgtfaaa T/A ttgaaaaggcaagaatagta	4169
UCHL3	49	intron 8 + 252	agacattgtcattatattcc C/G agattttcatcaaatccagga	4170
UCHL3	50	intron 8 + (883-892)	tttacactgaataatcatatc (T)9-10 octocataggtatgcataga	4171
DDOST	1	intron2 629	attctgttaagaagttctta T/C attaagaataattgtctct	4172
DDOST	2	intron2 3125	ggaatataggagcttctgc G/A tatgctgaaagtcagtcag	4173
DDOST	3	intron2 3920	attactcatttaaatgaataa A/G tggattactgacactgtct	4174
DDOST	4	intron3 189	actgtgtccaggggtccat C/T tgggctgagccagcgtgga	4175
DDOST	5	intron6 185	ctgtcctcttgttcggagg C/T gtggcagcttttcccttact	4176
DDOST	6	exon8 37	aactatgaactagctgtggc C/T ctctcccgctgggtttcaa	4177
DDOST	7	intron9 37	tcttgcccaagaatgtgcc A/Δ aaaaacggccacagccctca	4178
DDOST	8	intron2 + 1299	attcttgatgactggctt C/T ggtgcagtaactgggtttg	4179
DDOST	9	intron2 + 1581	gatactgttggtggagaaa T/C gacagagagtgtaaaacagt	4180
DDOST	10	intron2 + 2822	gtttctcaacaggtgcattc T/G tgacgtttcagactggataa	4181
DDOST	11	intron2 + 3392	cagaagggtggaggcctgc C/T ggcctccctcgtgtctgc	4182
DDOST	12	intron5 + 495	attgcttgaaccacaggggc G/A gaggttcagtgagccaaag	4183
DDOST	13	intron6 + 226	ggaactgcttgggtcacagc C/T tegtittgttccagtatcc	4184
DDOST	14	intron8 + 303	aagagaatataggtcattagg A/T tgaatttgttagcaagaga	4185
DDOST	15	3' flanking + 40	caacagctggagacggggca G/A ggagggggttattaggatt	4186
NTE	1	5' flanking - 535	cagatctgtccctccgattc C/T tgttaactotagactttcg	4187
NTE	2	5' flanking - 15	gtaaatcccgccgcaaaaacc A/G ggcgccttgcgaagccac	4188
NTE	3	5' flanking - 748	agcatggcggggagagg G/T gtggagaggtcggagaggac	4189
NTE	4	5' flanking - 690	tgaataatttaaaaggcccg T/C gcctgcggagccggcgcaa	4190
NTE	5	intron6 + 605	tcttgccataataacttagtg A/G ggggtctacatcagggttt	4191
NTE	6	intron6 + 748	agcctcagcctctctctc C/T ggggttattctcaggcatct	4192
NTE	7	intron6 + 987	gggtcgtggctctgggattccc C/T gtgcgtcatgtagtctacct	4193
NTE	8	intron6 + 1882	tggcctcaagcaatctccc G/A cctggcctcccaaaagtct	4194
NTE	9	intron6 + 2222	gaatgtttatgtagaacaga G/A agactgtatctggtgtcttc	4195
NTE	10	intron12 + 166	tatctggtaaccgaggagct C/G tggcctcgtcccaaggcc	4196
NTE	11	intron13 + 69	atccaggctcaccgcctgcc C/T gcttgattgttttaactcg	4197

Table 1

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NTE	12	intron14 + 8	agcccccgtcgggtaaggc C/I tgggaacctgcccgttgggtg	4198
NTE	13	intron16 - 113	gcaacggccctggcctt I/C atattttttaaccttcc	4199
NTE	14	intron21 + 34	agagccggccggccagagc A/G tctggagatgtatccgg	4200
NTE	15	intron21 + 128	gaagaaatcgtgcccctgag G/A gttaaaacctaaagtagga	4201
NTE	16	intron21 + 151	ttcaaaccttaagttagacc C/G aggtgcagagcattctgggg	4202
NTE	17	intron21 + 651	ccactgtactccagccggga C/I gacagagctagaacctgttt	4203
NTE	18	intron21 + 737	tggaaaatagctgtgatt G/I tigttagactctggcac	4204
NTE	19	intron21 + 1752	acagctggtctaggctgta G/C tggagaaactgggaagcaac	4205
NTE	20	intron21 + 1788	gaagcaacagctgggtcaaa A/ Δ gtactttttttctggc	4206
NTE	21	intron21 + 1907	cactgaacctgtgctccc A/G ggttcaagtgttctctgc	4207
NTE	22	intron21 + 2065	ctgctcgtttttatgttcag G/I tccccattagacagaggaa	4208
NTE	23	intron21 + 2336	agctgggagcacagaggca G/A gaatttcagataaggaggaa	4209
NTE	24	intron23 + 41	tggggagggtgtgggtggg G/C ctggagcctcaattcttc	4210
NTE	25	intron23 + 71	caattcttcagacctgag I/C tcaagttctcggttccaac	4211
NTE	26	intron23 + 81	caacctgagttcaagtct C/I ggttccaaacccagggcct	4212
NTE	27	intron24 + 150	gtggggcggtgtgtgacctc A/C ggcctccgtattccgcagct	4213
NTE	28	intron29 + 37	gcctgcagcaacgcctgacg I/C cagctgggtgtgggggag	4214
NTE	29	intron29 + 370	cgctccaggttcagcgagccc G/A tggggccgctgggctccg	4215
NTE	30	intron30 + 56	acctccgcaccacacacac G/A cacacgcttgggcacacaa	4216
NTE	31	intron30 + 358	aaaaatacaaaaataaac A/G ggtgtgggtgtgctgt	4217
NTE	32	intron30 + 372	ttaccaggcgtgtgggtg I/C gcctgtaatcccagctact	4218
NTE	33	intron30 + 430	aaatcacitgaacctggag G/I tggaggttcagtgagctga	4219
NTE	34	intron30 + 655	gtgtcacaccagctatata I/C gcaaatgtttctctcagg	4220
NTE	35	intron30 + 659	gcacacagctatatatgca A/C atgctttctctcaggggcag	4221
NTE	36	intron30 + 760	tgaatataggccattggcaa C/I gcatgccagtctgctccgtt	4222
NTE	37	intron30 + 835	gcacacagctagataggatg I/C ggcacotctgacogagttaa	4223
NTE	38	intron31 + 40	tgtgtcctgcatagggtggc I/C ggcctaggtttgtacttaa	4224
NTE	39	intron31 + 41	ggctgcctgcataggtgtgt G/A gctaagctttgtacttaa	4225
NTE	40	intron31 + 1329	gtctgtcaaggccagagacag G/A ggtgtgtaggcaggtgtgc	4226
NTE	41	intron35 + 31	aatggcttcctgtcttctt G/A gactggggcccccactctg	4227
LICAM	1	intron 1 + 767	tttgacttcctacatgggt G/A actgtgtgagtcactctgtt	4228
LICAM	2	intron 1 + 862	gcattgggtcattgtatgt G/C tgaatggggtgaatgtaag	4229
LICAM	3	intron 1 + 1332	caggatgaaggagcagagc C/I gctgagagccacacaggtg	4230
LICAM	4	intron 4 + 502	tttccctggggtttccctt I/C gcatccatctctccctgagc	4231
LICAM	5	intron 18 + 147	agcgacttaagaaattccc C/A acattcacatttctataat	4232
LICAM	6	intron 24 + 221	ctcttagccccccagagg C/I cccaaactttaagagcatact	4233
AANAT	1	5' flanking-542	aggggtgcaggatgggtgt G/I agctggagggcagggggtag	4234
AANAT	2	5' flanking-263	ccccacacataagaggtgg C/G tigtocaagactccgaggga	4235
AANAT	3	intron3 39	cgccagctccagggagggc I/A ctgaagacagaggtcagcca	4236
AANAT	4	exon4 150	cafcggcgctgcggggc C/I ggcctcatgtgcaggagcgc	4237

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ARD1	1	intron1 + 317	ccgtcggtctgtctcgccccc C/G ctccctcgggctgggcagg	4238
ARD1	2	intron6 + 322	gtccctcagcatctgtctac G/A ccagggaacccacacctctct	4239
ARD1	3	intron6 + 1095	aggctccatctcctgagacaa A/C aagtcacagtgtacctgccc	4240
ARD1	4	intron6 + 1179	aggagaaagaccctgataccc A/G gggacacccctcctccactcc	4241
ARD1	5	intron7 + 159	ctccagggtgttaggcaga C/T ggcctcctctaaagccocagg	4242
ARD1	6	intron7 + 295	tgaccagccctgcccccga G/T gagccttgggcagacccttg	4243
ARD1	7	intron7 + 416	actacocatggagcccccac G/A acagagcgtgcccttgac	4244
NAT1	1	3' UTR 215	ataataataataataataa A/T aatgtattttaagatggc	4245
NAT2	1	exon2 867	cgtgccaaacccctgggatg G/A atcccttaactattagaata	4246
NAT2	2	3' flank 521	caatccatactttgcacaa G/A agaaggaacatgagctttat	4247
NAT2	3	3' flank 573	gattgaaatcctgtggaca C/T ggggtgaattacttttaaaa	4248
NAT2	4	3' flank 918	attttgtgttgtaattcc A/G gtatcaggcgtatagttaa	4249
NAT2	5	3' flank 979	actattcctcctcttgact C/T gtagactataataatctt	4250
NAT2	6	3' flank 1958	taactattgaagtaagccta C/T gtcataatccactatttgtt	4251
NAT2	7	3' flank 2034	ccactgattccagagctag T/G toattaagaagacagtgcct	4252
NAT2	8	3' flank 2201	cagattactggagggtact G/A ttgtctacccaatgcaaatg	4253
NAT2	9	3' flank 2818	gggatattgtctctttct C/G ccagtgcatgttggaacc	4254
NAT2	10	3' flank 3237	atataattccaaataaaaa A/ Δ caaataaatttcgaaact	4255
NAT2	11	3' flank 3386	caacaagagattttttaaa G/A ctttttaaacaccagacag	4256
NAT2	12	3' flank 3660	cagcaattatcgcaataga A/G agatgtggaatcaatctaaa	4257
NAT2	13	3' flank 3973	agcagaaaaataaataatg C/T gtactaggcttactactcgc	4258
NAT2	14	3' flank 4029	caaacacaaaccccatgaca I/C gagttatctatataacaaa	4259
NAT2	15	3' flank 4118	ataagattaaatactgcata C/A aatctttgtttacagcttg	4260
NAT2	16	3' flank 4146	tgtttacagcttgttatata C/T tgaattatgtctgtccccc	4261
NAT2	17	3' flank 4279	ttaatctgatagattgggt G/C ctttataagaaaaagaaaag	4262
NAT2	18	3' flank 4323	ttgtctctccccagtcag I/G taccagggaaggccatgig	4263
NAT2	19	3' flank 4446	tcaattggctttatctgcga I/C tctggaatcaggcaatactc	4264
NAT2	20	3' flank 4462	ggattctggaatcagcga I/C actccatttcataaaaacaga	4265
NAT2	21	exon2 + 288	atgttaggagggtattttta C/T atccctcagtttaacaaata	4266
NAT2	22	5' flank - 2053	ctggattgcaacattttaat I/C ccagggtcaggtttccaac	4267
NAT2	23	5' flank - 1299	gaatcacccagtcgggaggt A/G taacagtgaaacccaagacac	4268
NAT2	24	5' flank - 1145	ctgtagaacacaaaggatatt C/T ggaggcagtttgtacatgcc	4269
NAT2	25	5' flank - 1036	ccttccacacaggtccocag T/A toatgtggcagcatgccaga	4270
NAT2	26	5' flank - 94	aagatttgcataagagattc G/A cagaggcaaccctgaggccct	4271
NAT2	27	5' flank - 643	atgtttatattttatataa I/C attaatgtaataaaaaattt	4272
ABC82	1	5' flanking - 673	agctaaagagtcaaagcaccc G/C gttttccaccagcctcgcg	4273
ABC82	2	5' flanking - 646	ccaccagcctcgctgctgt T/G tcccttcacggacactctag	4274
ABC82	3	5' flanking - 563	ttcgaagcgtgtgtgtctac A/C ggcgaacctccctgcgtccc	4275
ABC82	4	5' flanking - 236	gccttgcgcgcgcgtctaac G/T tctgtaggcagatctgccc	4276
ABC82	5	Intron3 + 408	aaggaaactgagccaagac C/T cttaatgtgaaactgcaca	4277

Table 1

Designation of Gene	No.	Location	Sequence	SEQ ID No
ABCB2	6	Exon4 + 153	ccctcaccatggtcaacctg A/G toacctgacctgtcttttc	4278
ABCB2	7	Intron4 + 289	gtattcttttagaatcaag G/I ggcatagtgtgtcttttc	4279
ABCB2	8	Intron4 + 291	attcttttagcatccaagg C/G catagctgtctcttttc	4280
ABCB2	9	Intron5 - 63	ttccttcaggtaataactg C/I ggtttttgtgtccctcca	4281
ABCB2	10	Intron7 - 185	gtctctgacctgtctttgc C/I gotttctctatctctactcc	4282
ABCB2	11	3' flanking + 71	agcgacatttcaagtcggg G/A tgtctctctttttatcatcc	4283
ABCB2	12	3' flanking + 129	aactgcatcaacctttccct I/C aagcttttaattctatga	4284
ABCB2	13	3' flanking + 459	cattcaggaggccaccagtc G/A tgtacgtogacagtgtcig	4285
ABCB3	1	Intron3+8	tcctcttggcaggtaggtg G/A tgggcagctgggtccatttg	4286
ABCB3	2	Intron4+104	cttcaacctatgccaggac C/I tggggatgcttttctctgt	4287
ABCB3	3	Intron10+219	ggacagtggtgtctccctc A/G tgggcagcccgccaggtcc	4288
ABCB3	4	Intron11+(317-319)	atgggtcccagggtggatgtg G/G/Δ tcatctcattctgcttt	4289
ABCB3	5	exon12+19	agctgcaggactggaattcc I/C gtgggatcgccagctgtcig	4290
ABCB3	6	exon12+ (356-357)	agctgggg'tggggtggggtg GG/IGTGGGIGGA ggcgtctgtgtccaggaaa	4291
GSTM3	1	5' flanking - 144	ccaaccccgcatattagtcgc G/I cctggcagcgcccttgga	4292
GSTM3	2	Intron 7 + 165	agcctaactctataacttg A/G aggcactgtctacaaaaa	4293
GSTM3	3	Intron 7 + 257	ctgttggactgggtgggtc I/G ttataagattgggtatttt	4294
GSTM3	4	exon 8 + 91	ccagtgggggcaacaagcct A/G tatgctgagcagaggagcaga	4295
GSTM4	1	Intron 4 + 67	ttggctggattgggg'tgcta I/C gctcagagtggctctgttt	4296
GSTM4	2	Intron 7 + 77	gatgcttccagtcctctgga I/G ctgcataaagaataaacttc	4297
GSTM4	3	Intron 7 + 80	gctttccagtccttgatct G/A cataaagaataaacttcatt	4298
ALDH7	1	Intron1+464	catgaatgactctgggaaag A/G atcattcttagcaatggact	4299
ALDH7	2	Intron1+2269	aatggaatccaacacagcaa G/C agacctccctcaccggtea	4300
ALDH7	3	Intron2+1349	actgagcttctgccacoggc C/I gctgccggccttcaigaga	4301
ALDH7	4	Intron2+1820	tcogtltggaaagcaccttc C/G ccagcctcagtggttagga	4302
ALDH7	5	Intron2+2046	aaactcaggggcgtgctcag C/G caggagccagcctggcccc	4303
ALDH7	6	Intron2+2939	aagcacgactgaacatgga G/A tgagttag'tgaocgaatgaa	4304
ALDH7	7	Intron3+7	tggccaagaaccttggtgagc C/I ggcggggctgaggcggcag	4305
ALDH7	8	Intron4+36	ggcccttcgggtcaccttc I/C cagctcagggcctcaggccc	4306
ALDH7	9	Intron6+(116-117)	attctctctctctctctct C/I/Δ ggaaccagctgggagcagtc	4307
ALDH7	10	Intron6+263	cagacotcatactgaccc I/C gctgccccccaggtctcttag	4308
HMGL1	1	3' untranslated + 864	cttcttgatttttgatagtc G/C gttgaagaaggagattttaa	4309

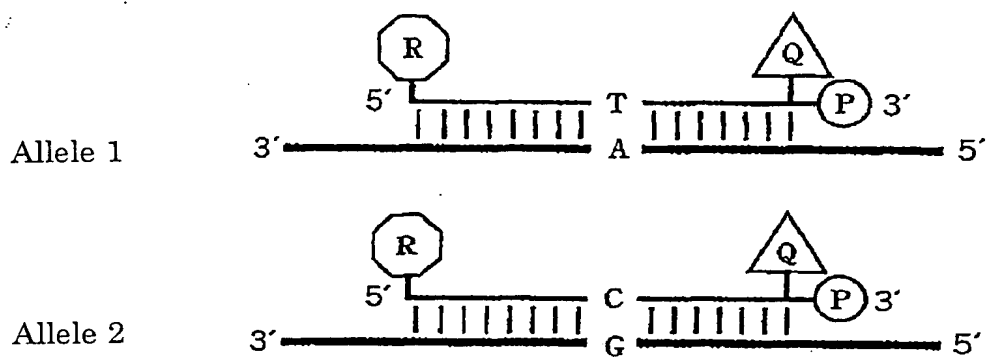


Fig. 2

a. Hybridization



b. PCR Reaction



c. 5' Nuclease Activity

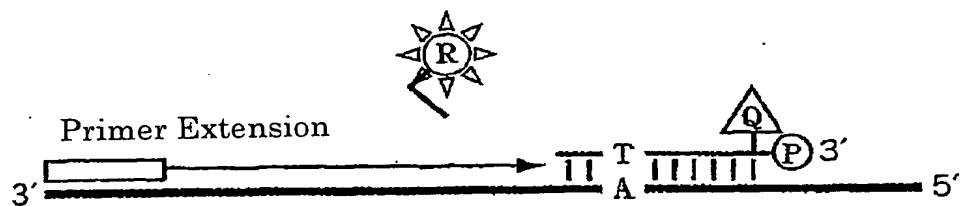


Fig. 3

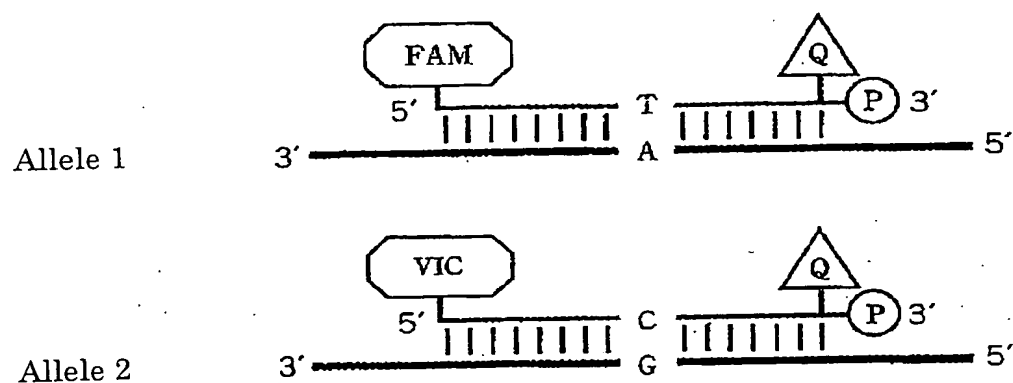
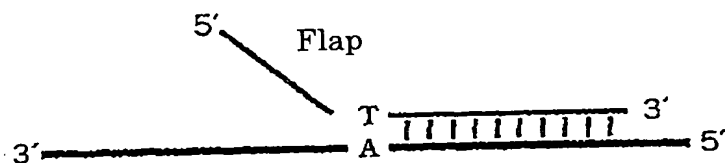


Fig. 4

a. Allele Probe



b. Invader Probe



c. 5' Nuclease Activity

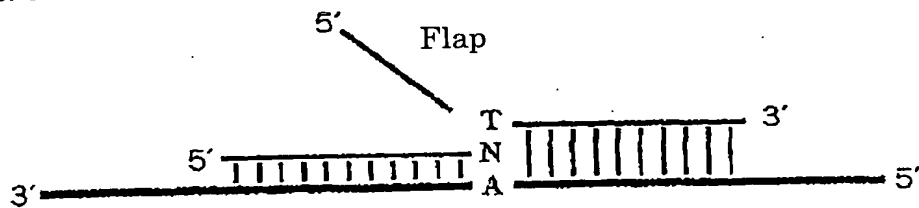


Fig. 5

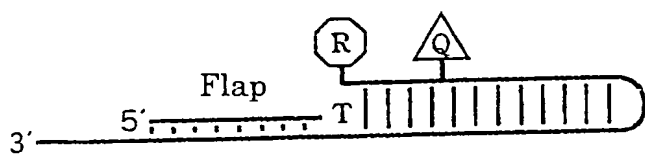
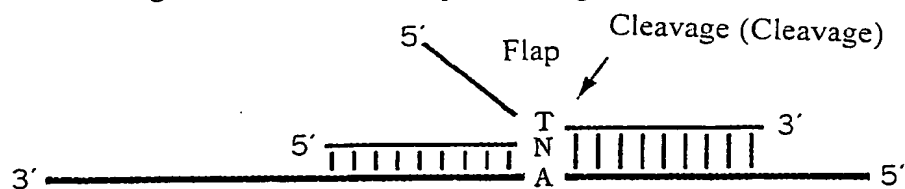
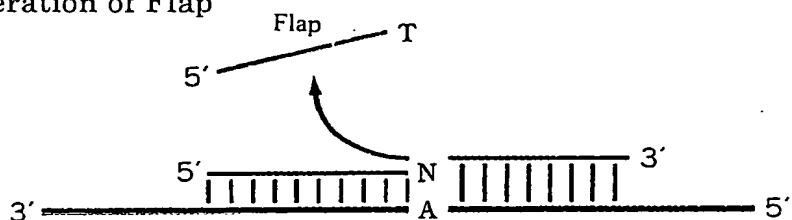


Fig. 6

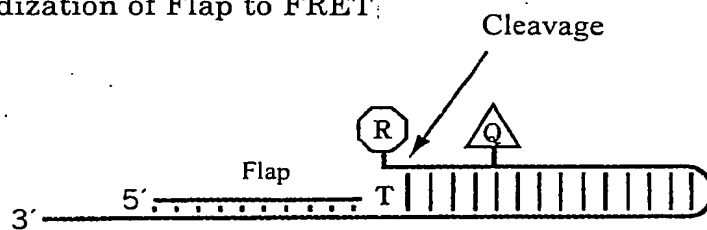
a. Cleavage of Allele Probe by Cleavage



b. Liberation of Flap



c. Hybridization of Flap to FRET



d. Liberation of Fluorescent Dye

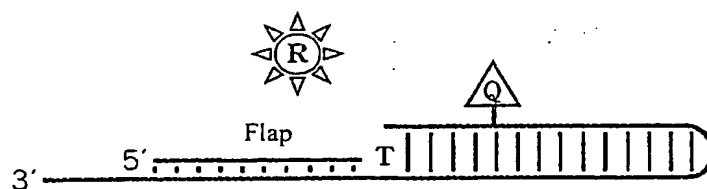


Fig. 7

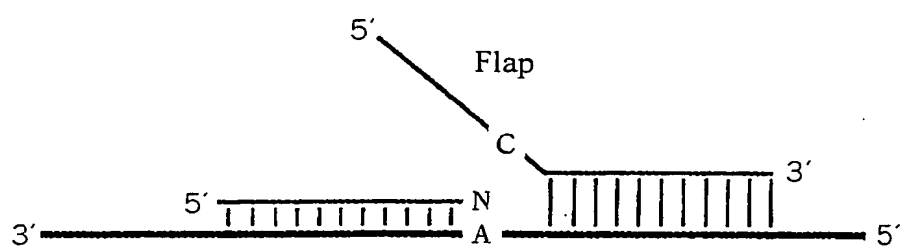


Fig. 8

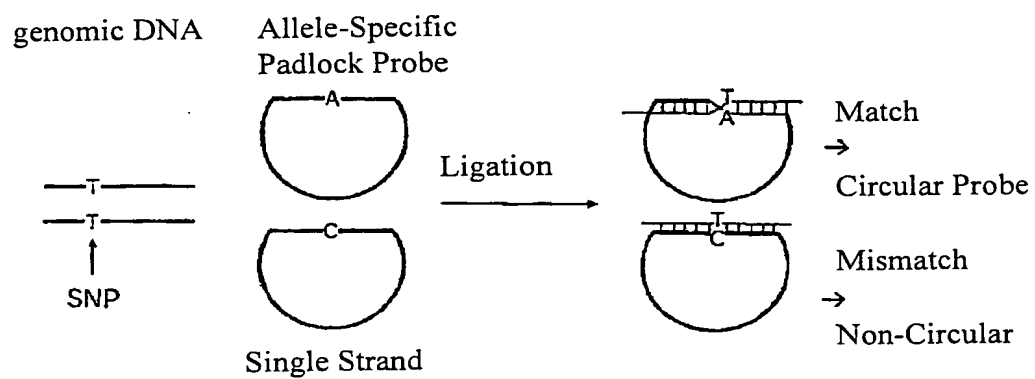


Fig.9A

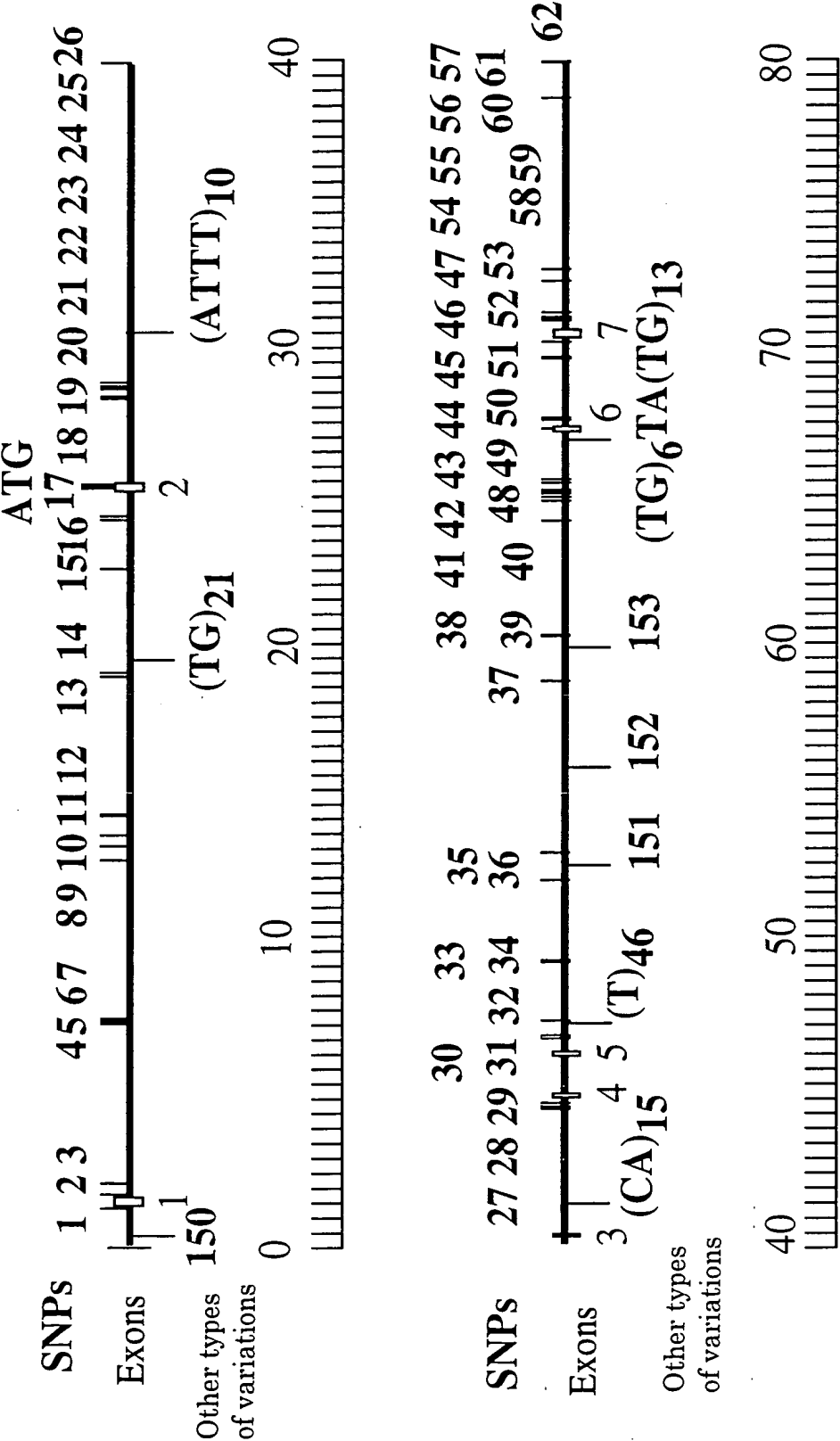


Fig.9B

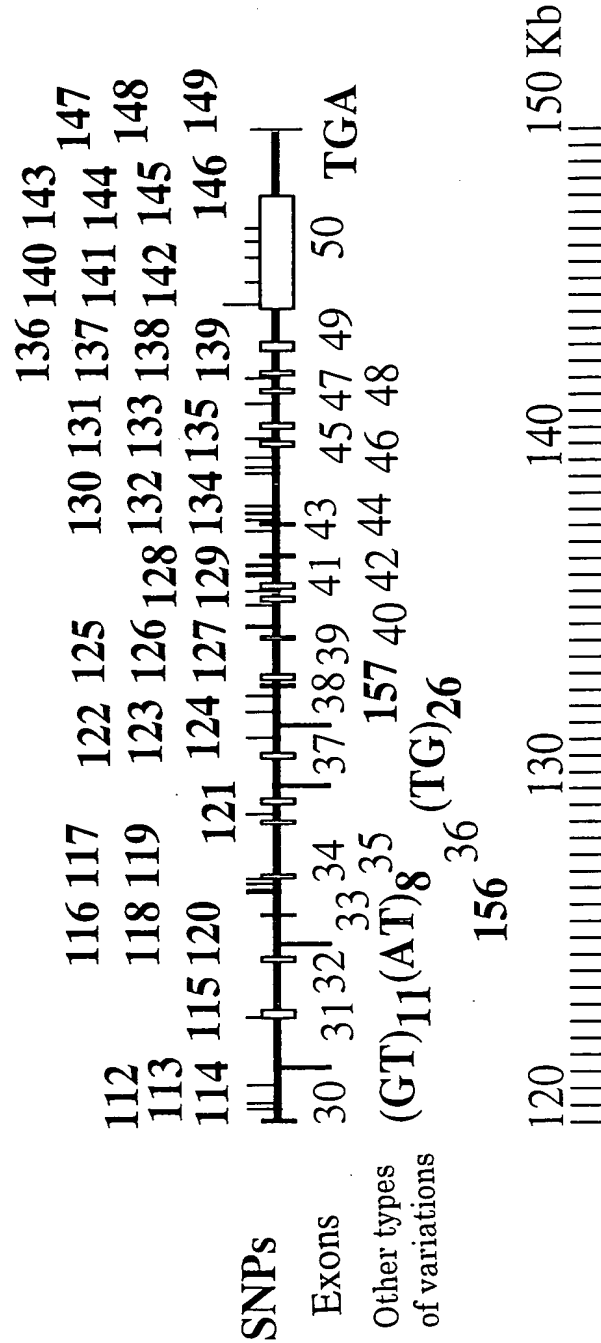
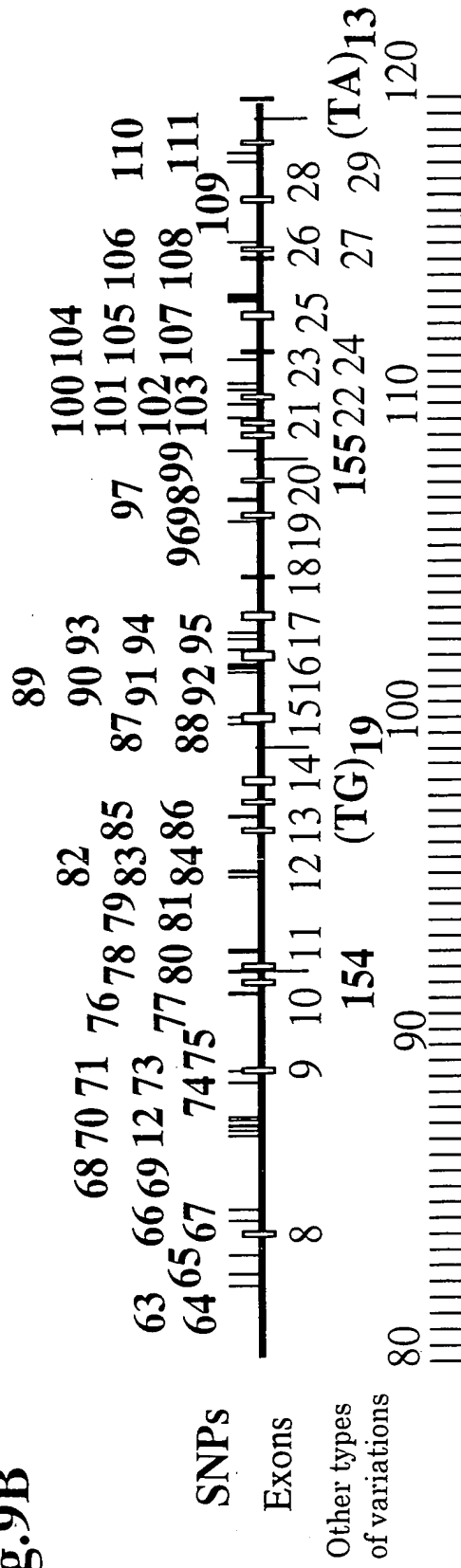


Fig. 10

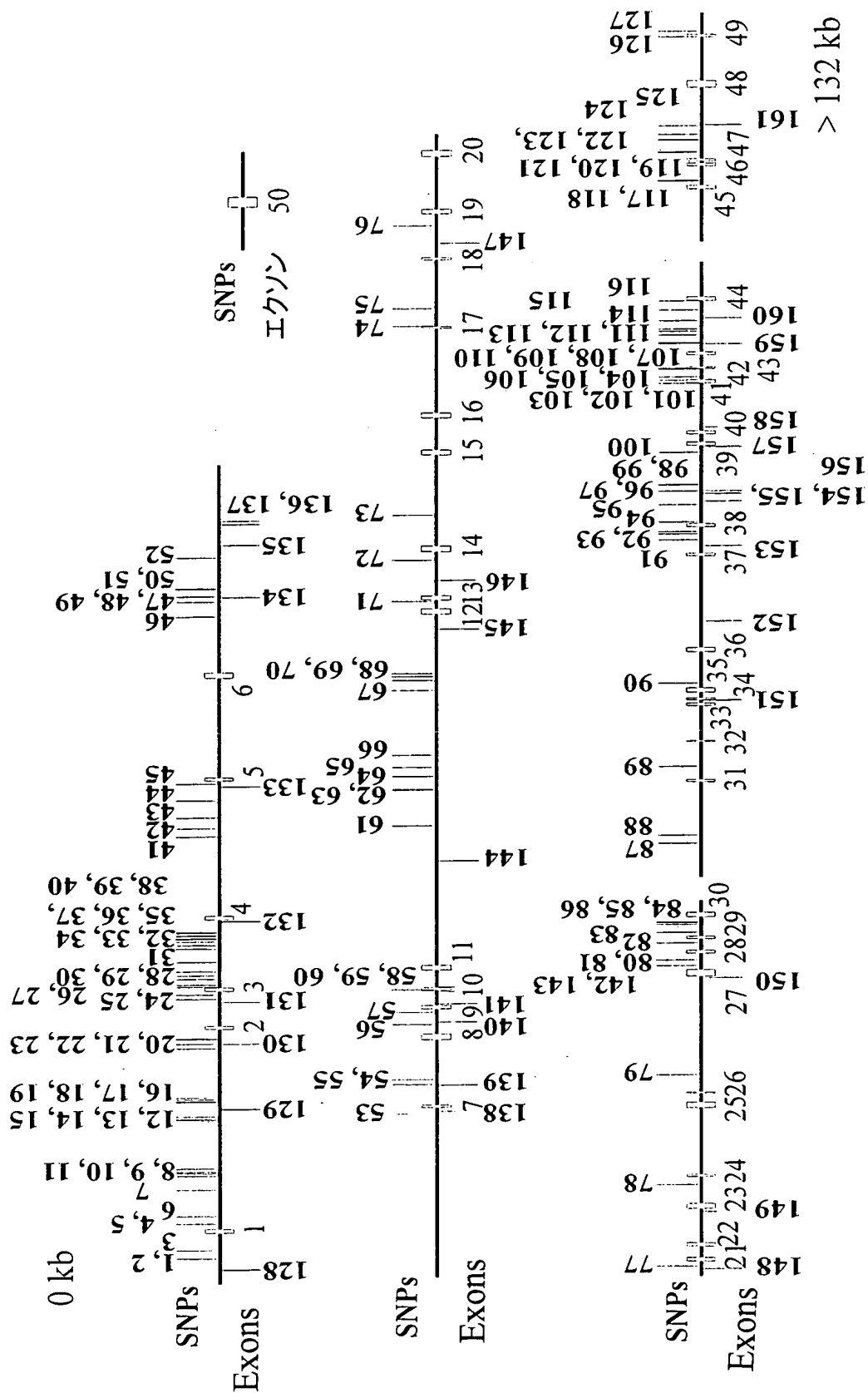


Fig. 11

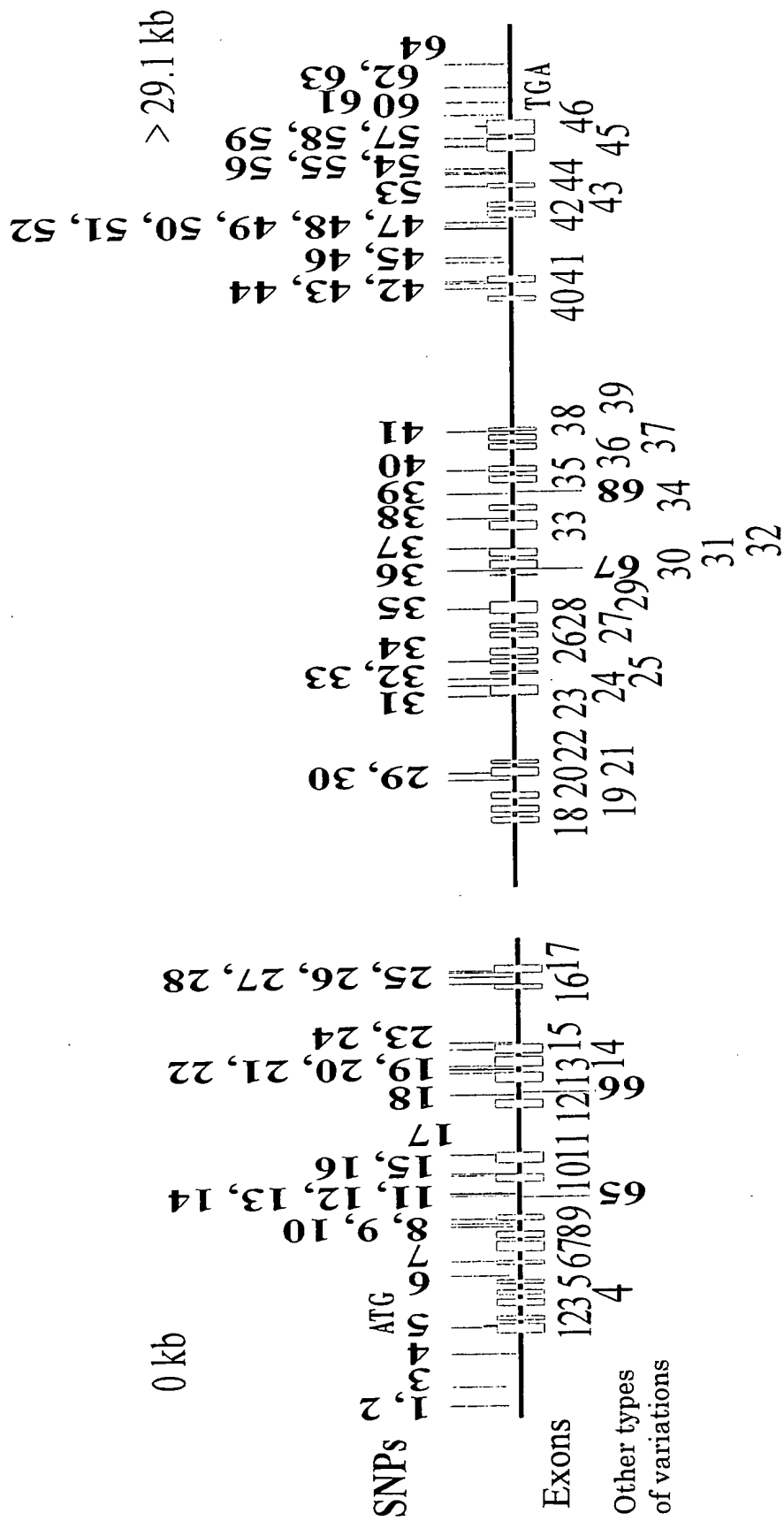


Fig. 12

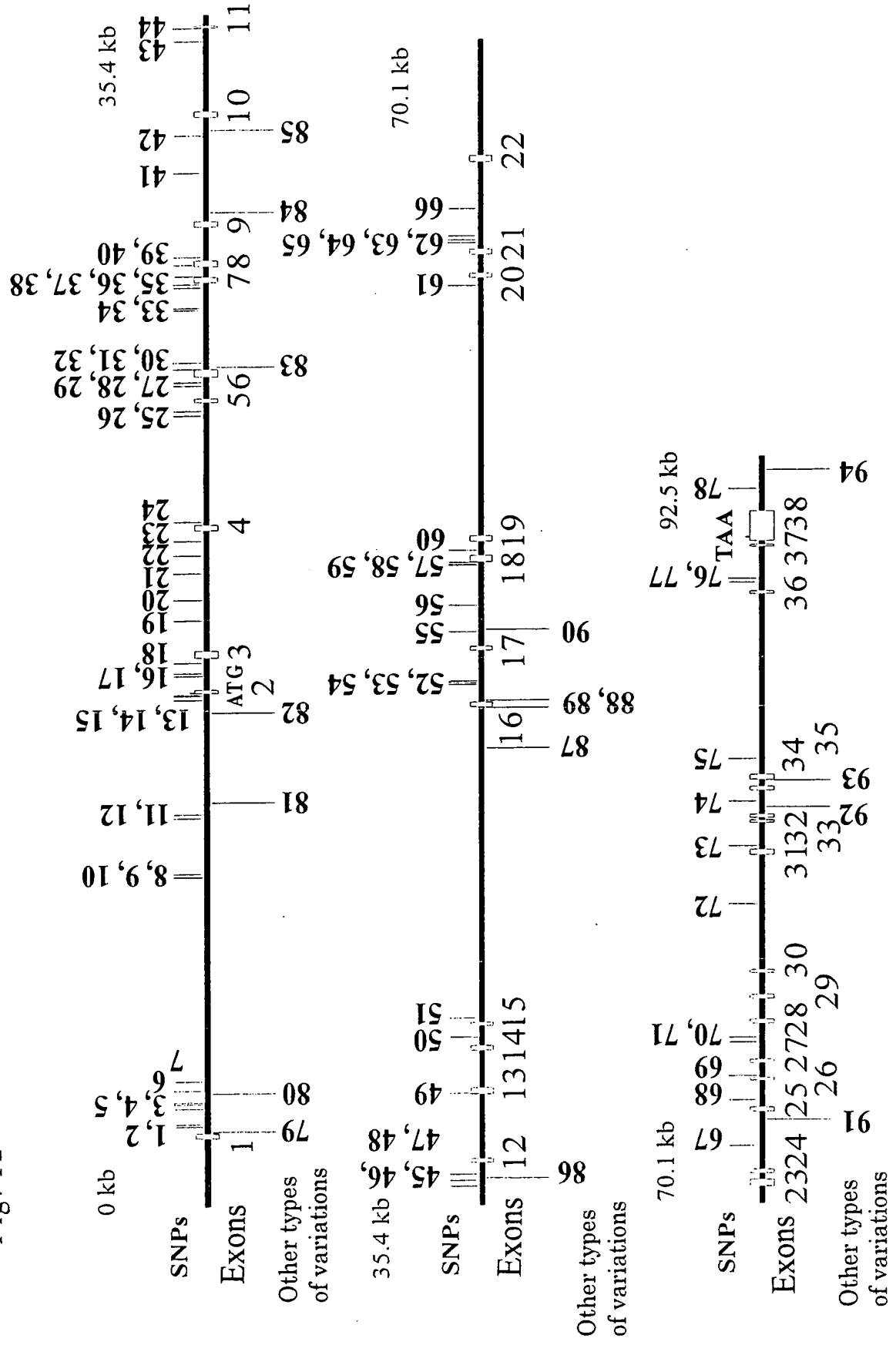


Fig.13

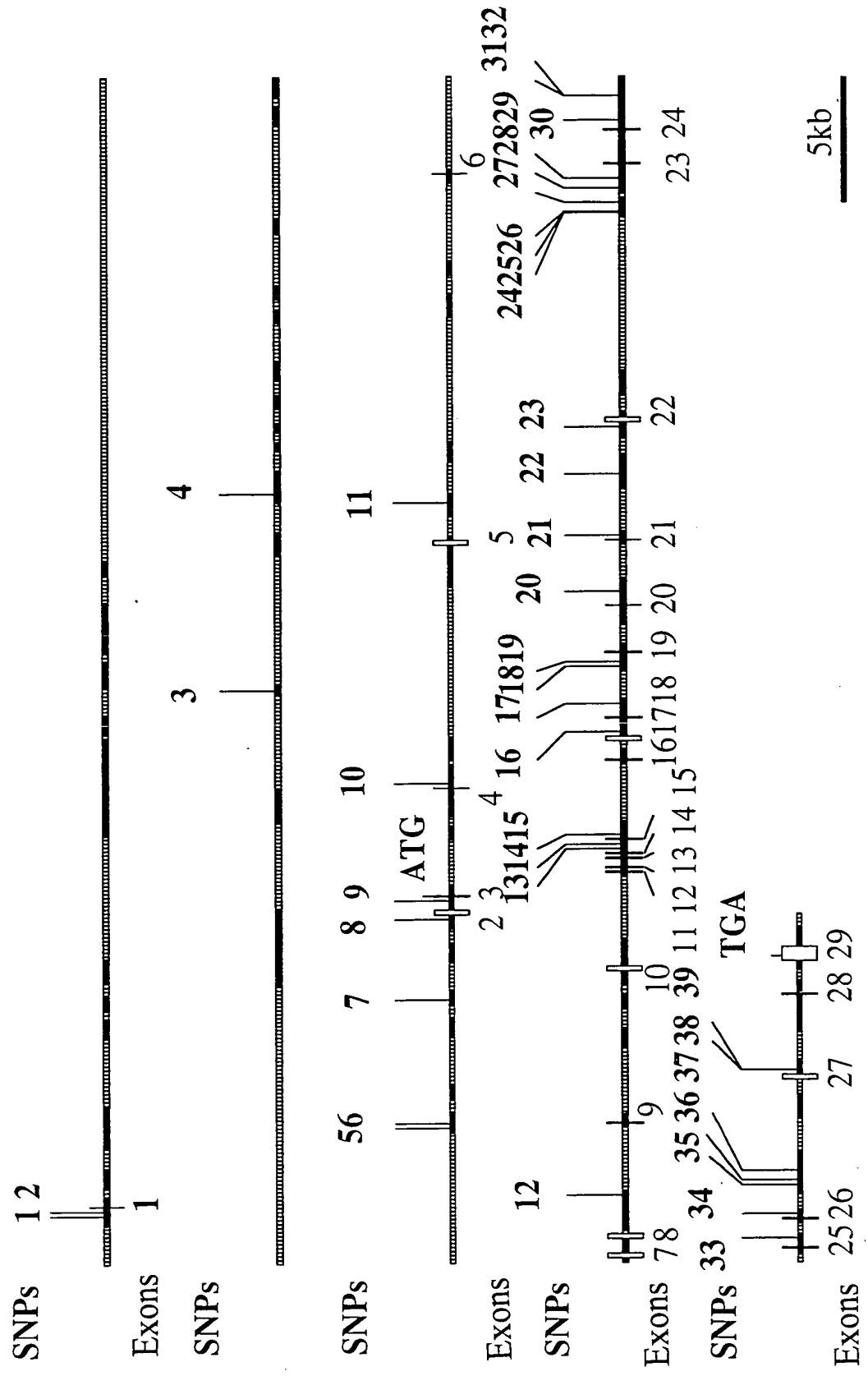


Fig.14

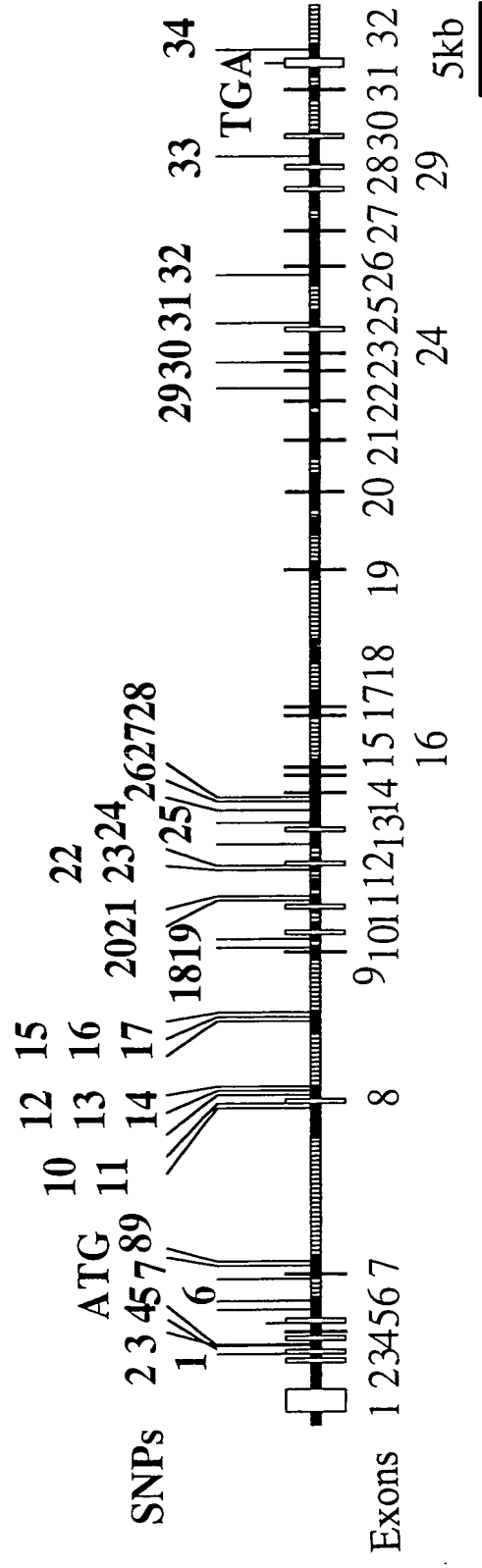


Fig.15

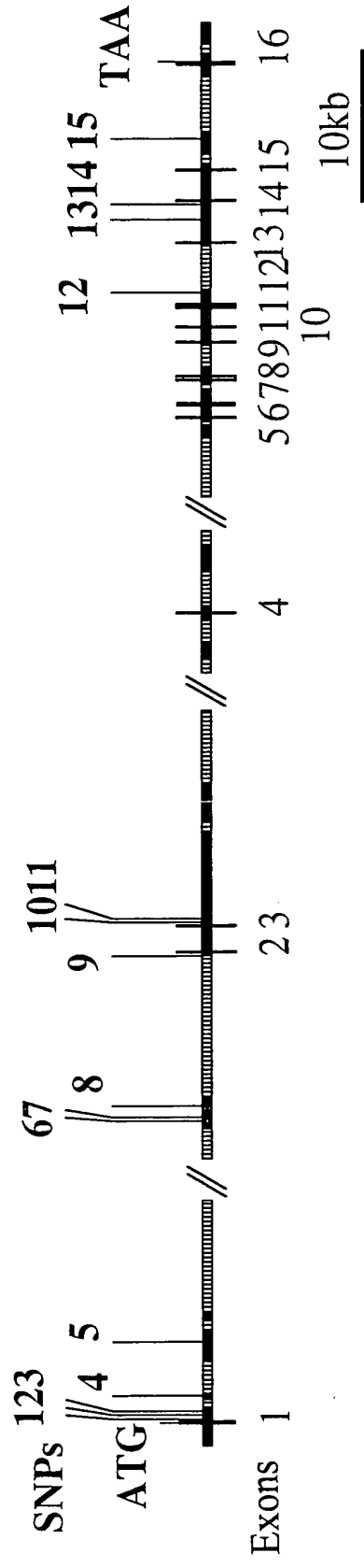


Fig.16

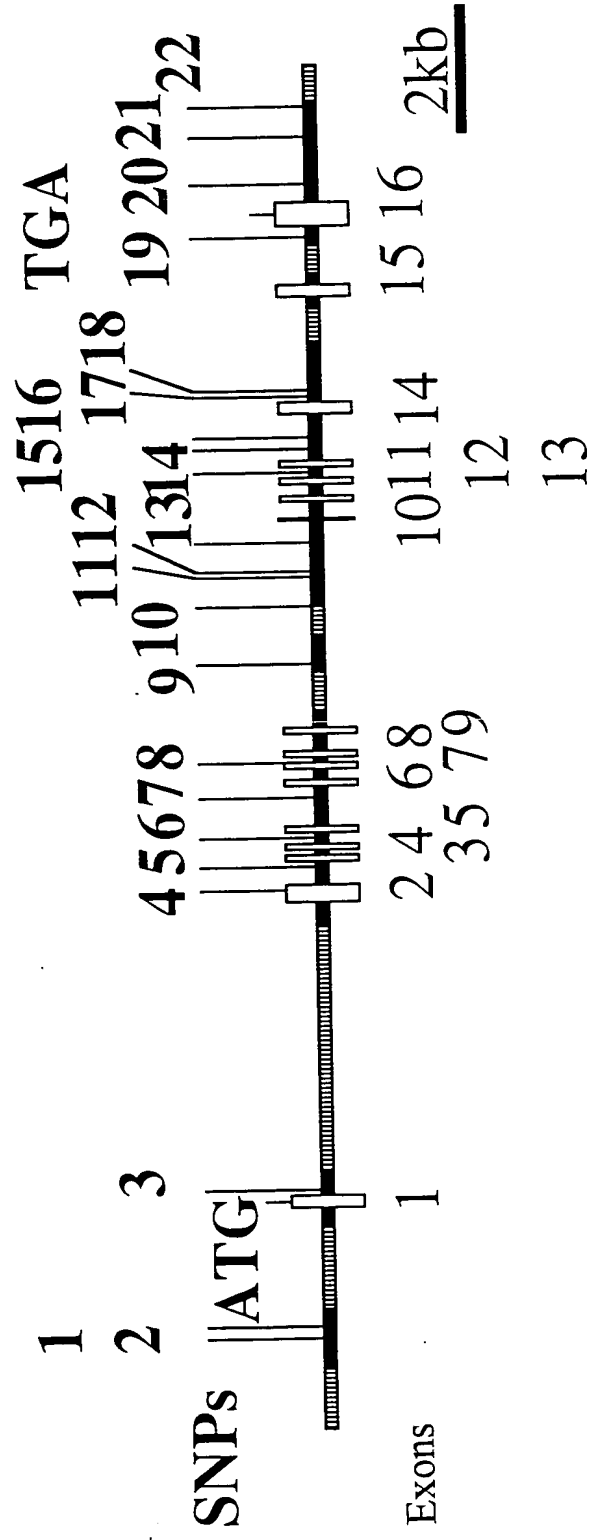


Fig.17

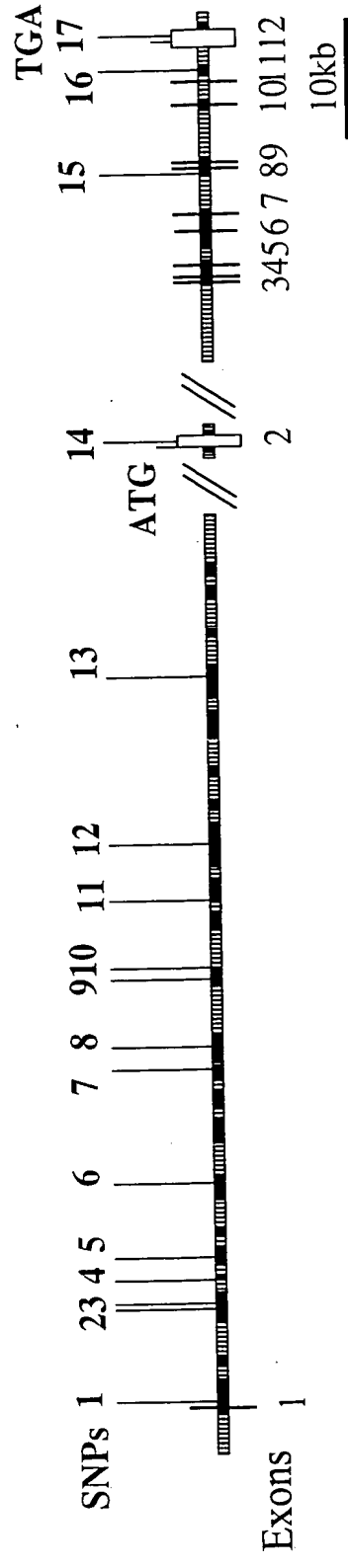


Fig.18

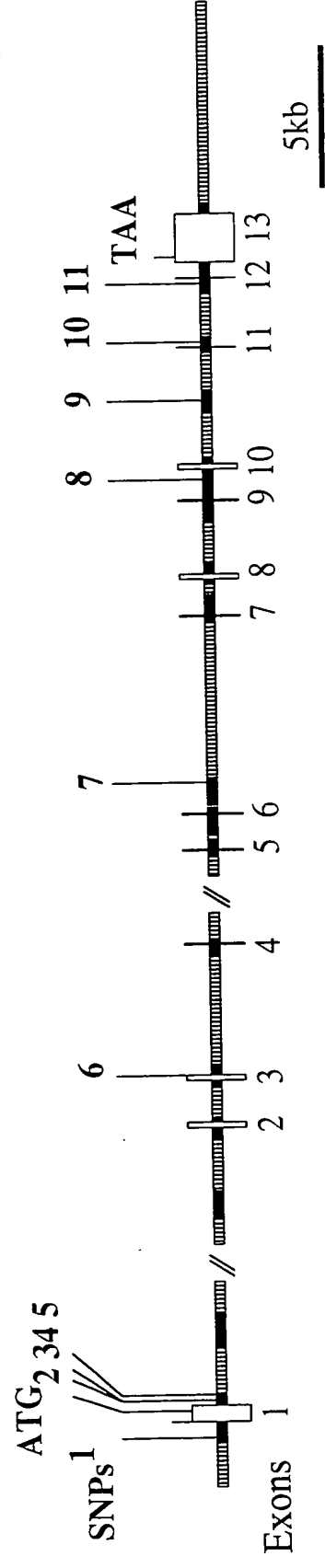


Fig.19

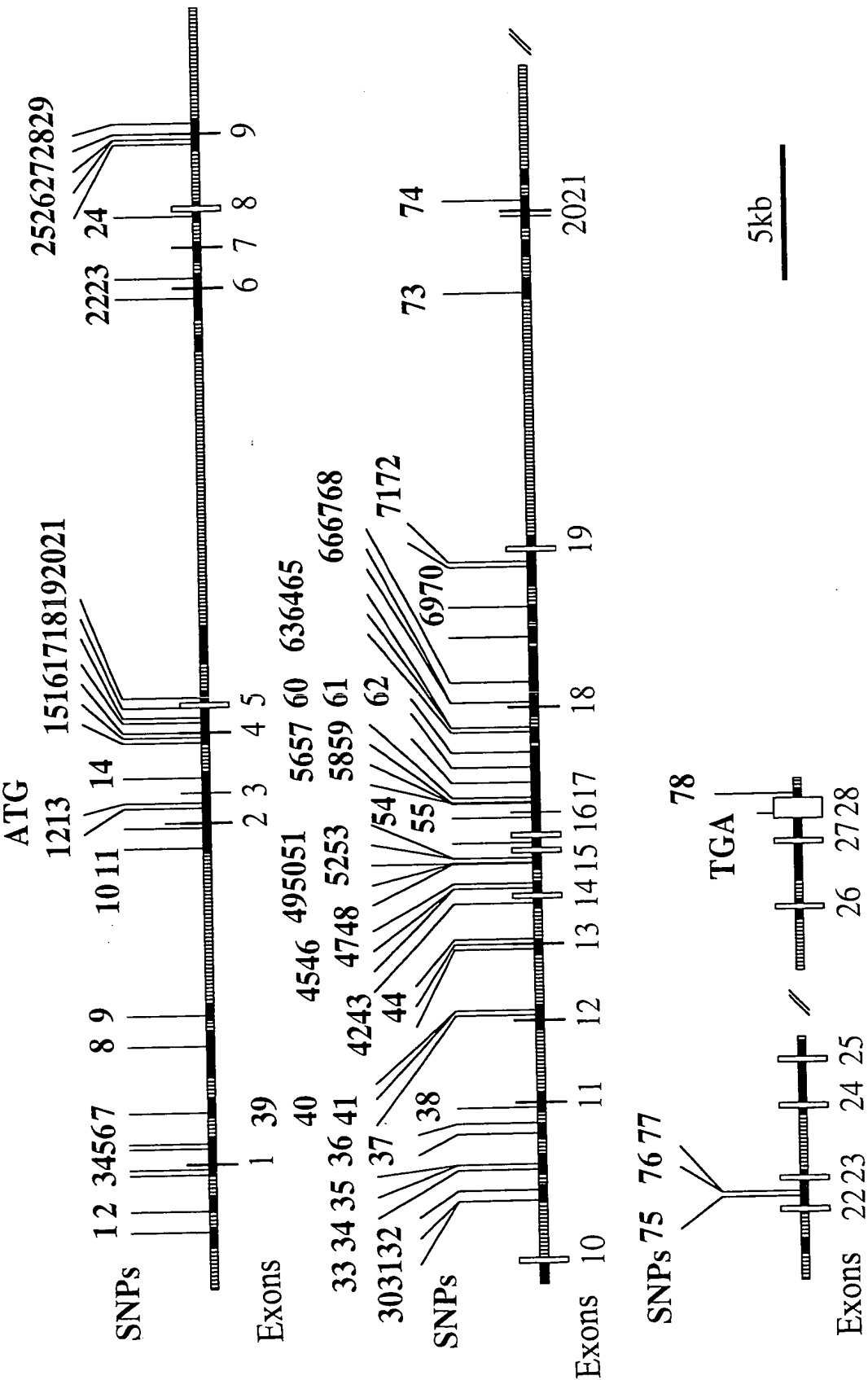


Fig.20

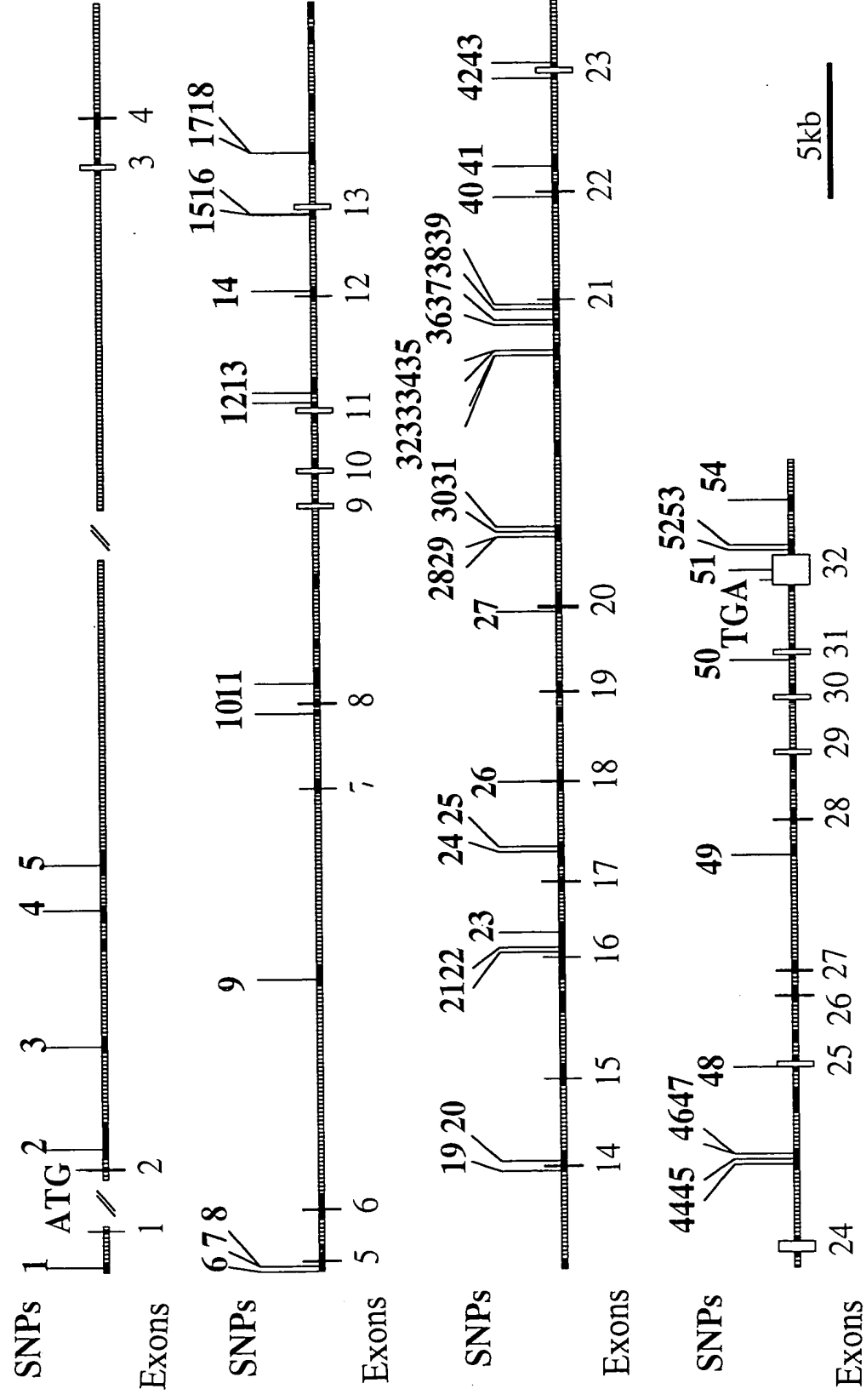


Fig.21

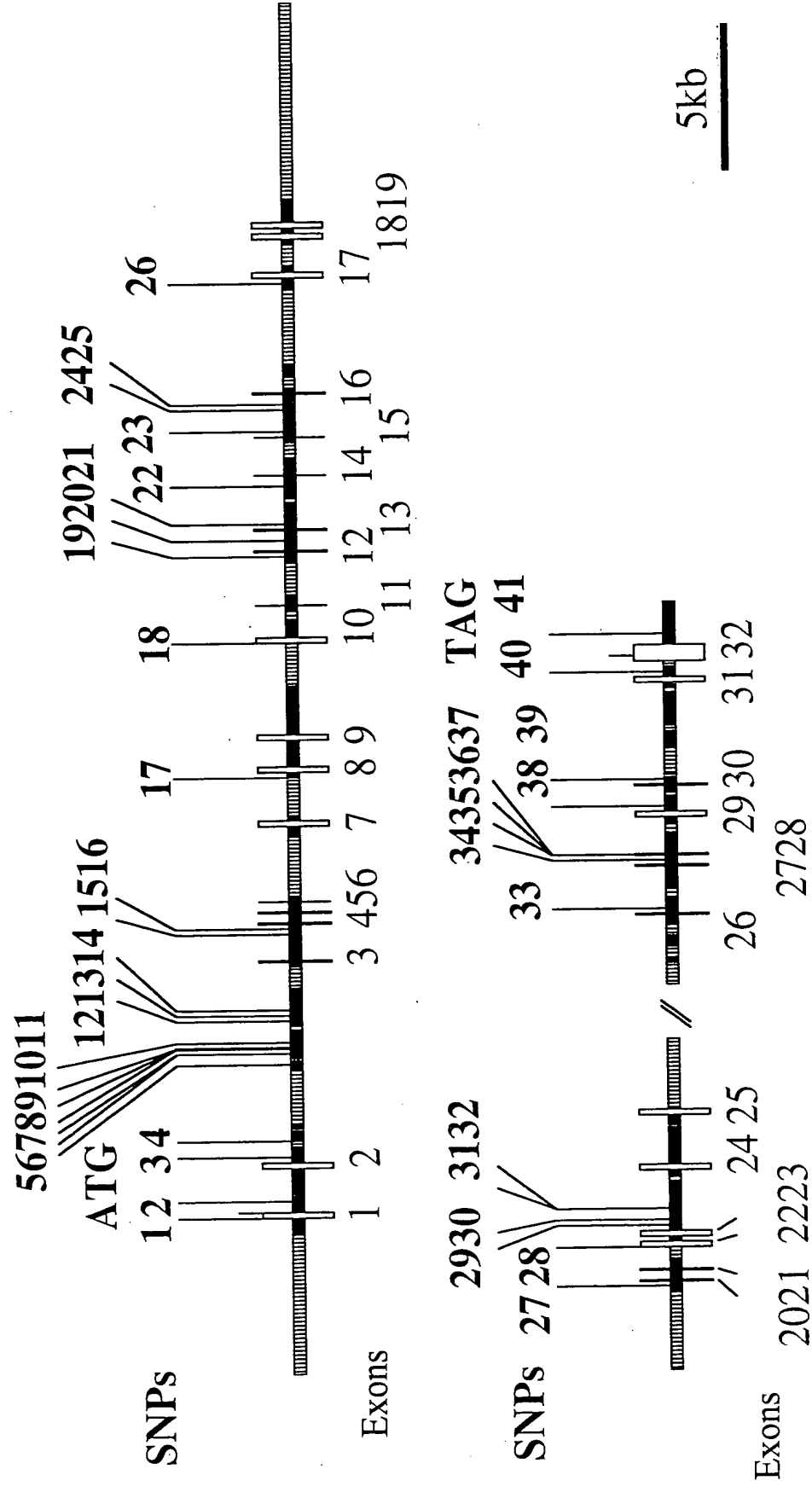


Fig.22

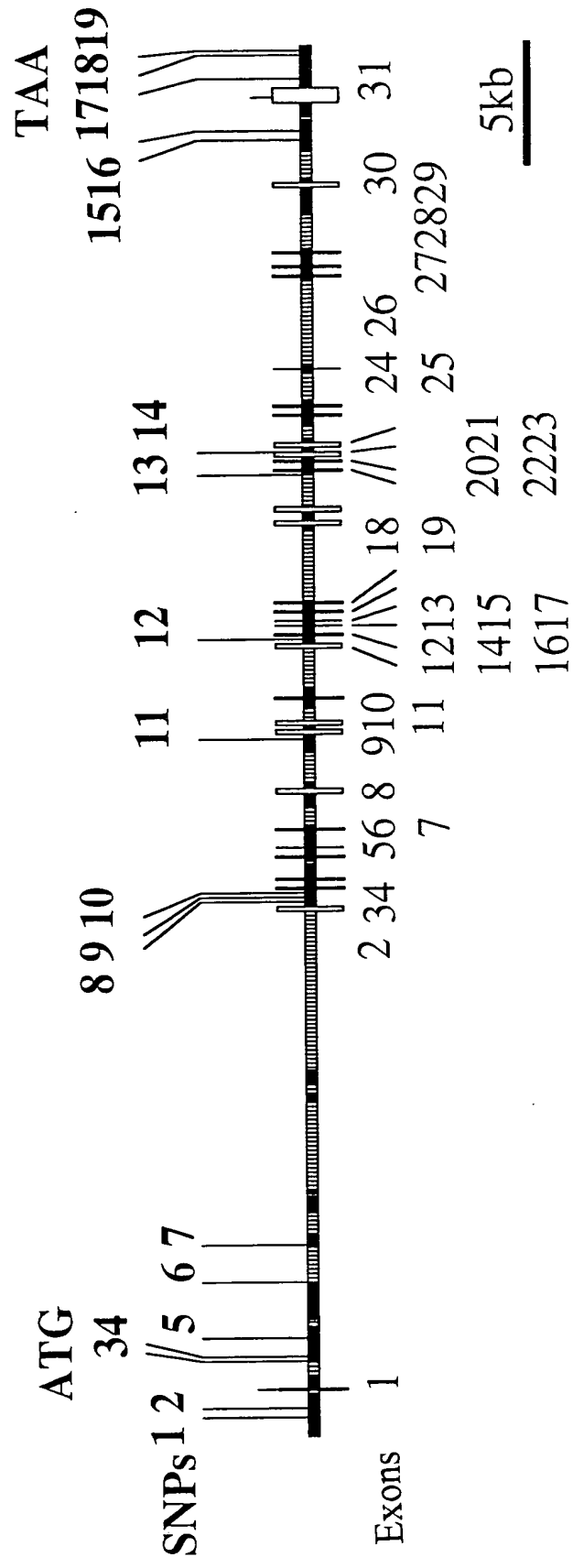


Fig.23A

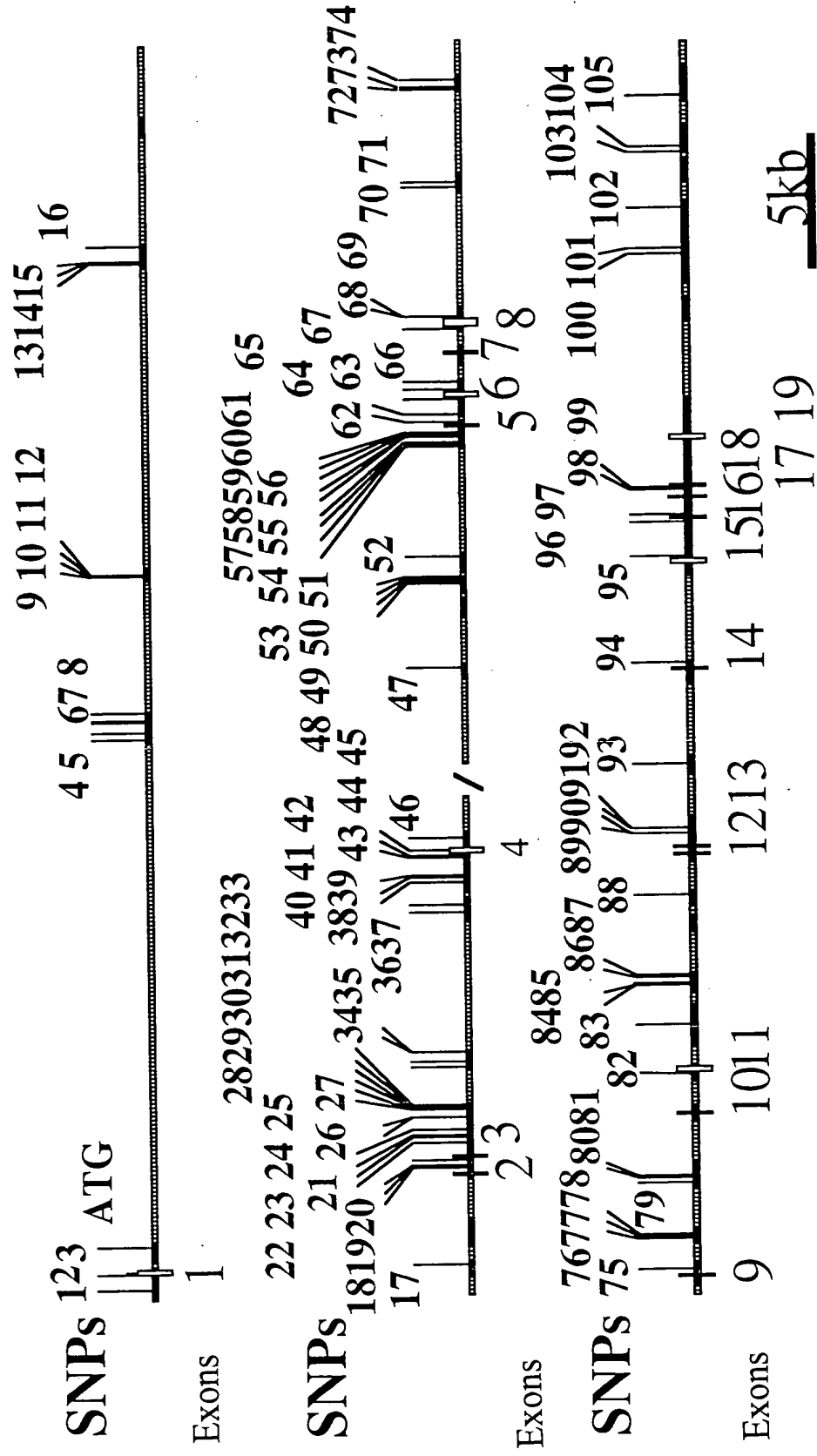


Fig.23B

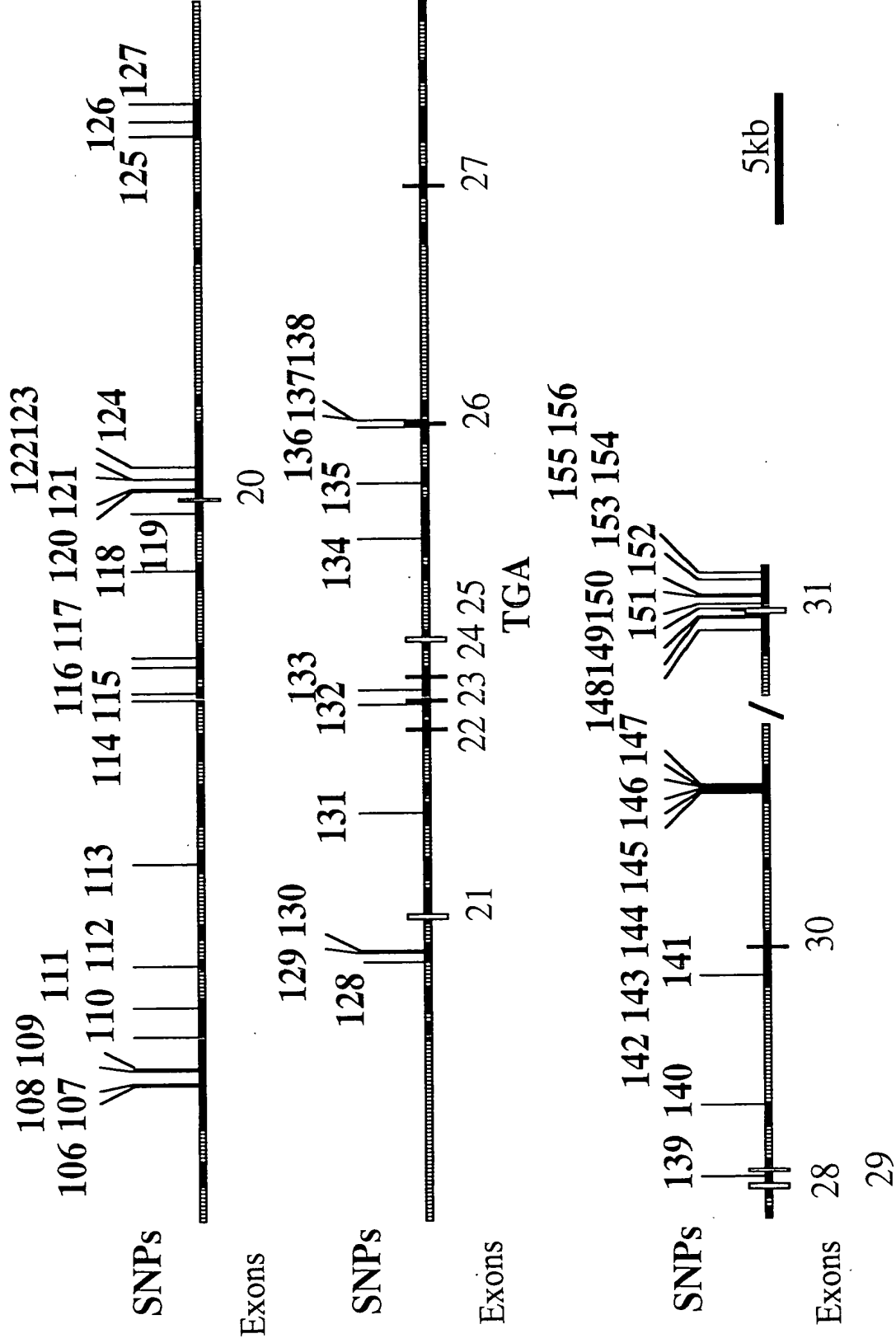


Fig.24

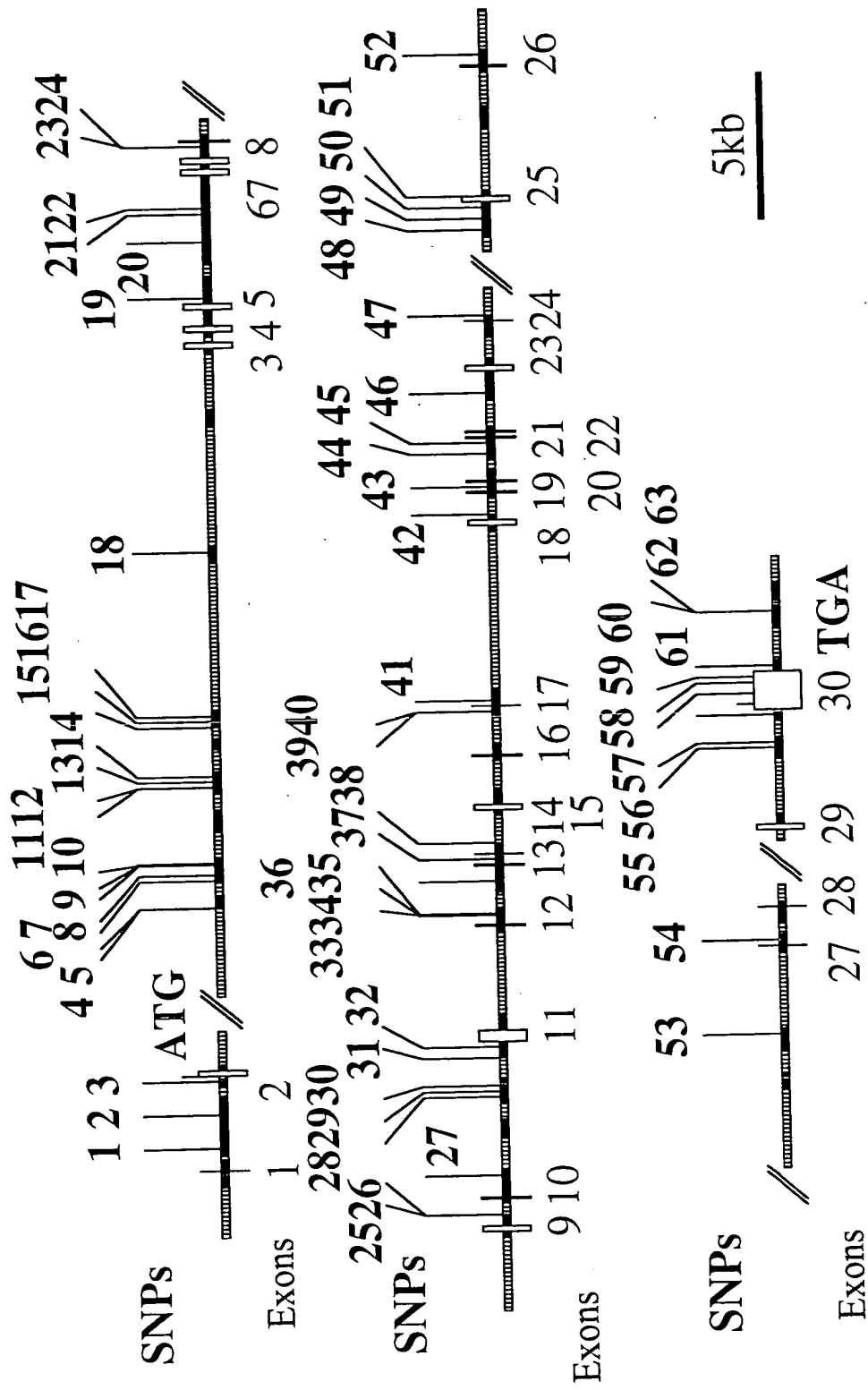


Fig.25

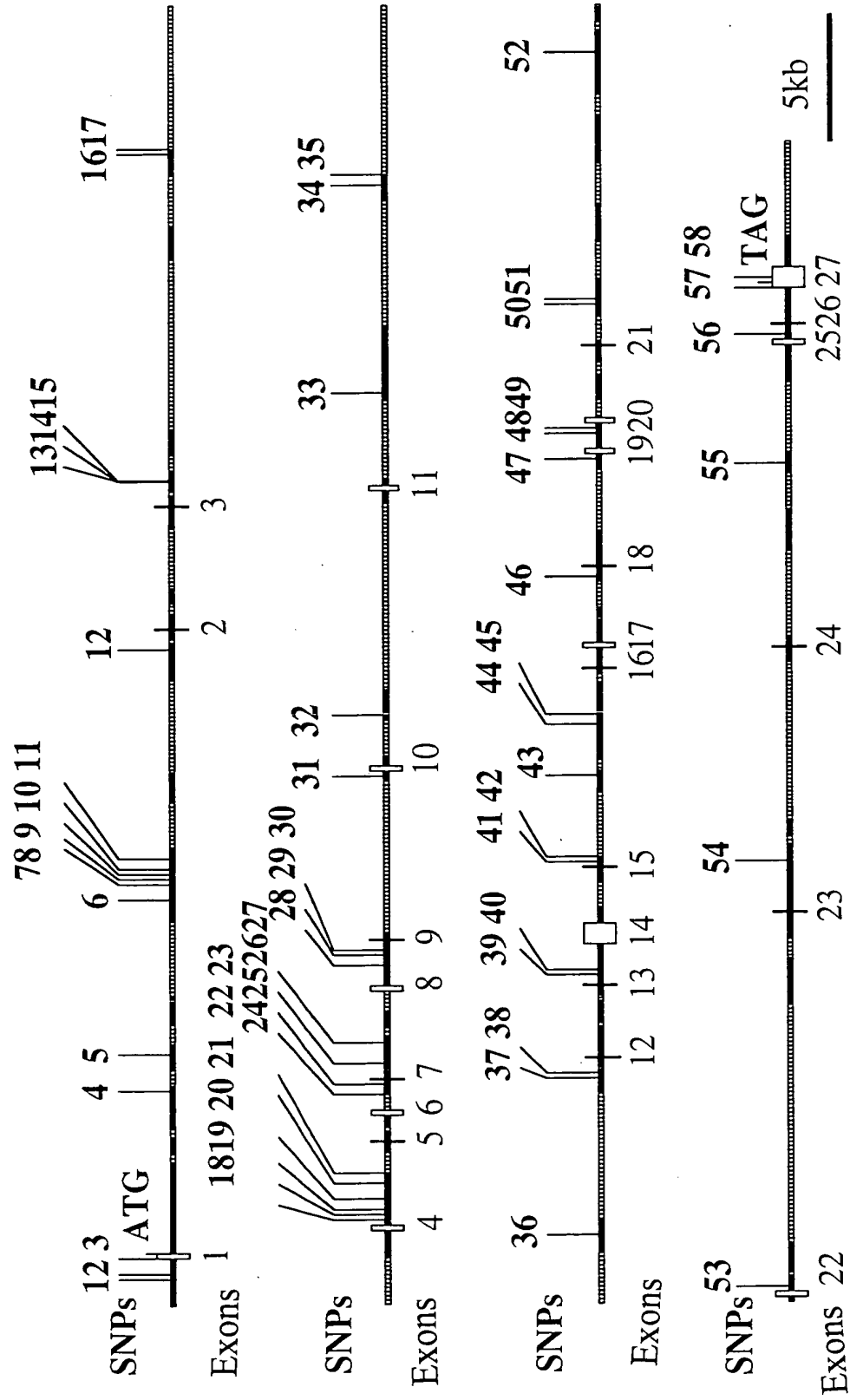


Fig.26

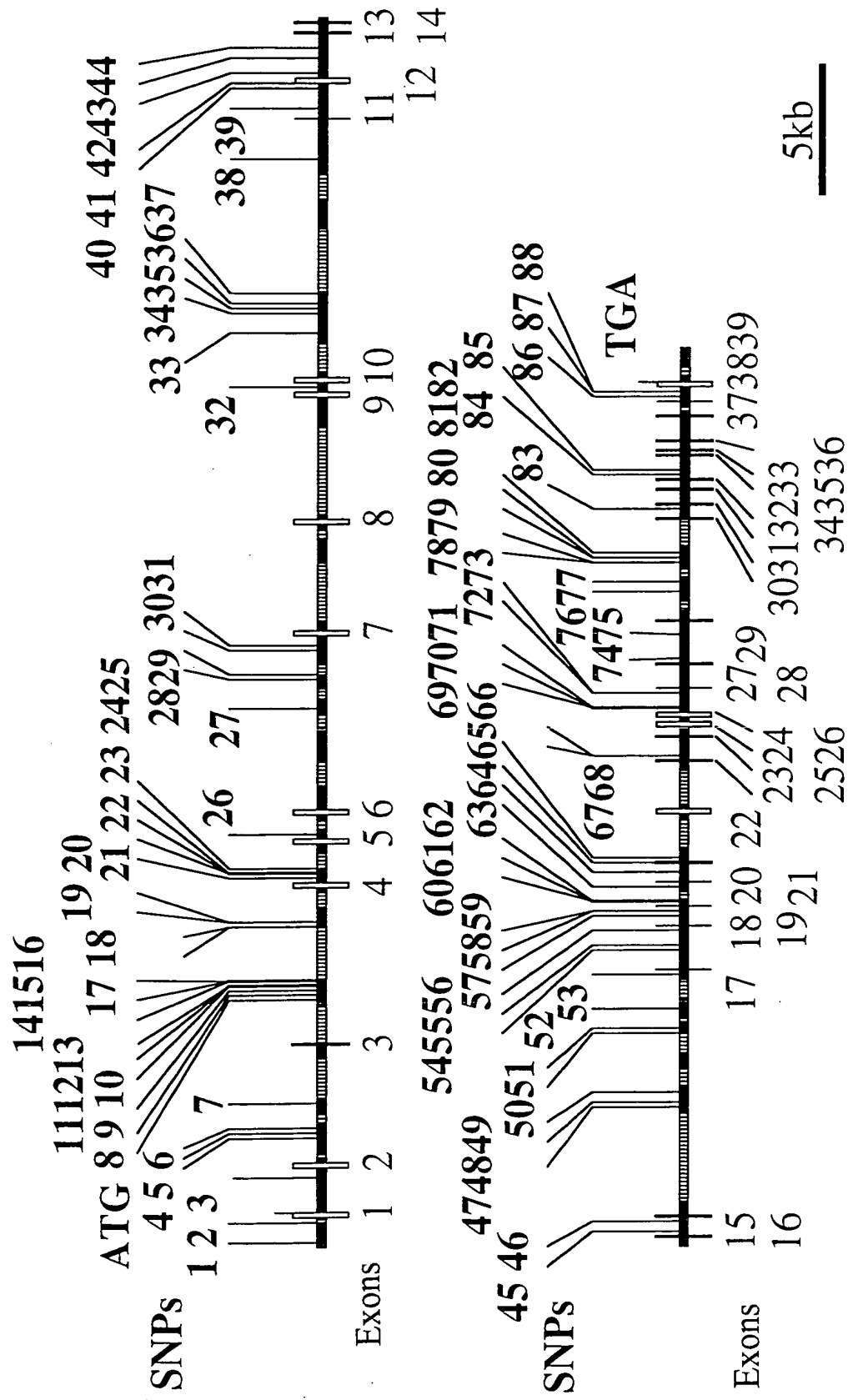


Fig.27

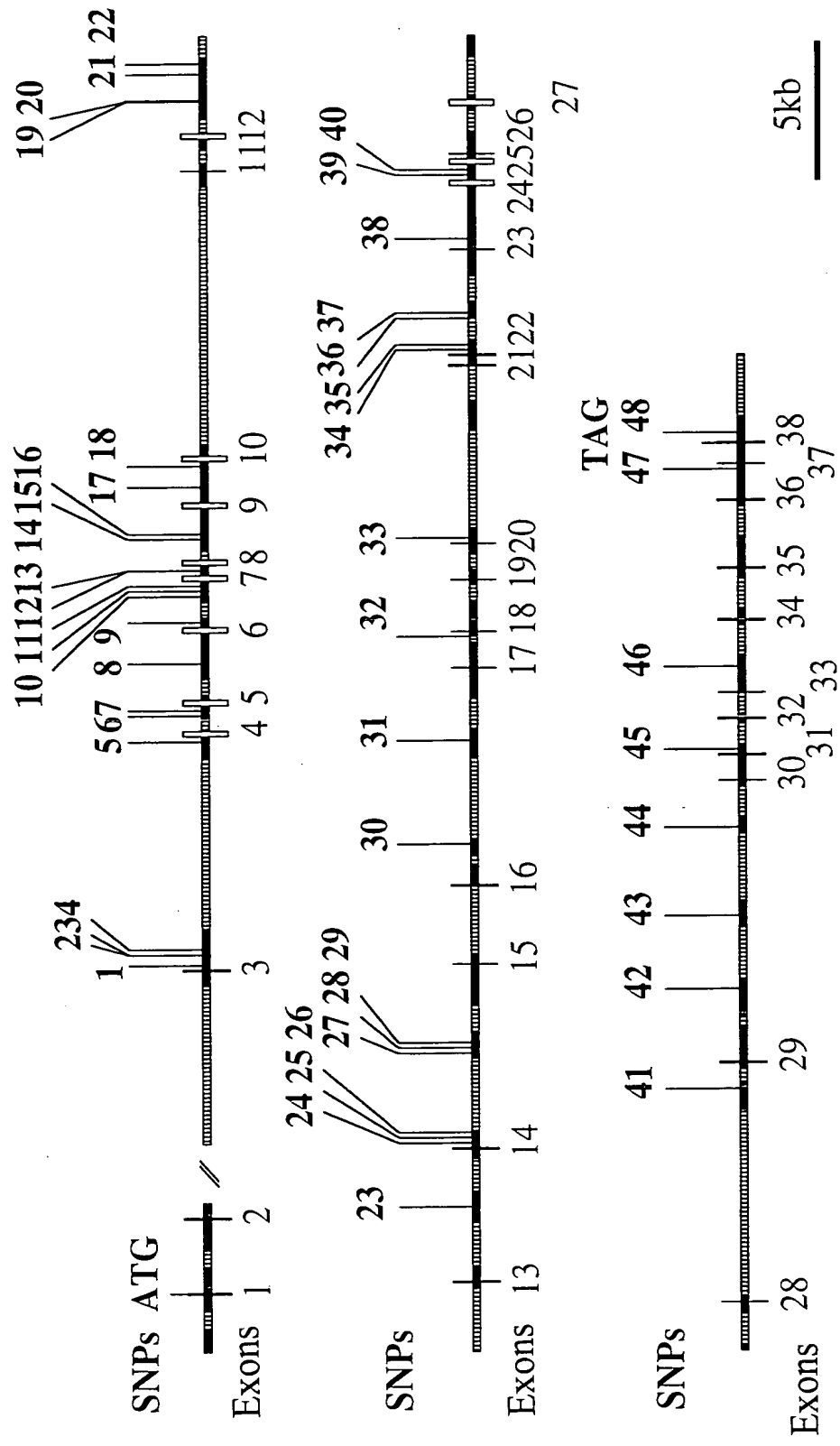


Fig. 28

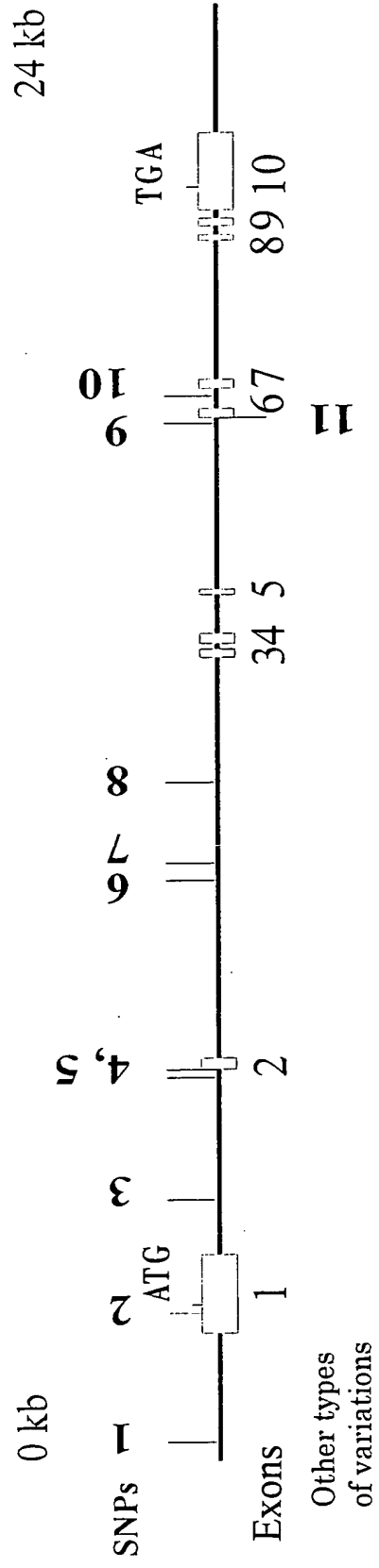


Fig. 29

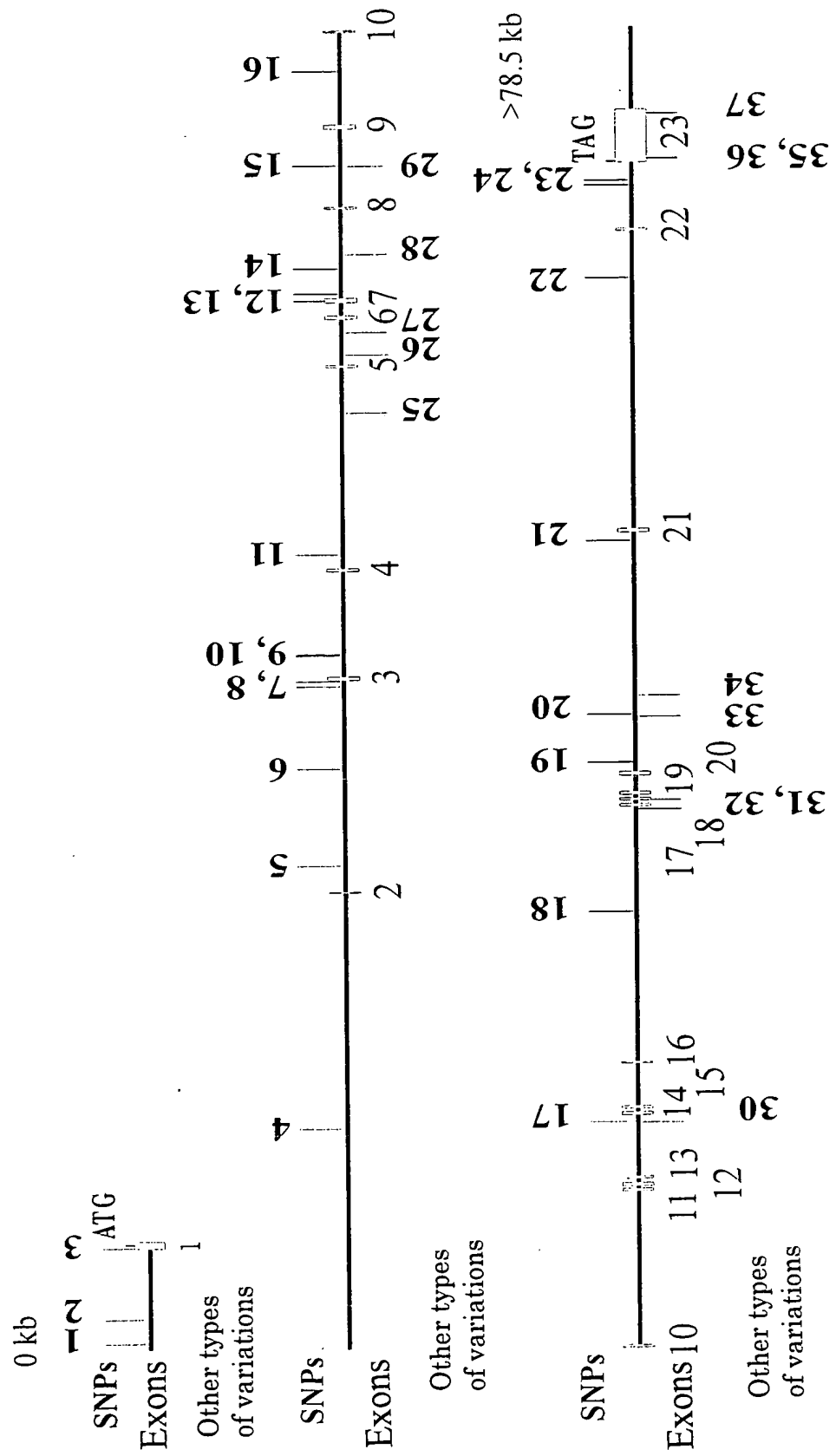


Fig. 30

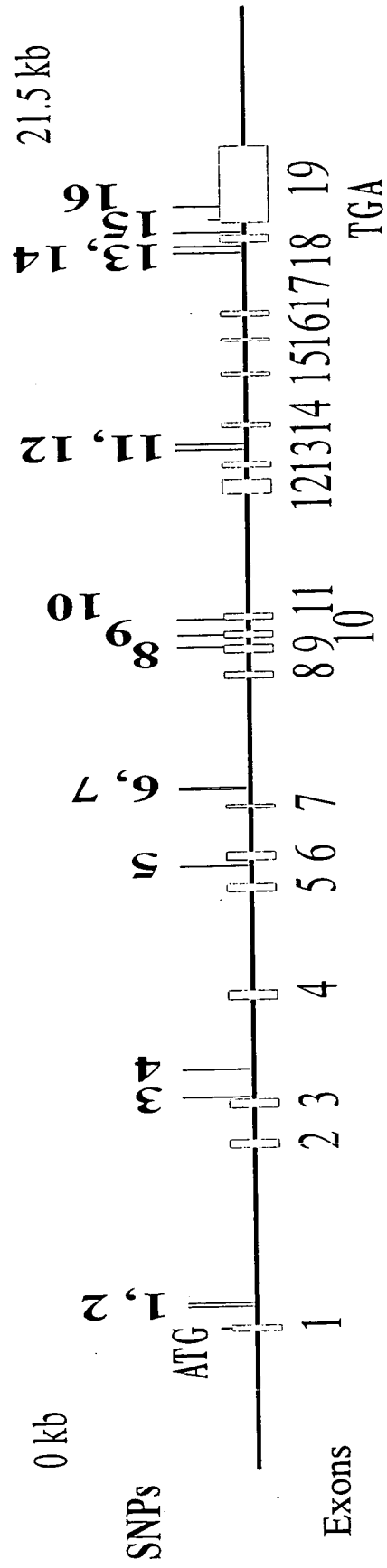


Fig. 31

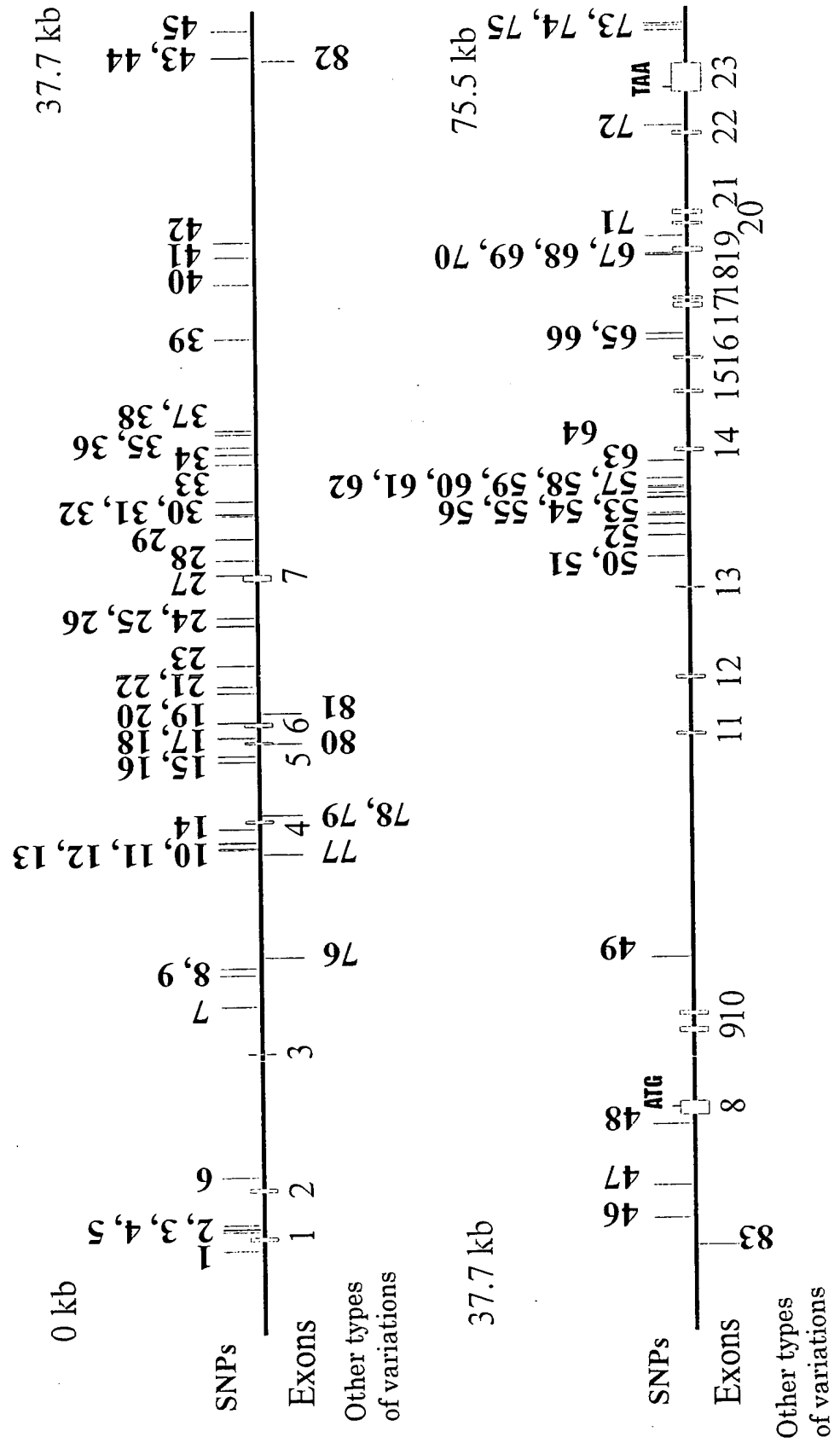


Fig. 32

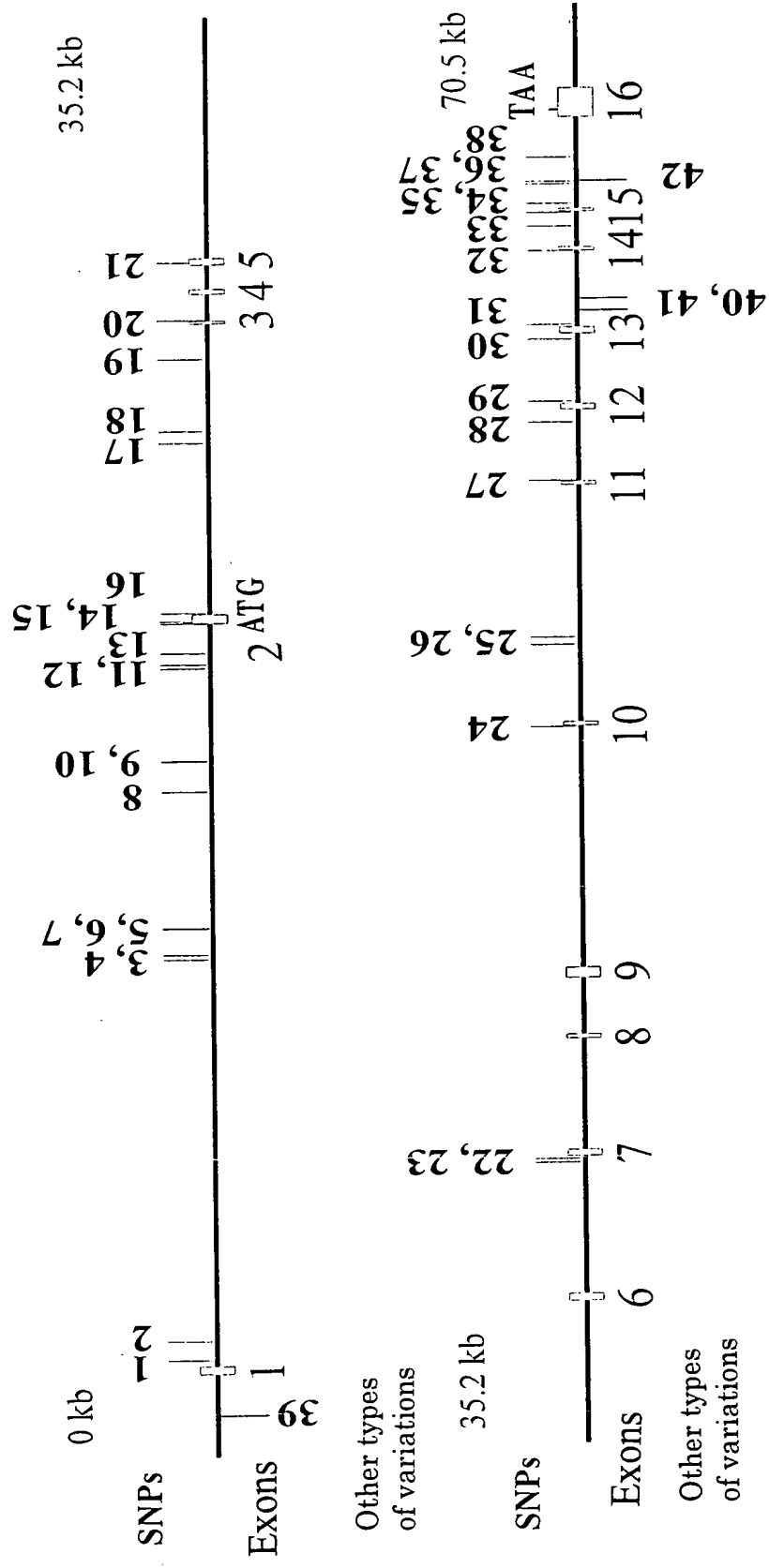


Fig. 33

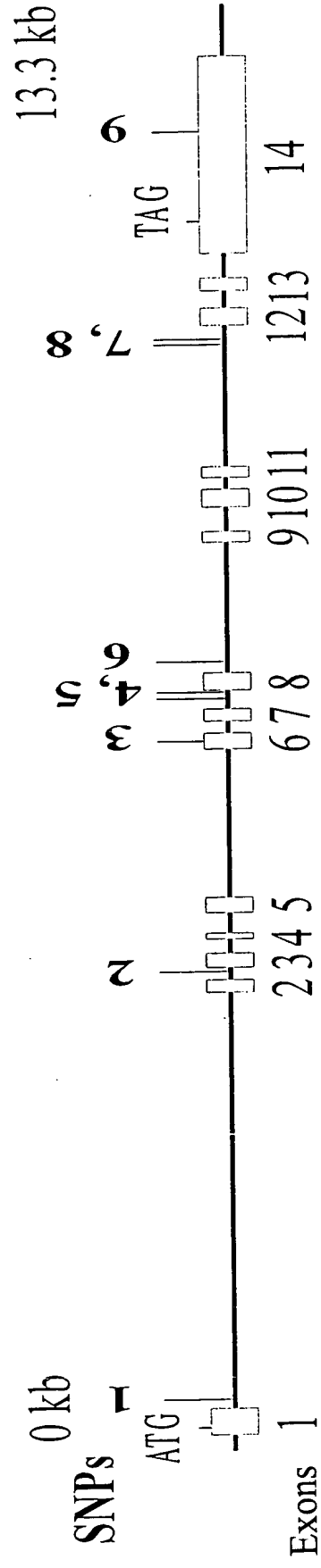


Fig. 34

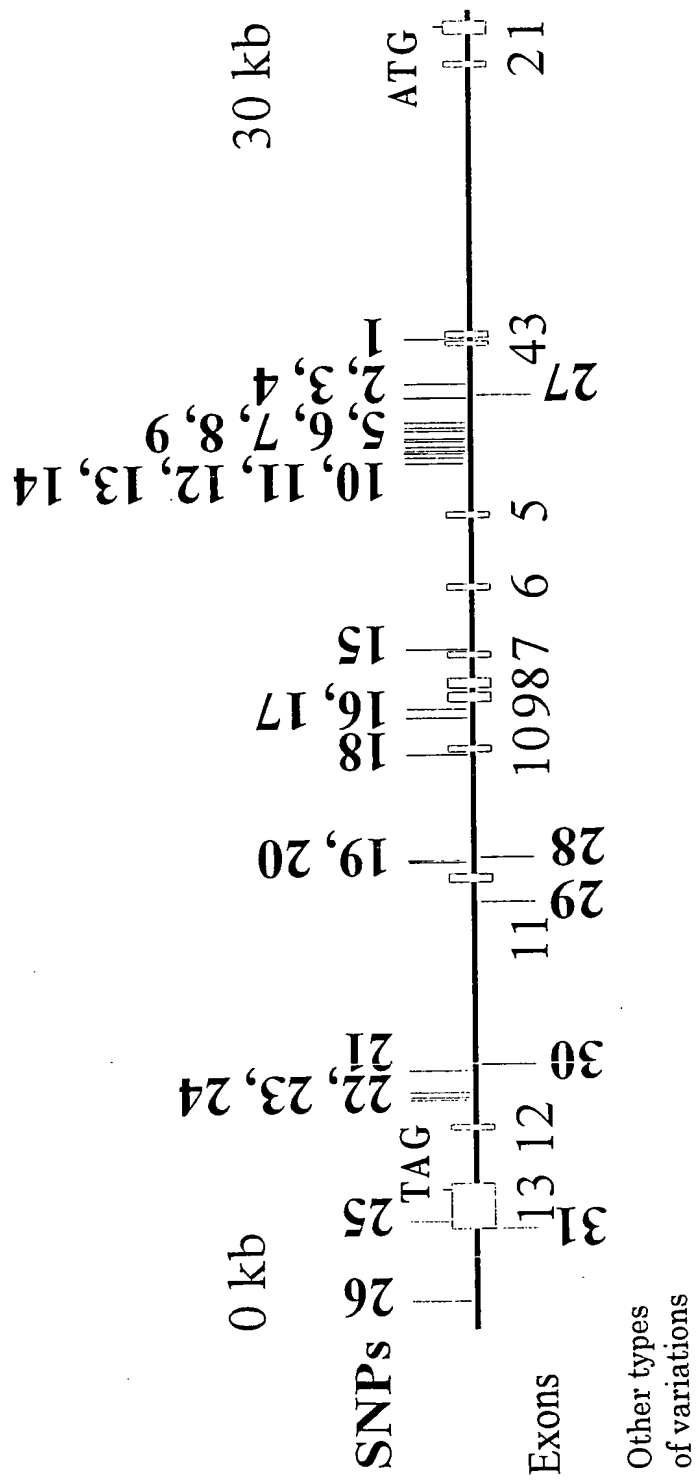


Fig. 35

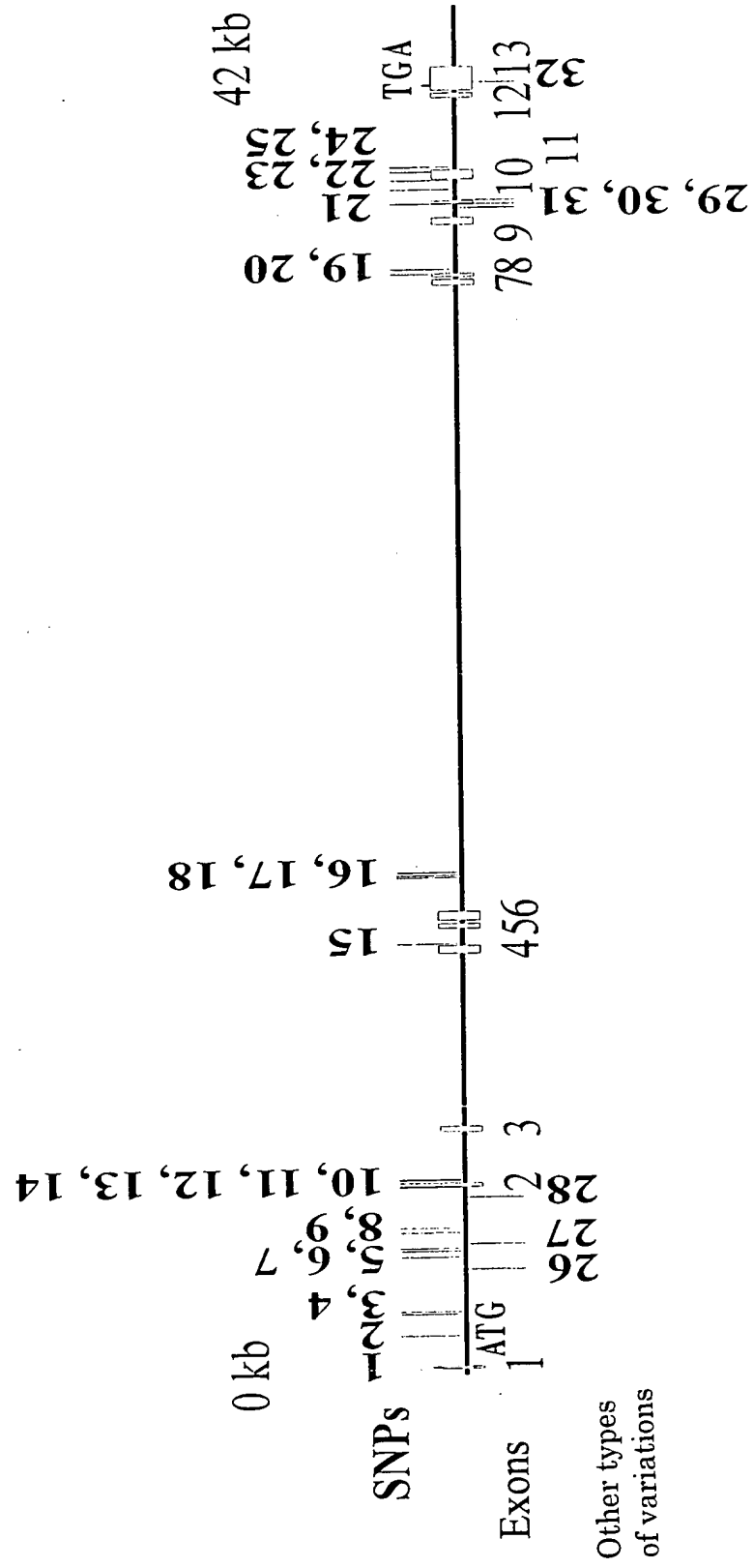


Fig. 36

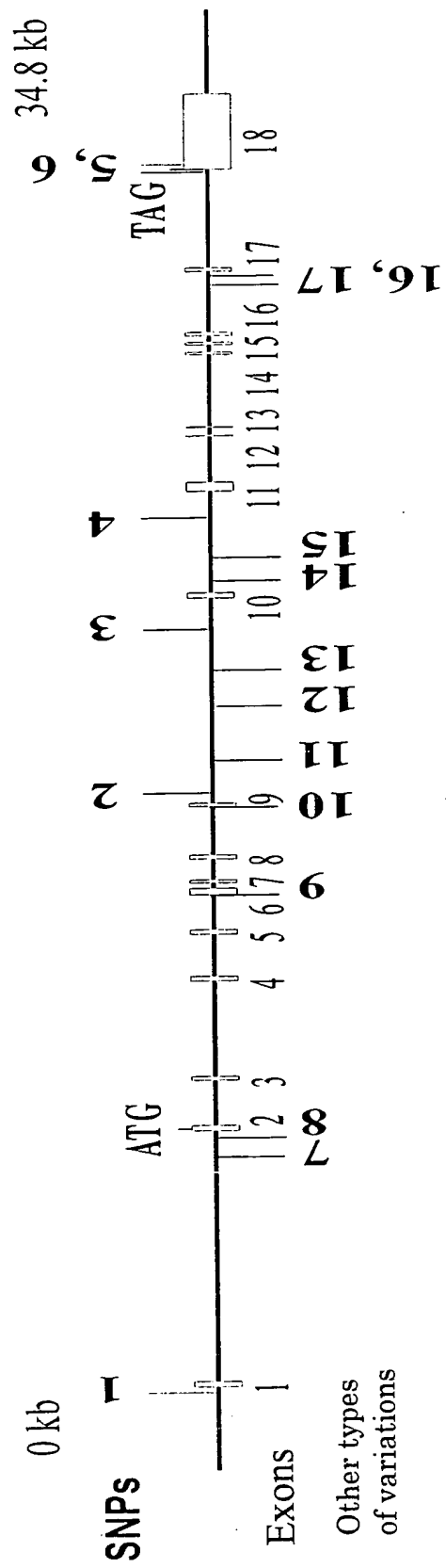


Fig. 37

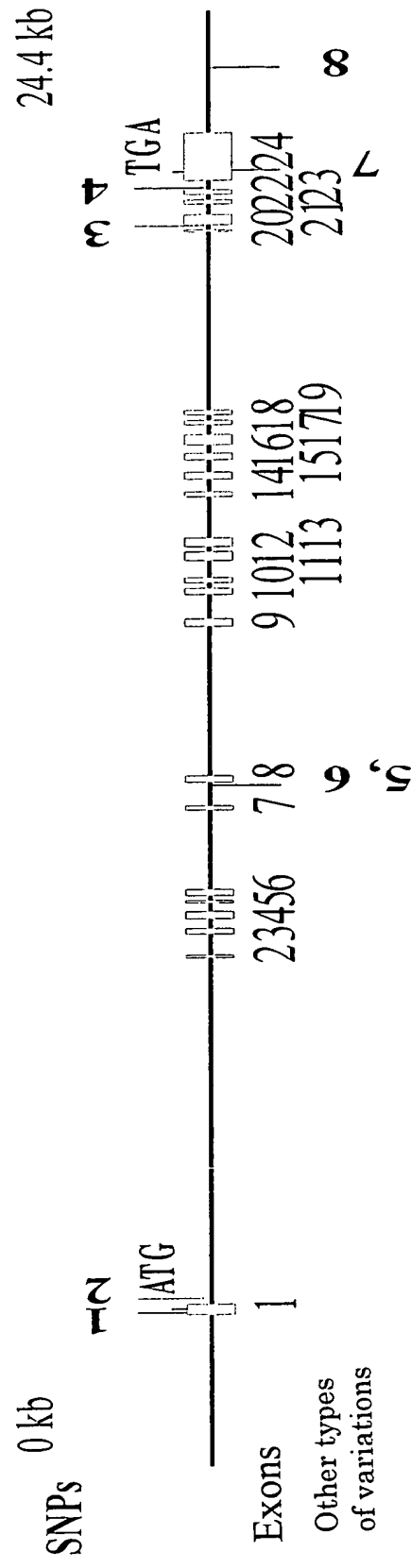


Fig. 38

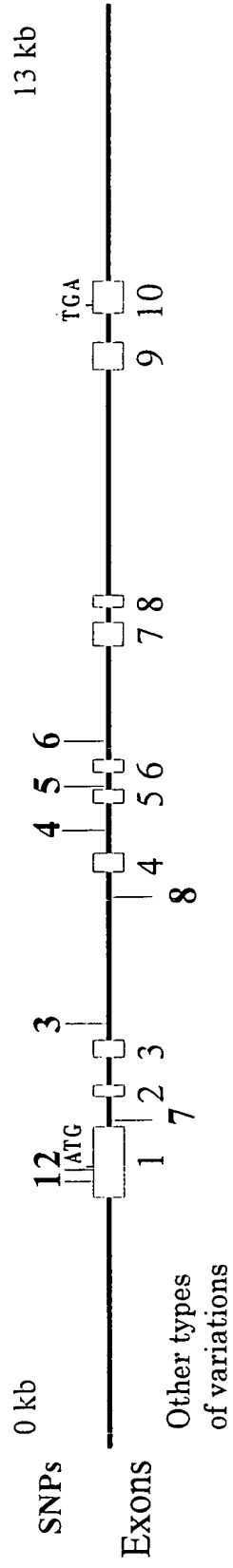


Fig. 39

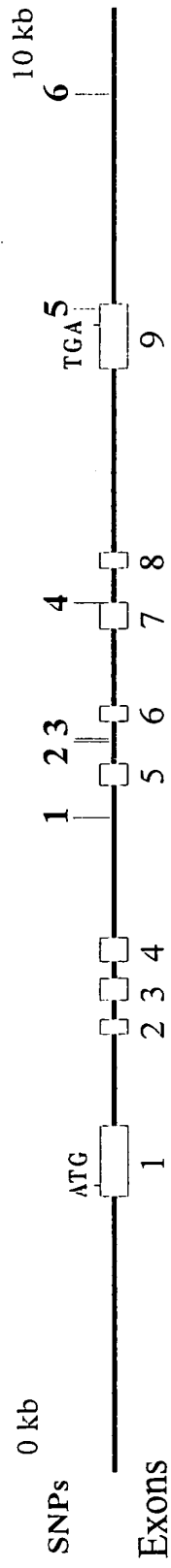


Fig. 40

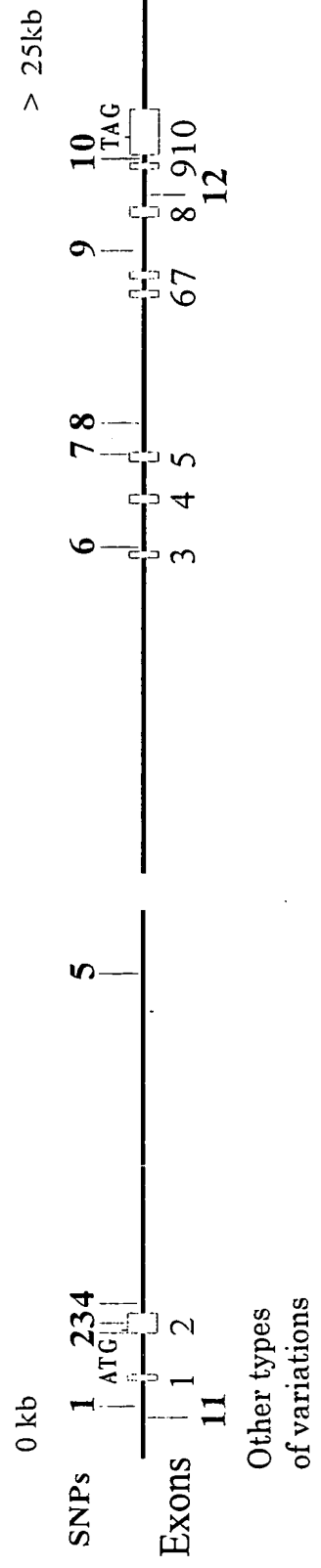


Fig. 41

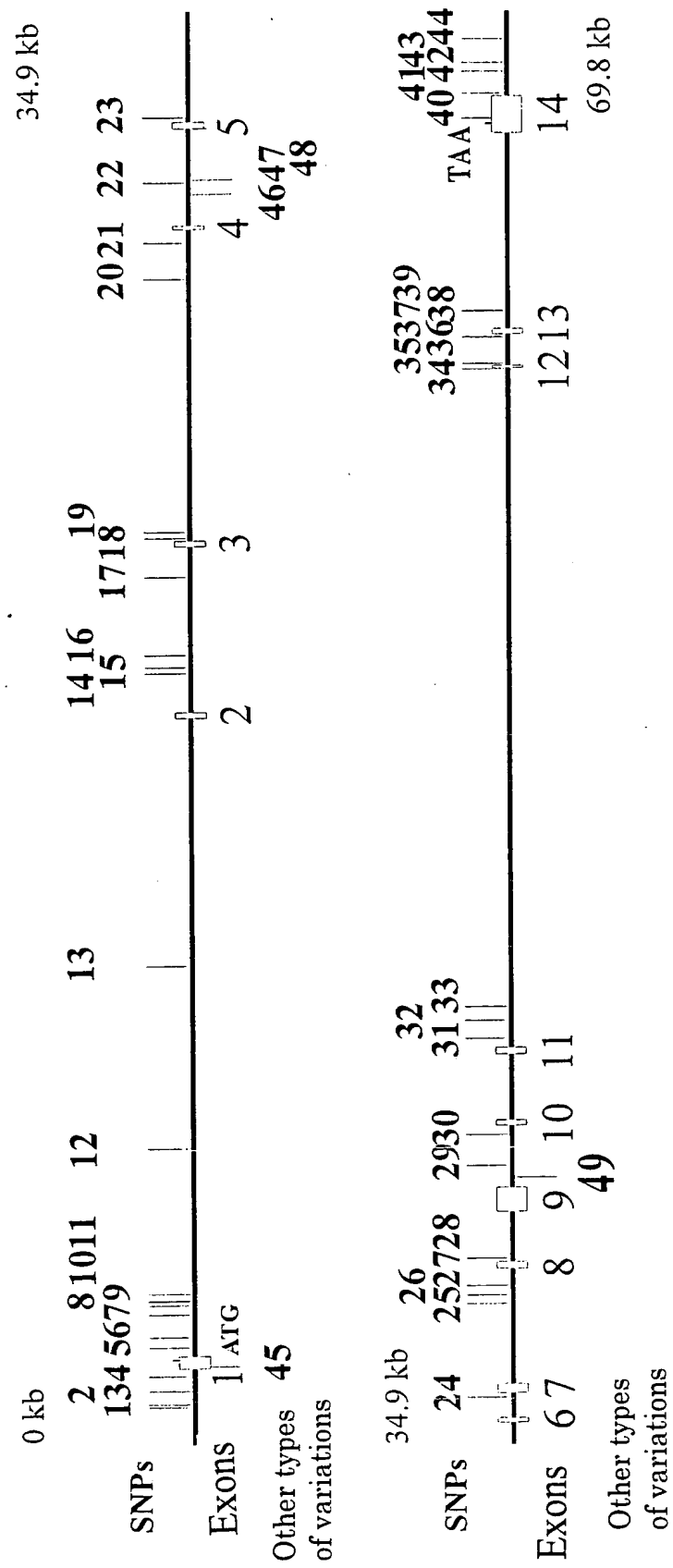


Fig. 42

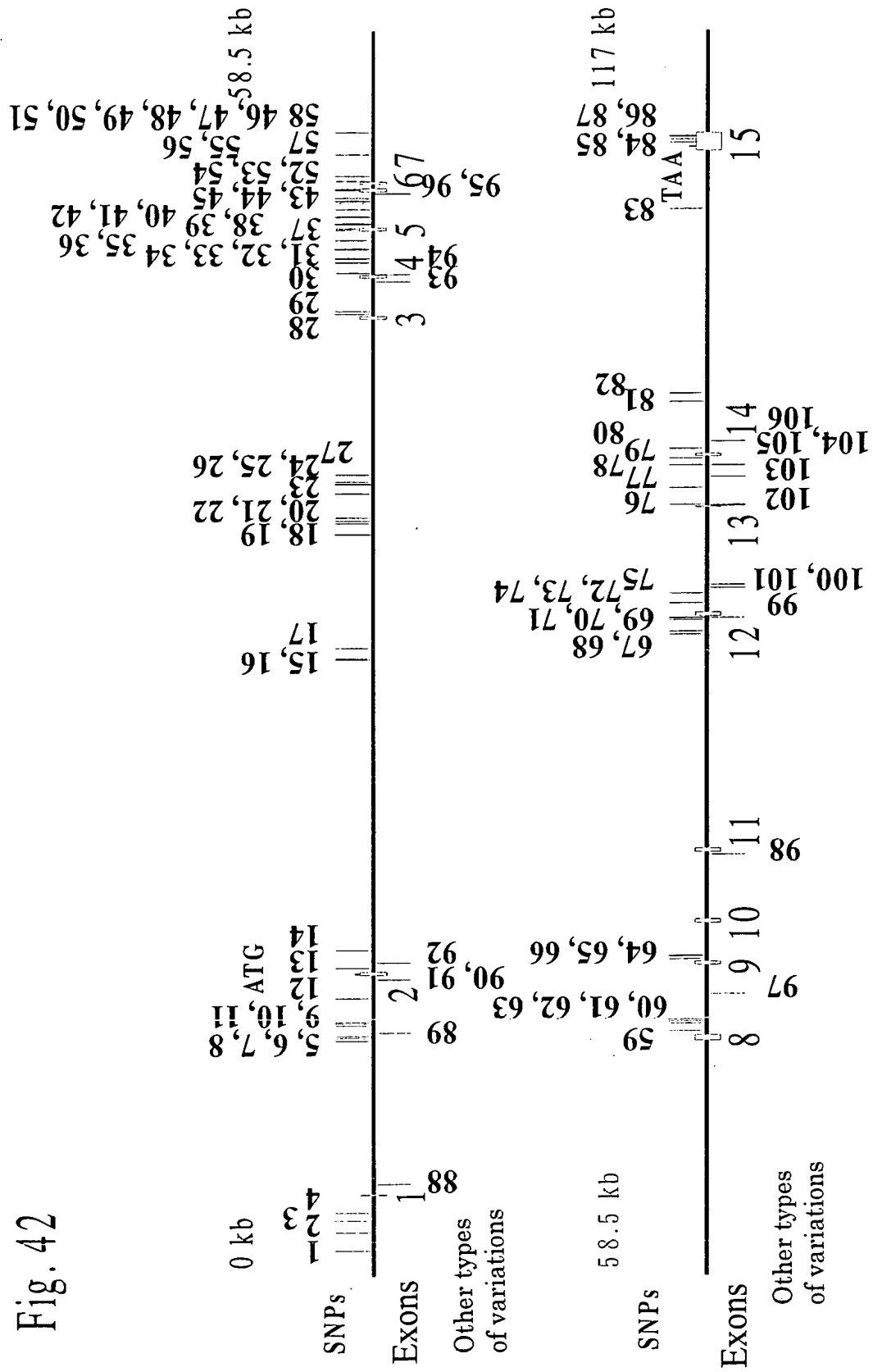


Fig. 43

0 kb

ATG

SNPs

Exons

Other types of variations

52.5 kb

TAA

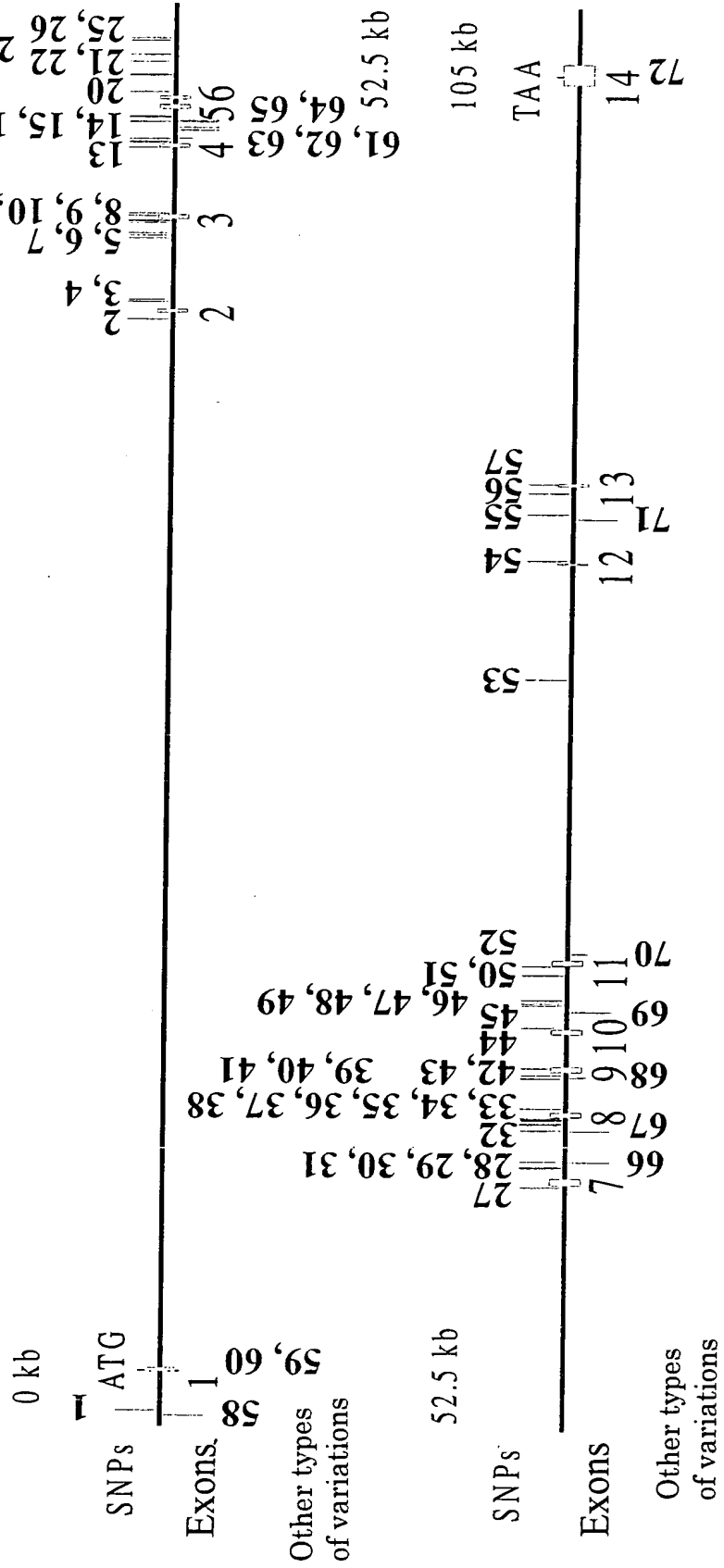


Fig.44

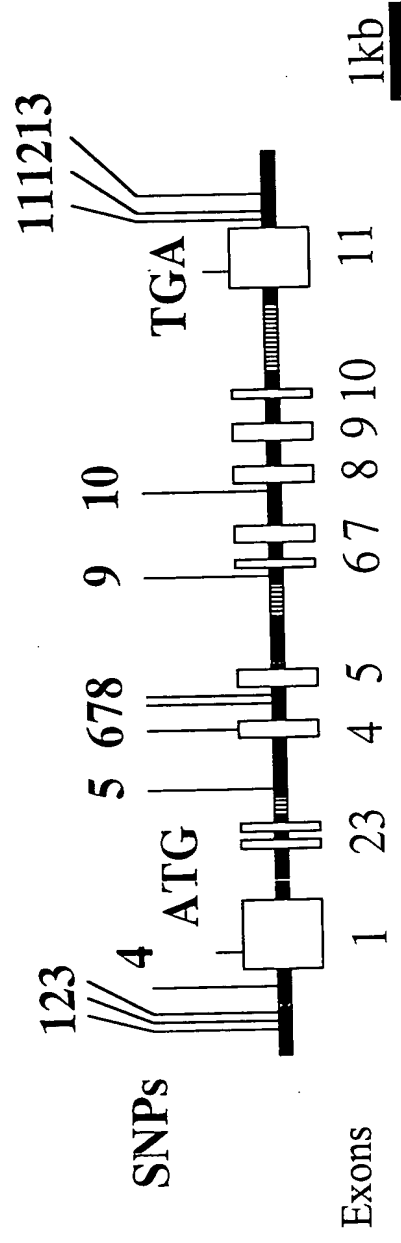


Fig.45

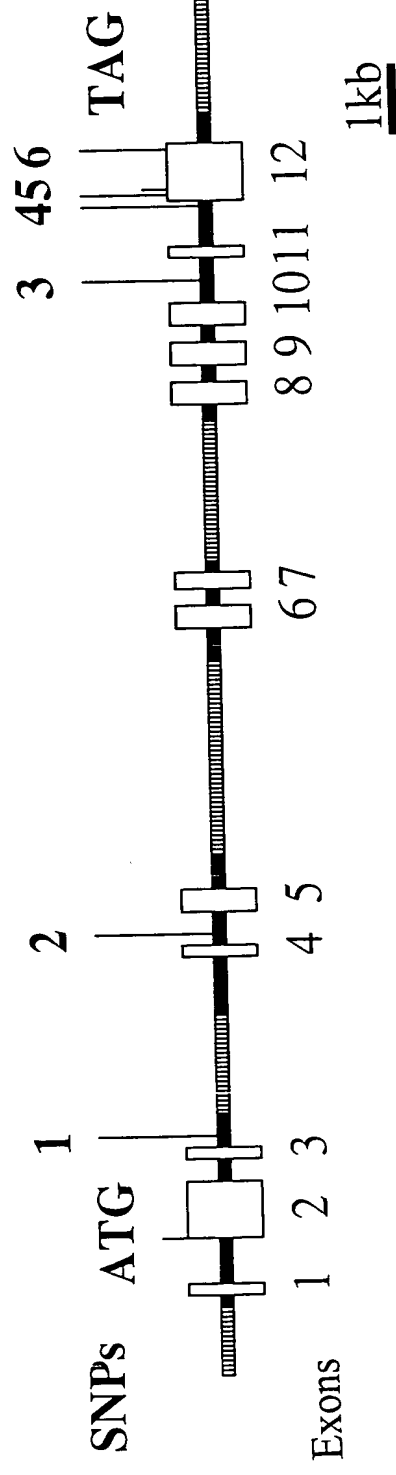


Fig.46

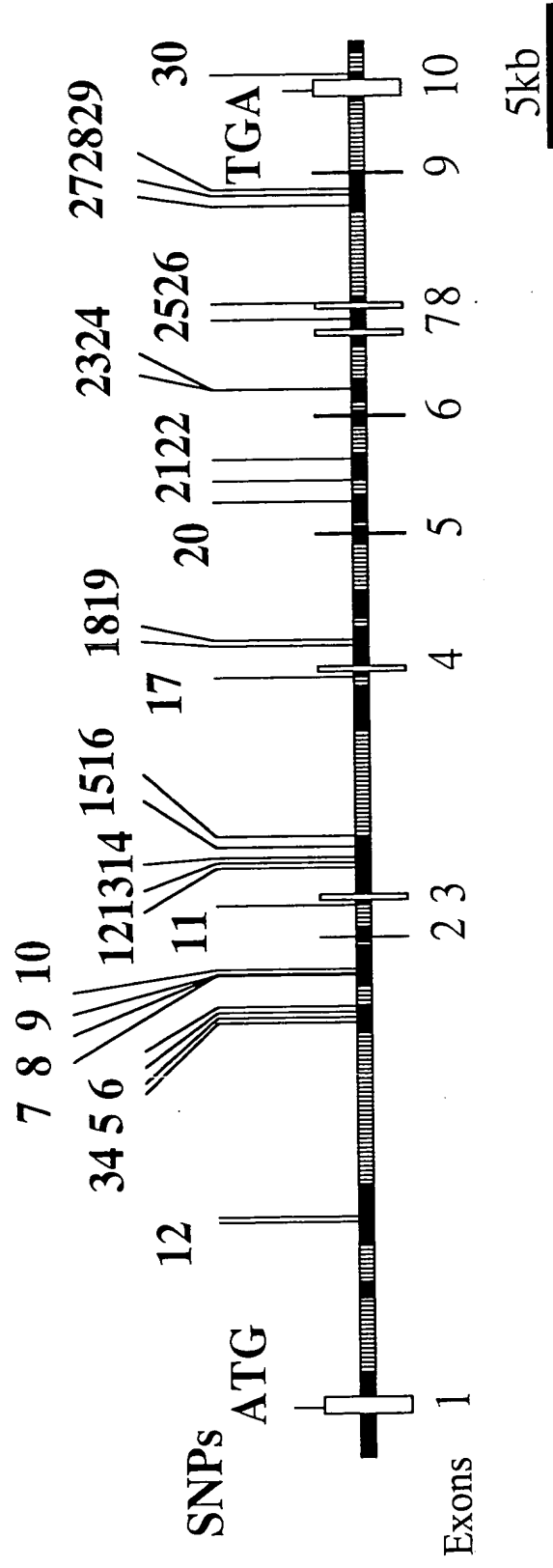


Fig.47

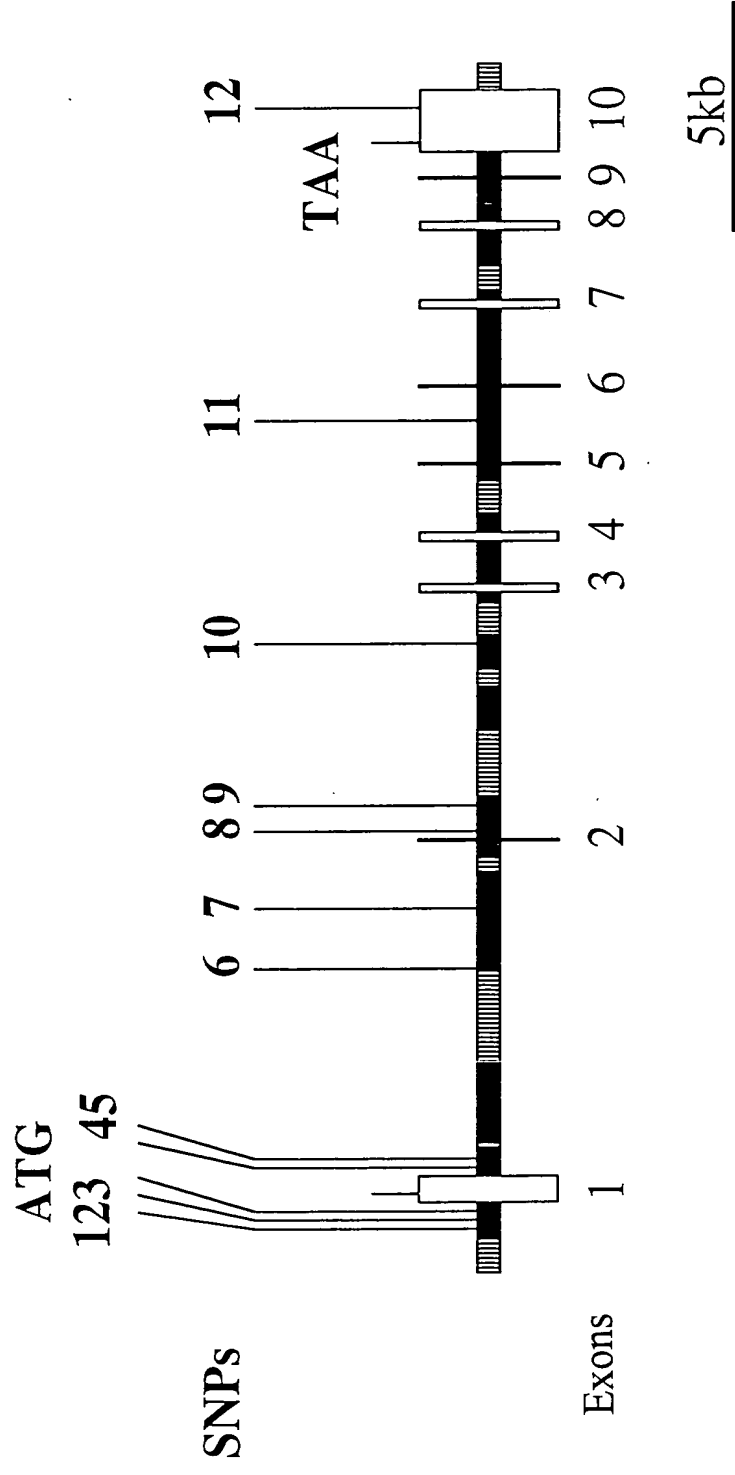


Fig.48

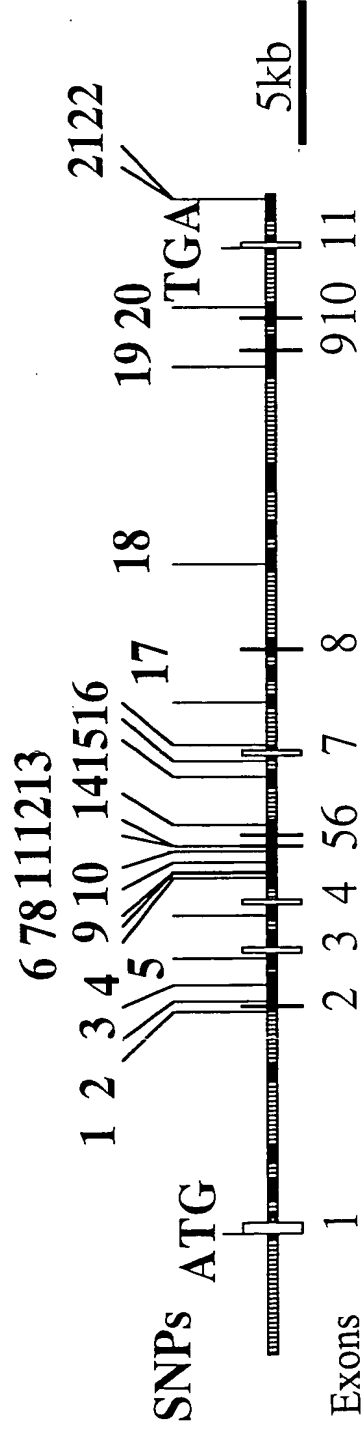


Fig.49

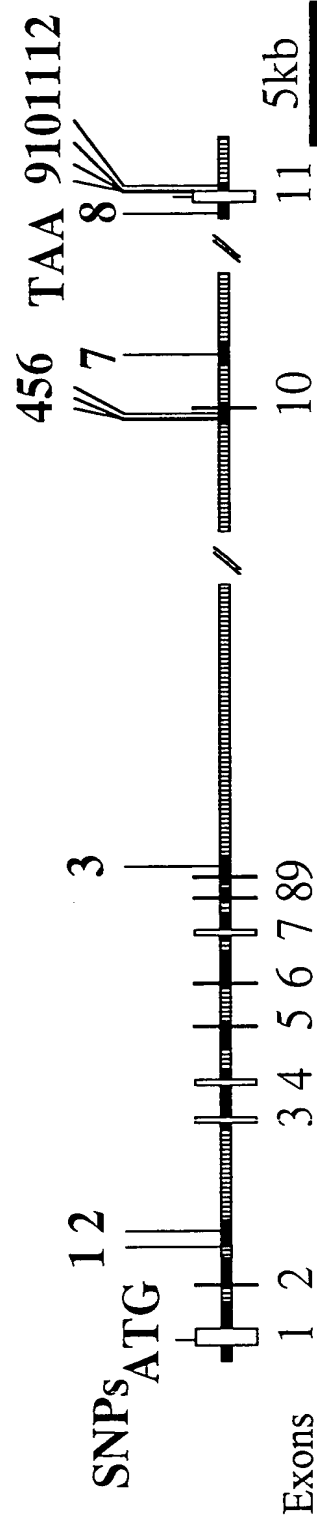


Fig.50

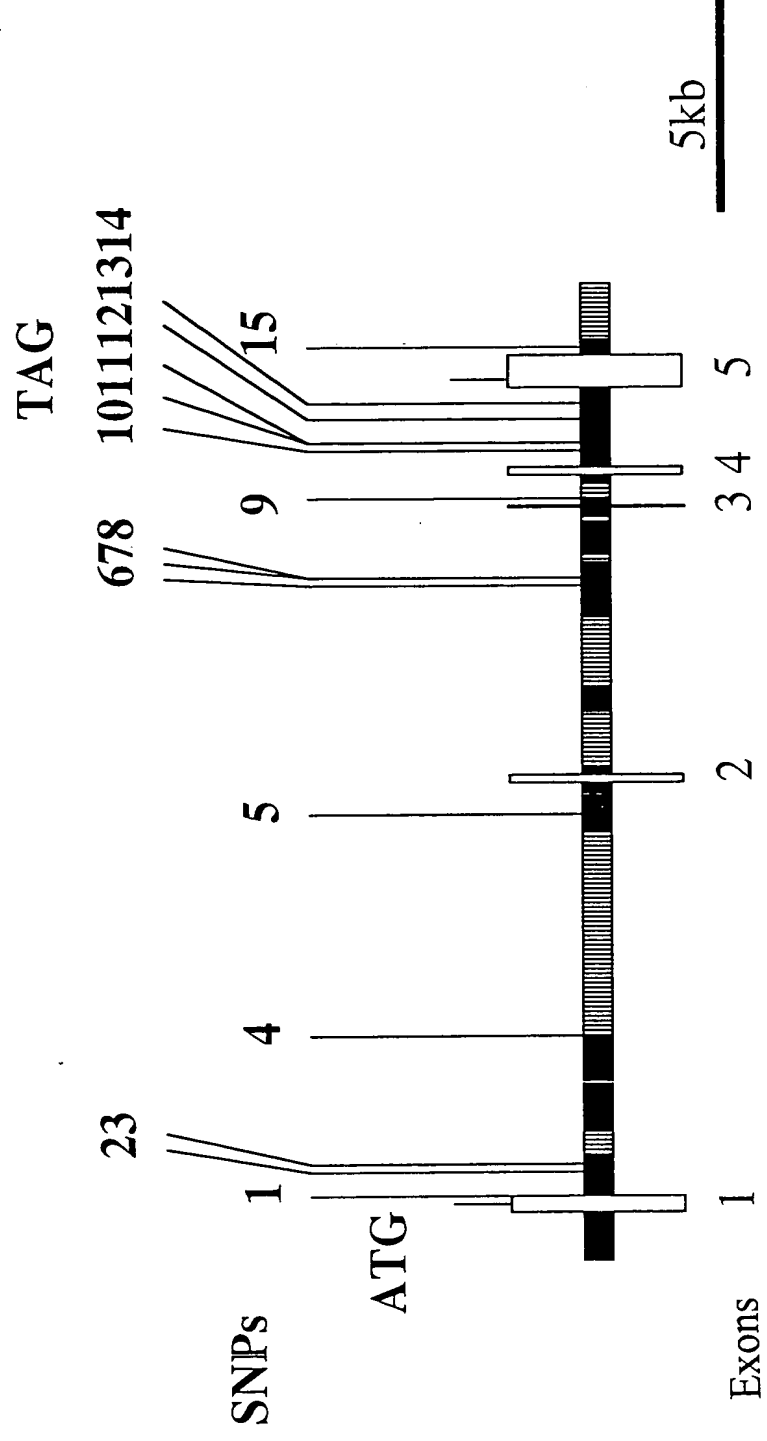


Fig.51

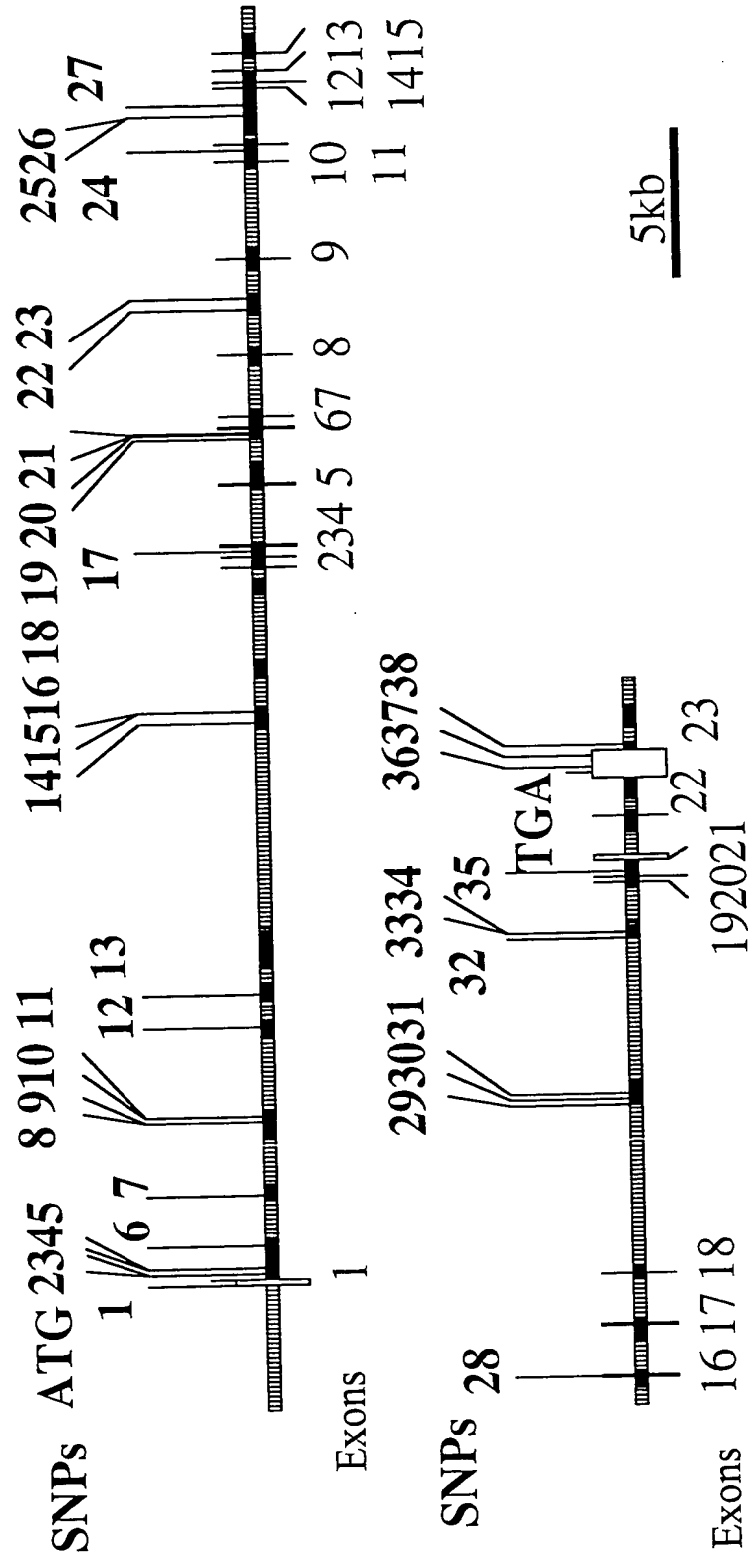


Fig.52

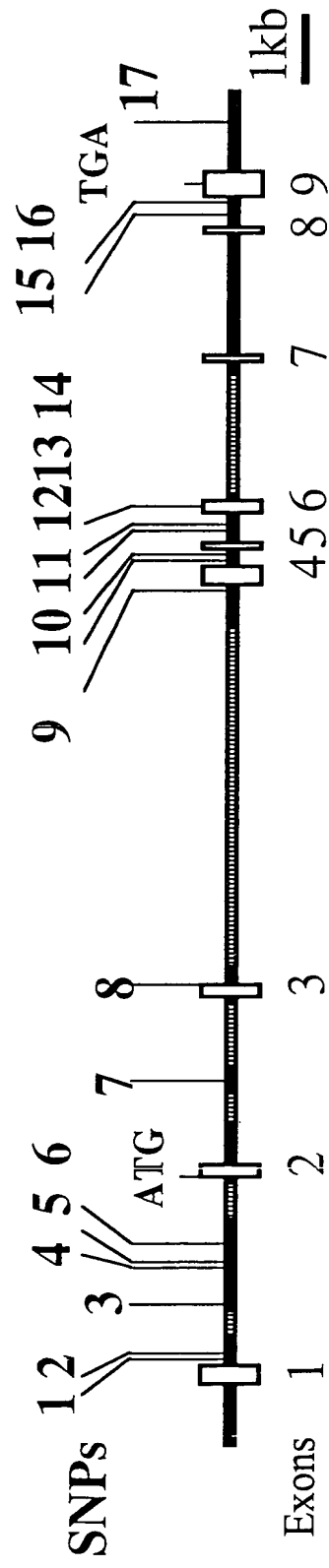


Fig.53

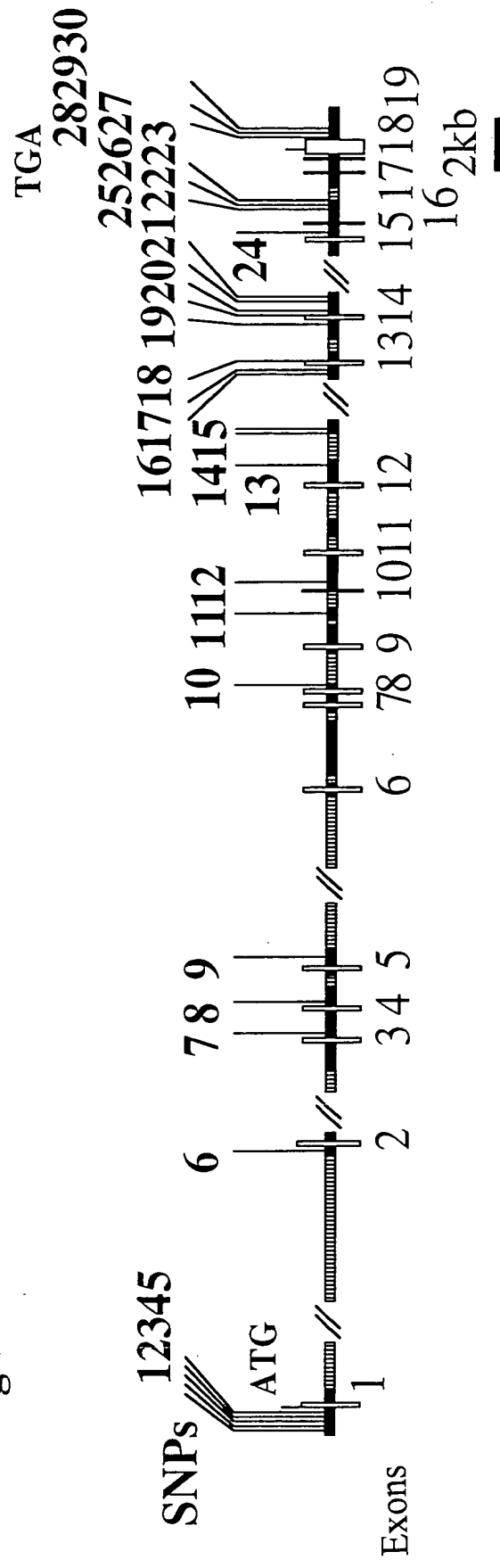


Fig.54

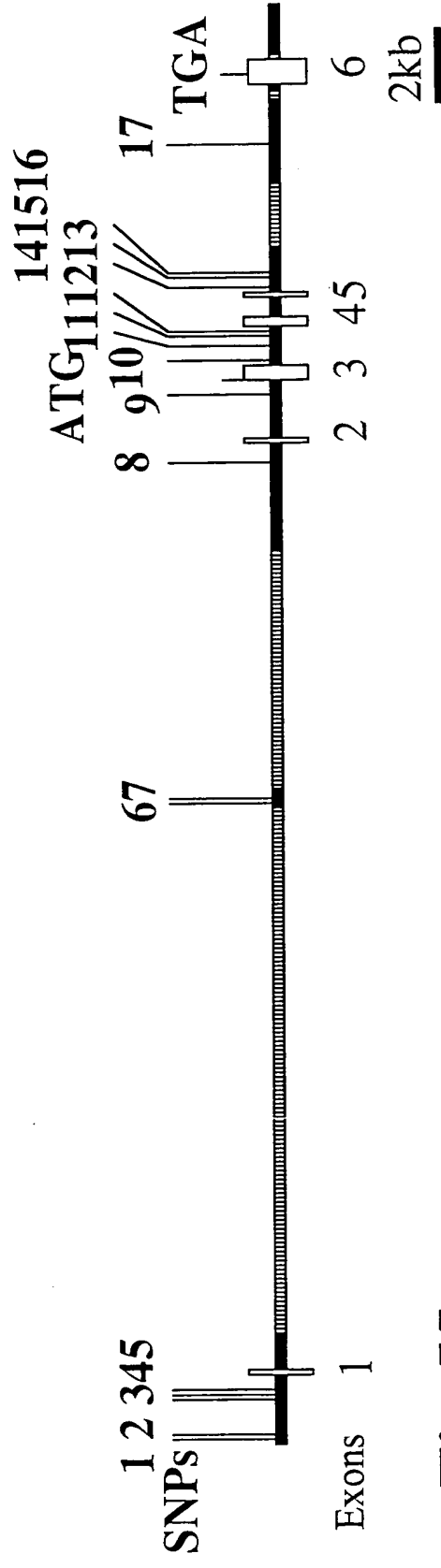


Fig.55

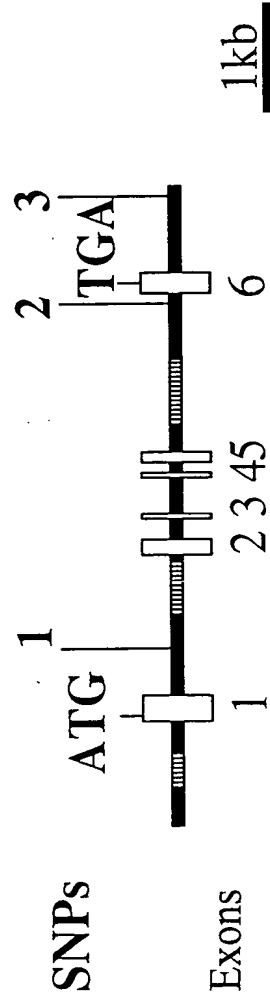


Fig.56

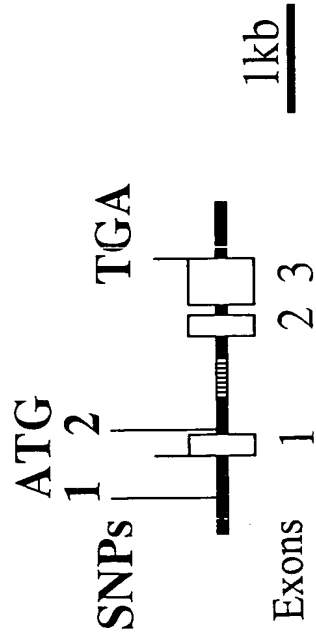


Fig.57

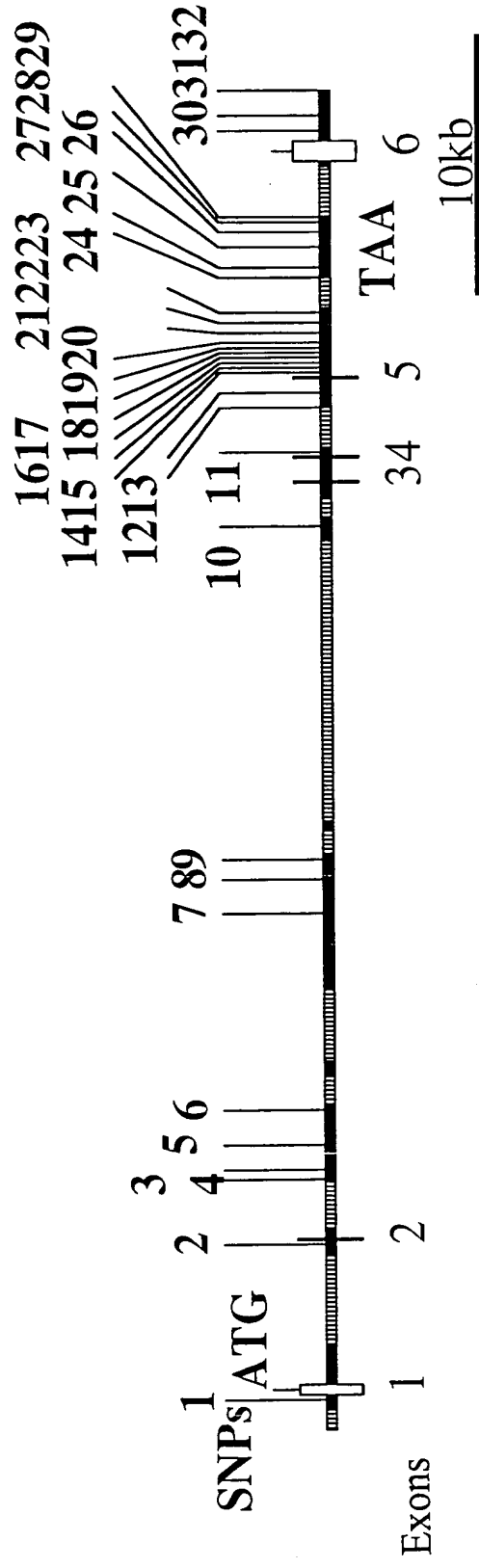


Fig.58

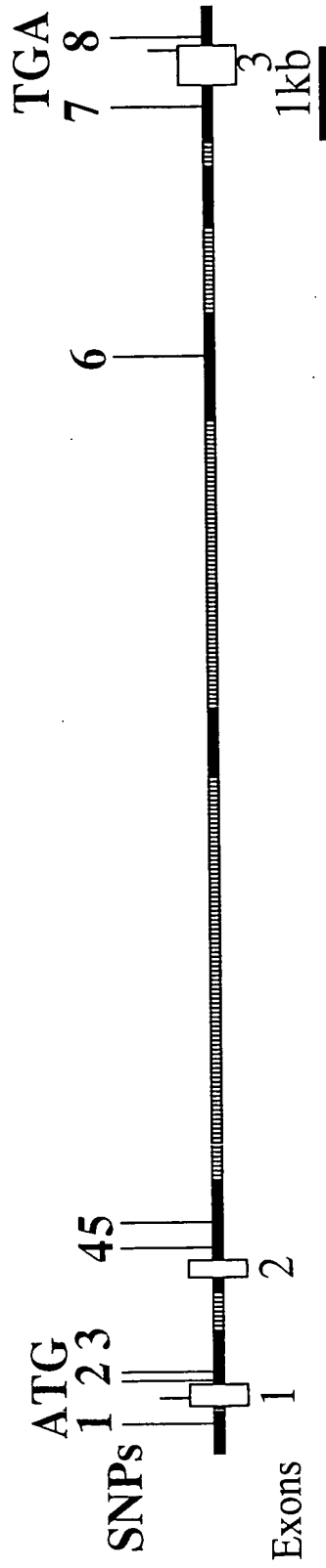


Fig.59

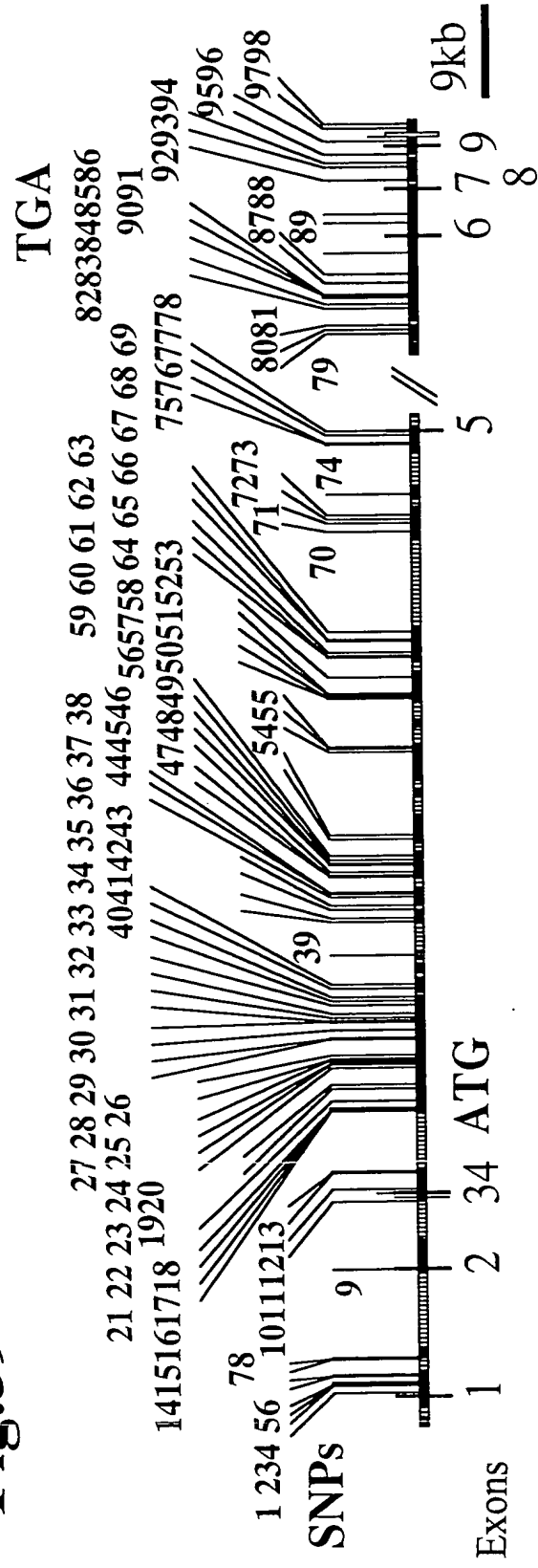


Fig.60

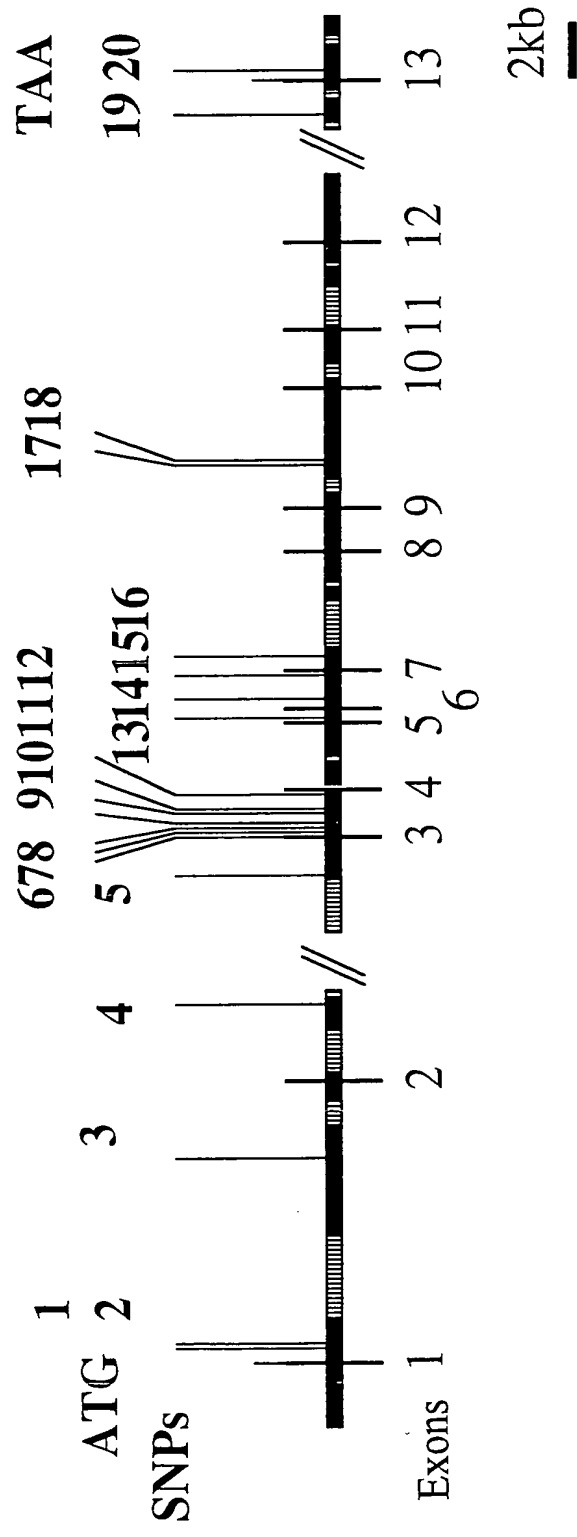


Fig. 62

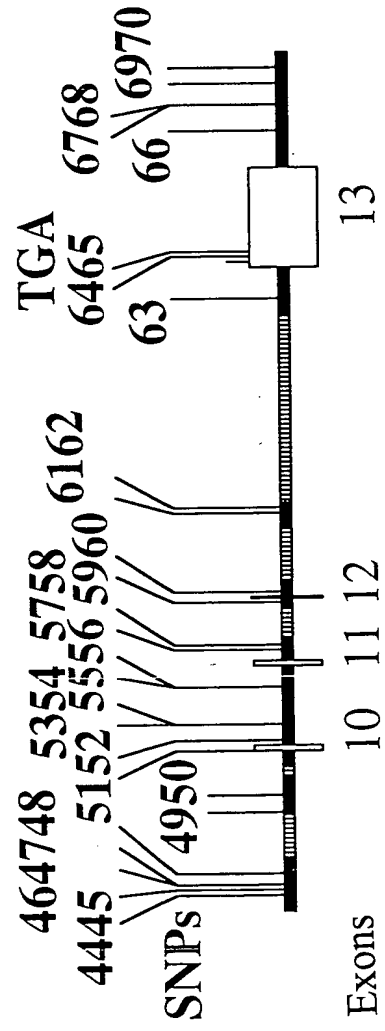
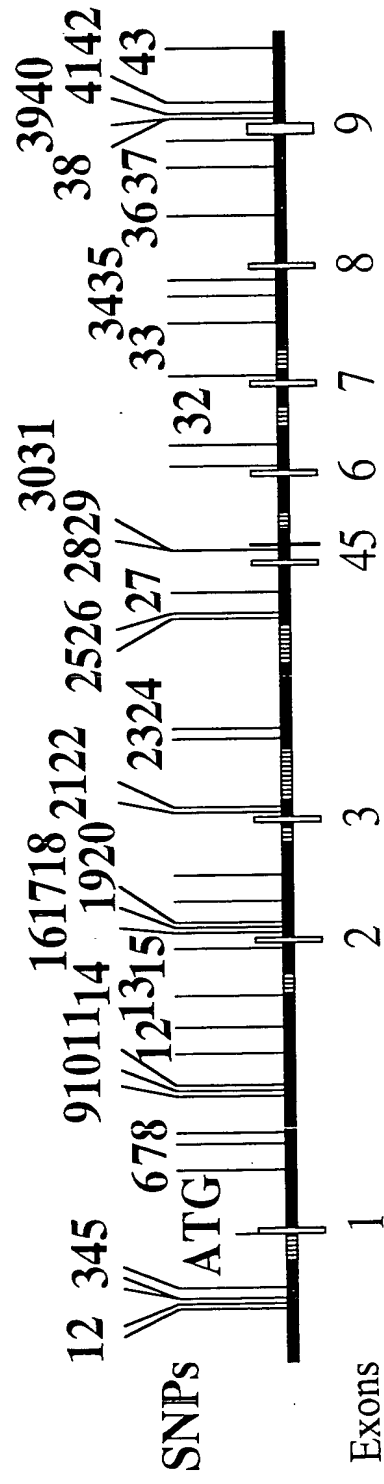


Fig. 63

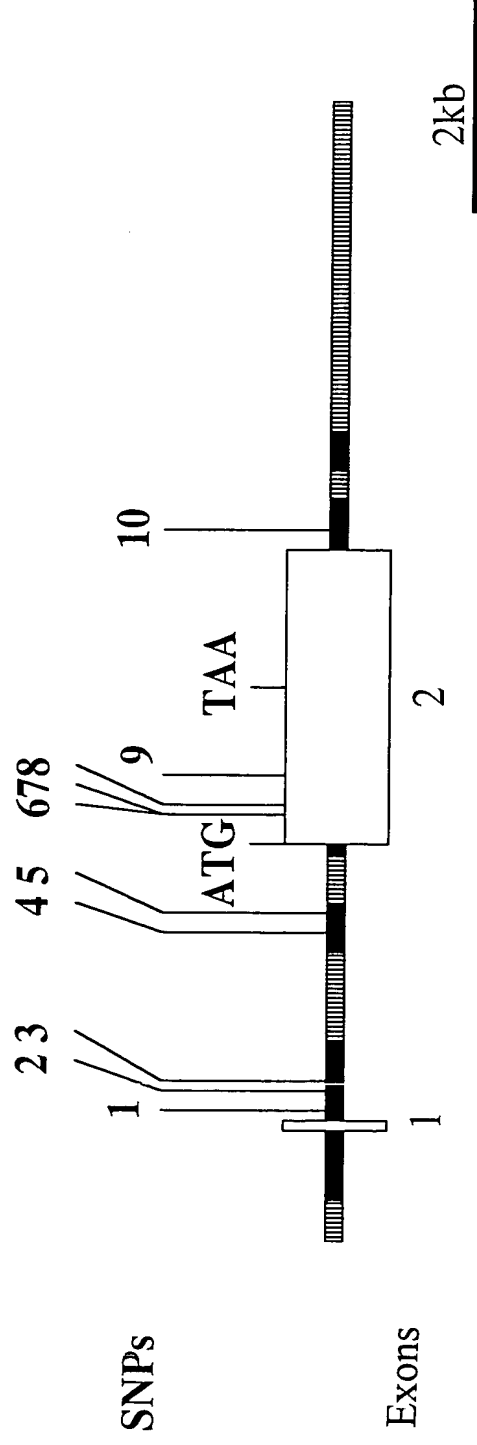
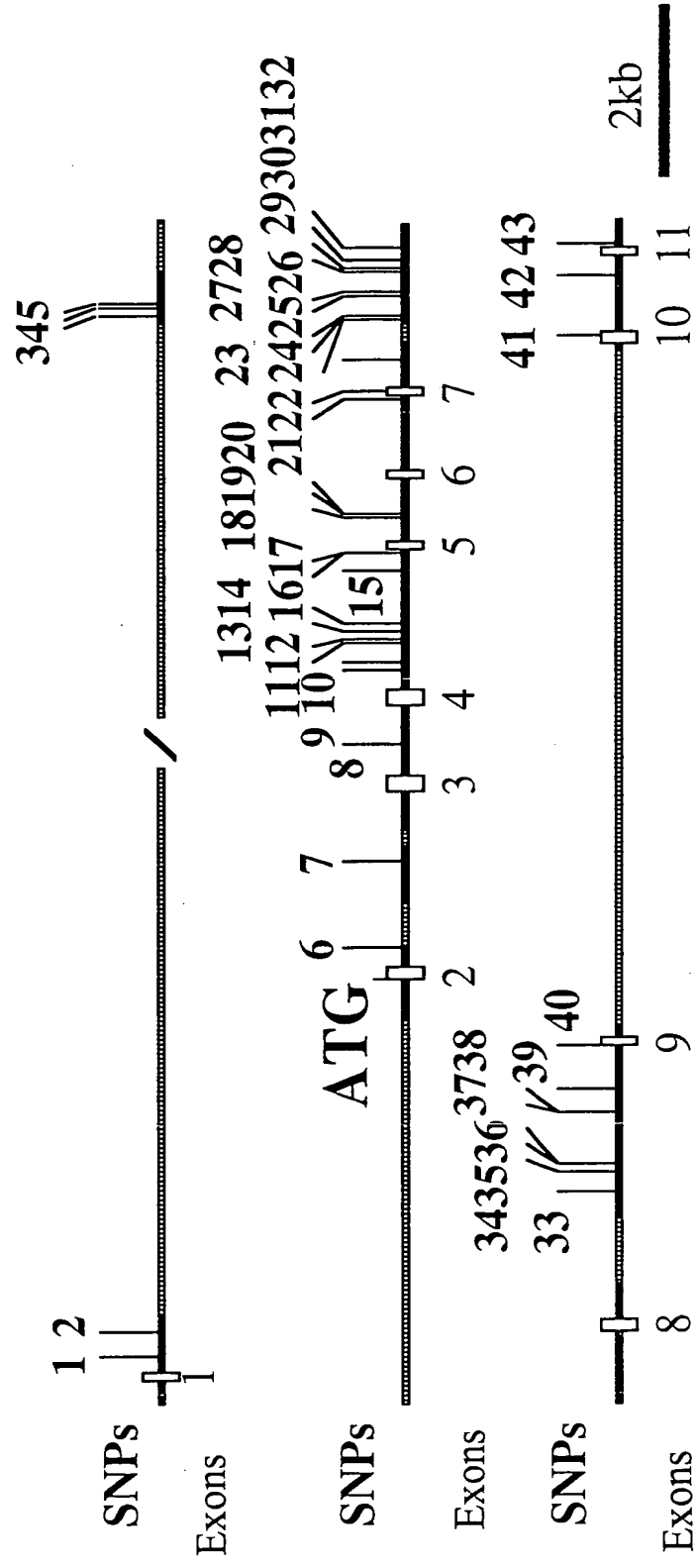


Fig. 64A



SNPs 99100101 104105106 110111 114115116
9798 102103 107108109 112113 118119120121

Exons 21 22 23

TGA

Fig.65

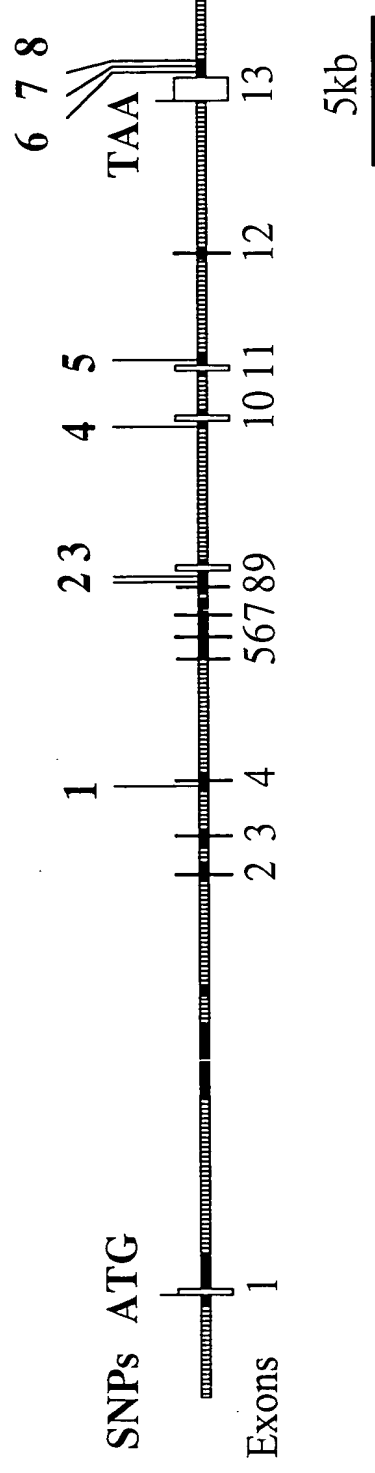


Fig.66

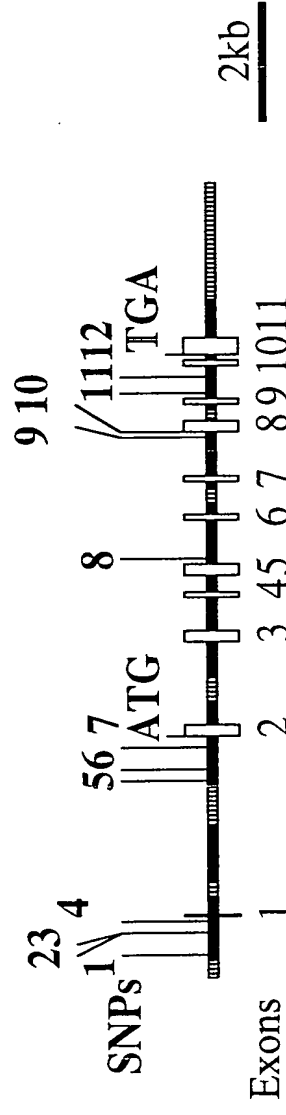


Fig.67

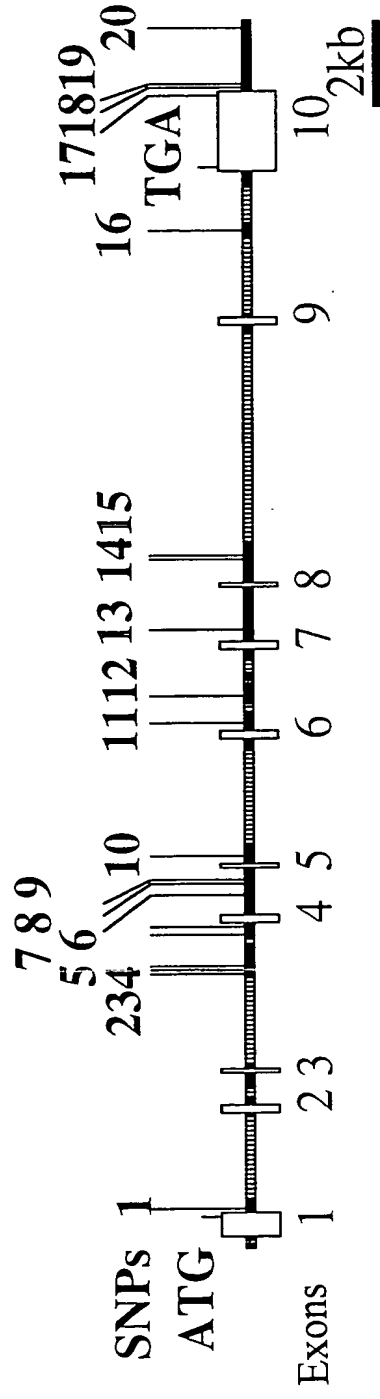


Fig.68

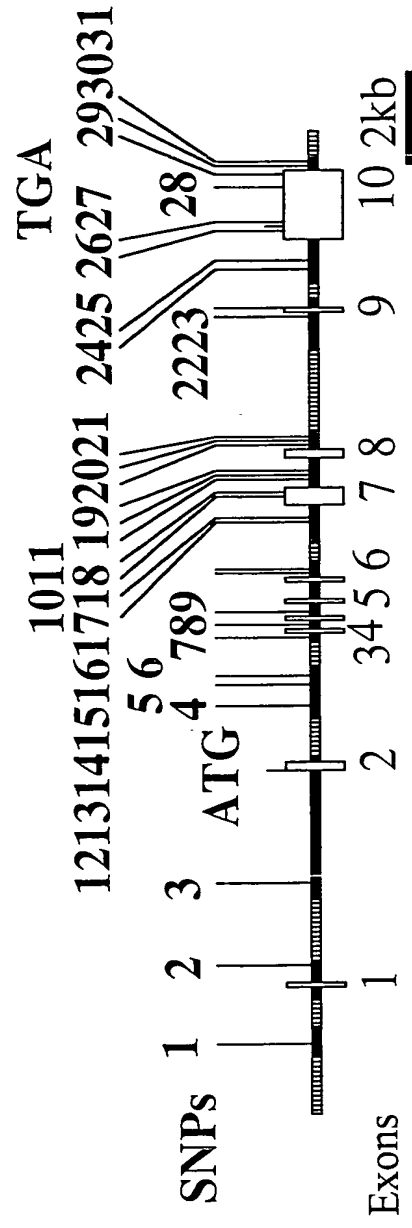


Fig.69

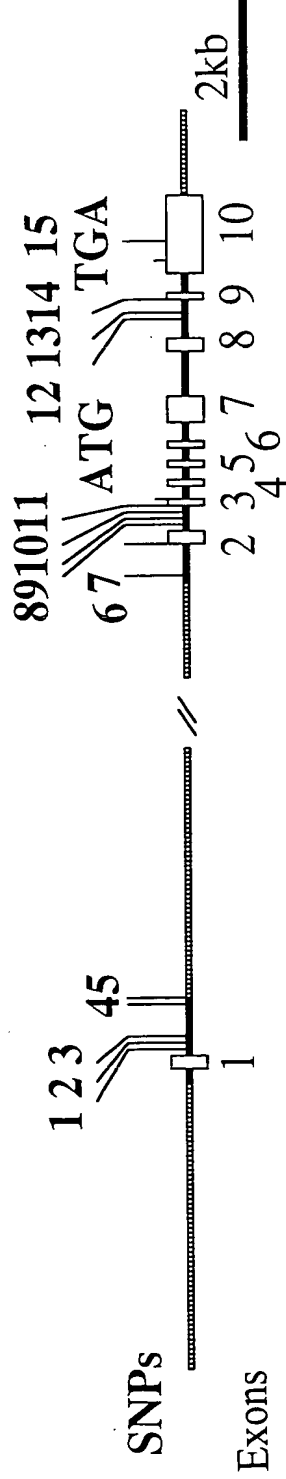


Fig.70

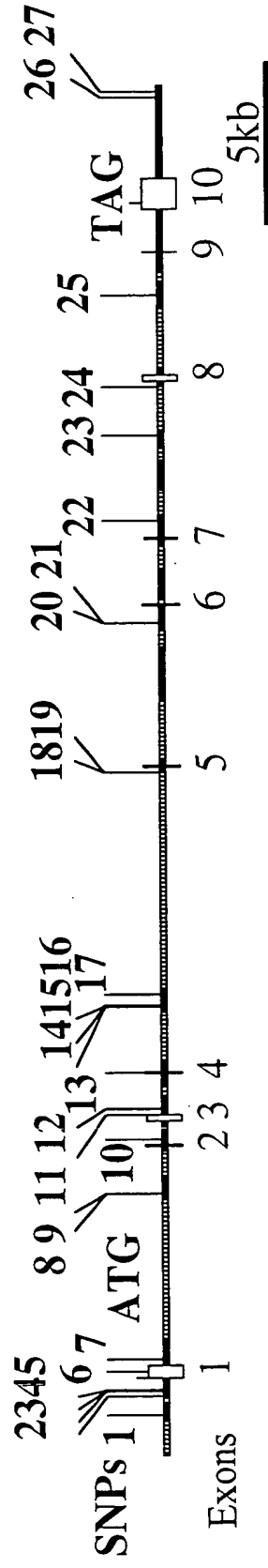


Fig.71

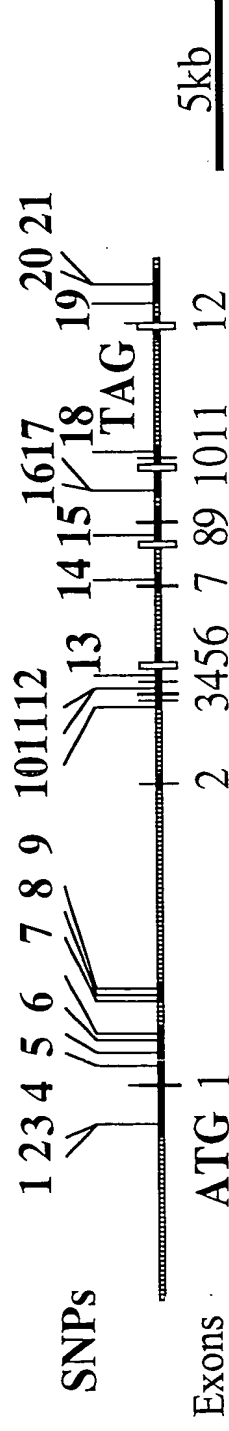


Fig.72

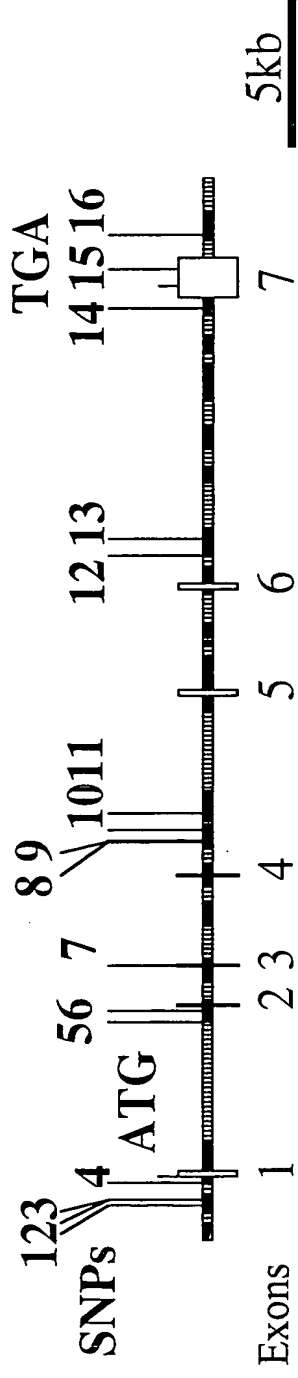


Fig.73

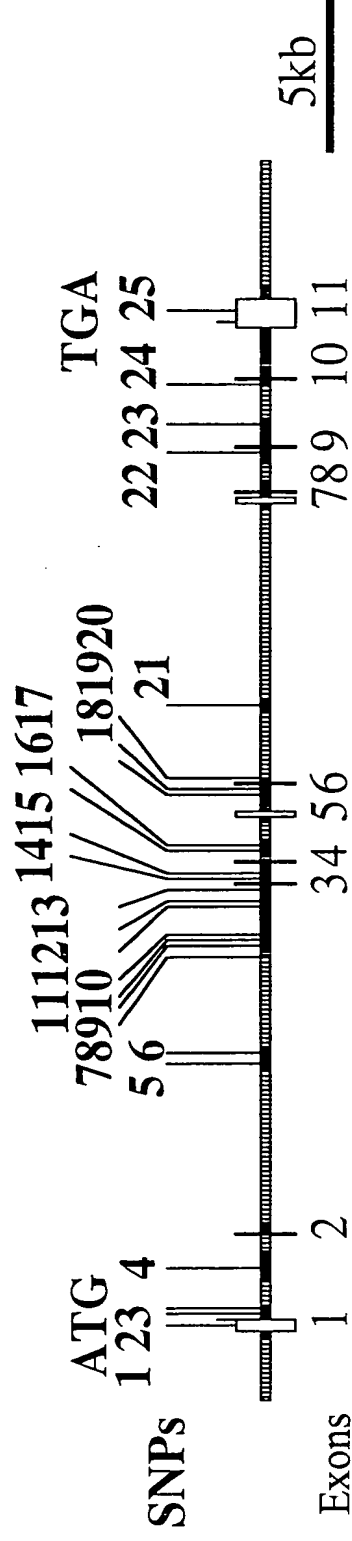


Fig.74

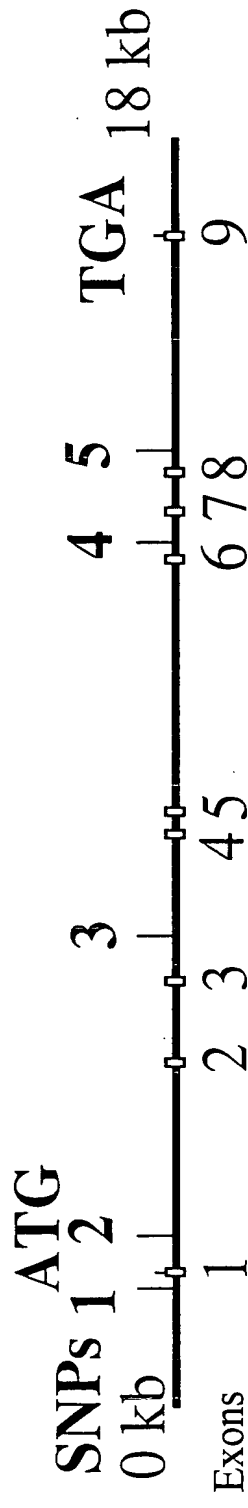


Fig.75

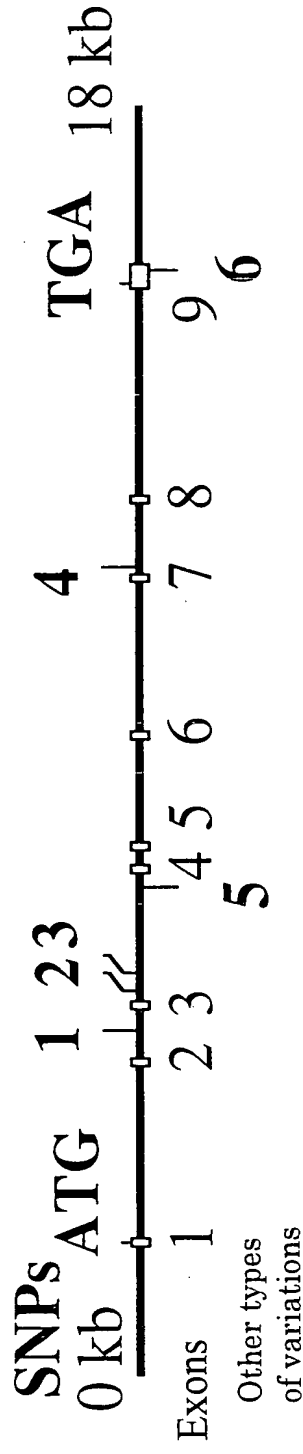


Fig.76

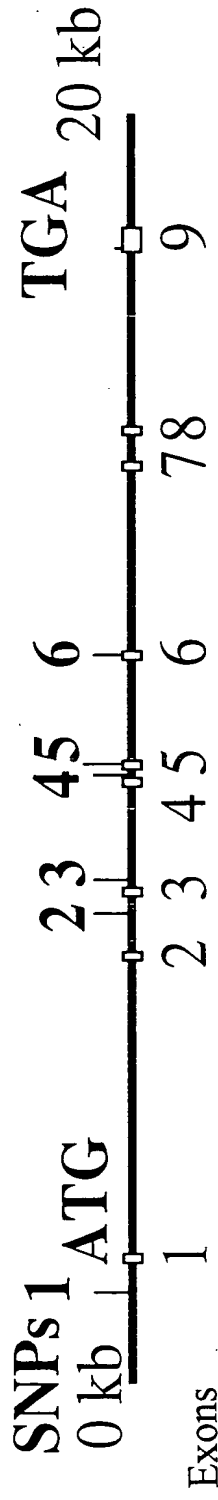


Fig. 77

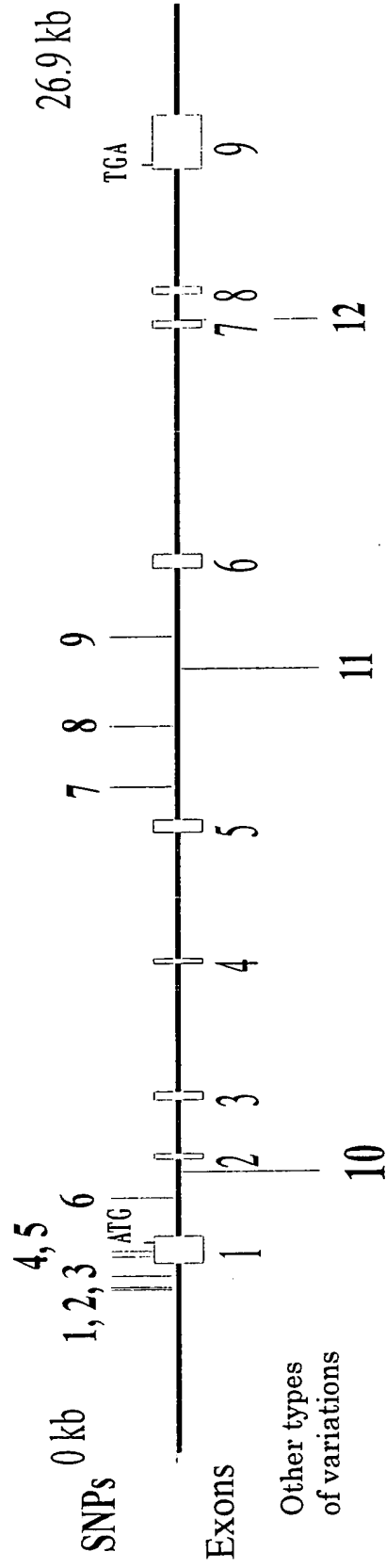


Fig.78

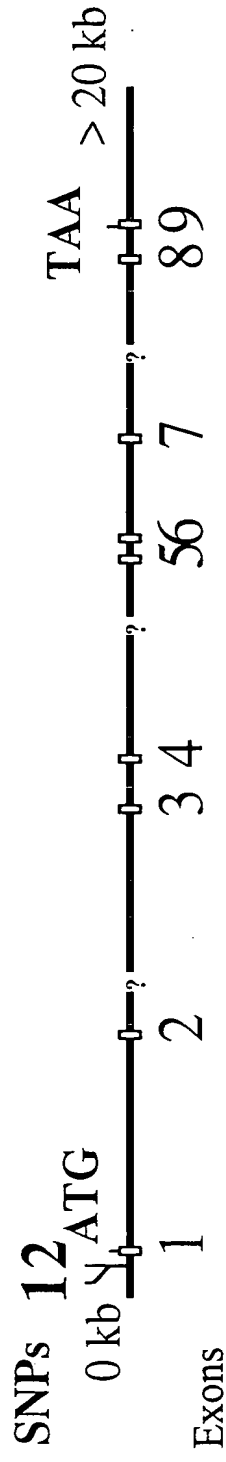


Fig.79

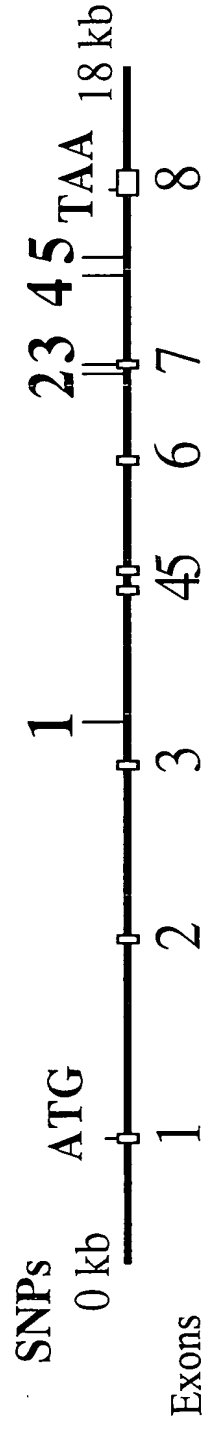


Fig.80

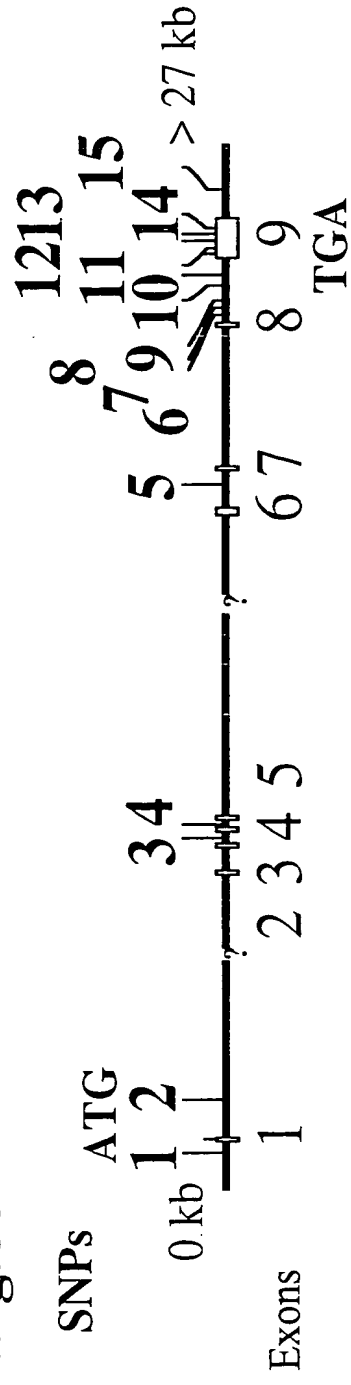


Fig.81

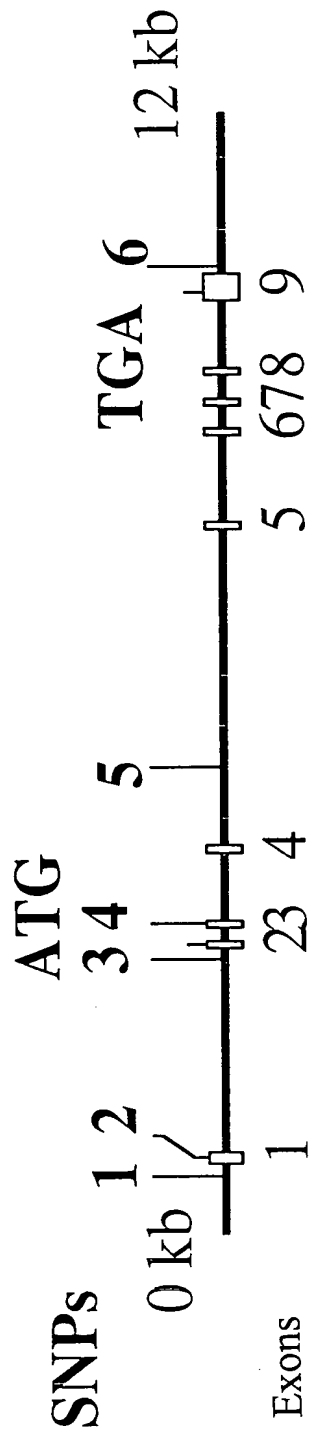


Fig.82

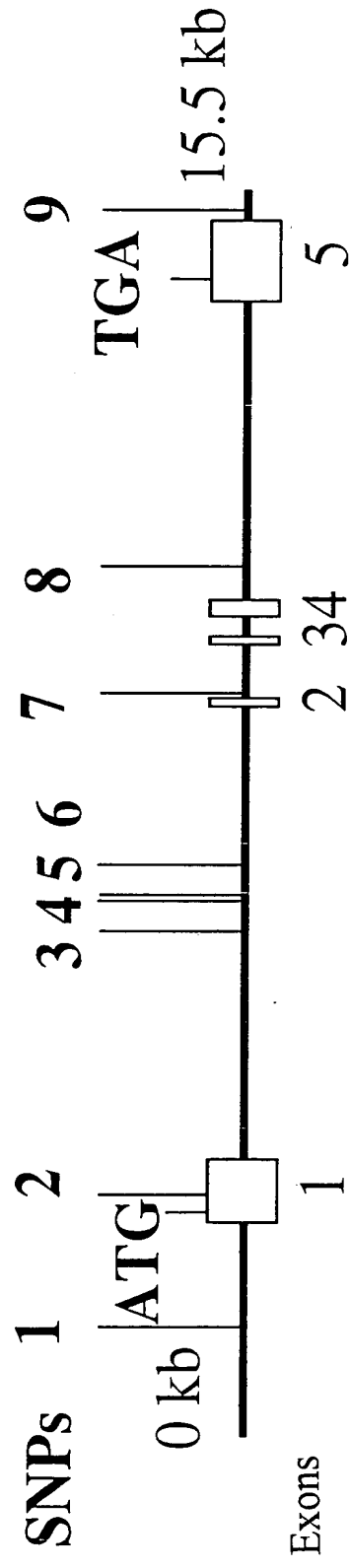


Fig. 83

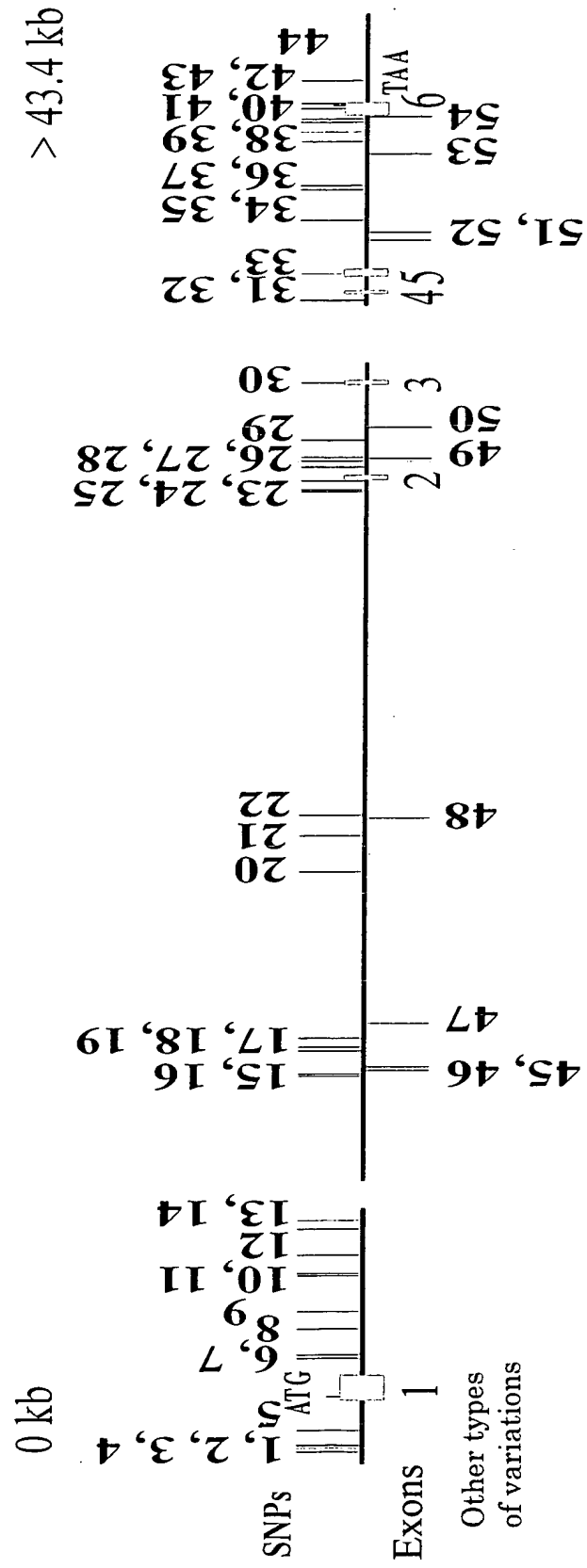


Fig. 84

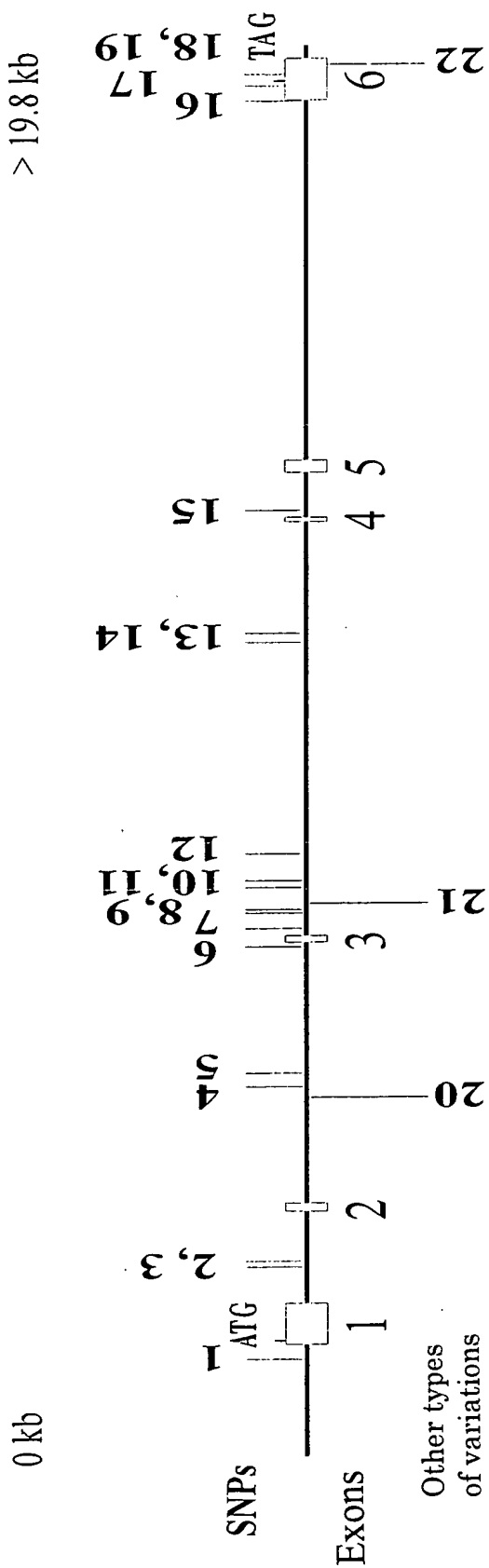


Fig. 85

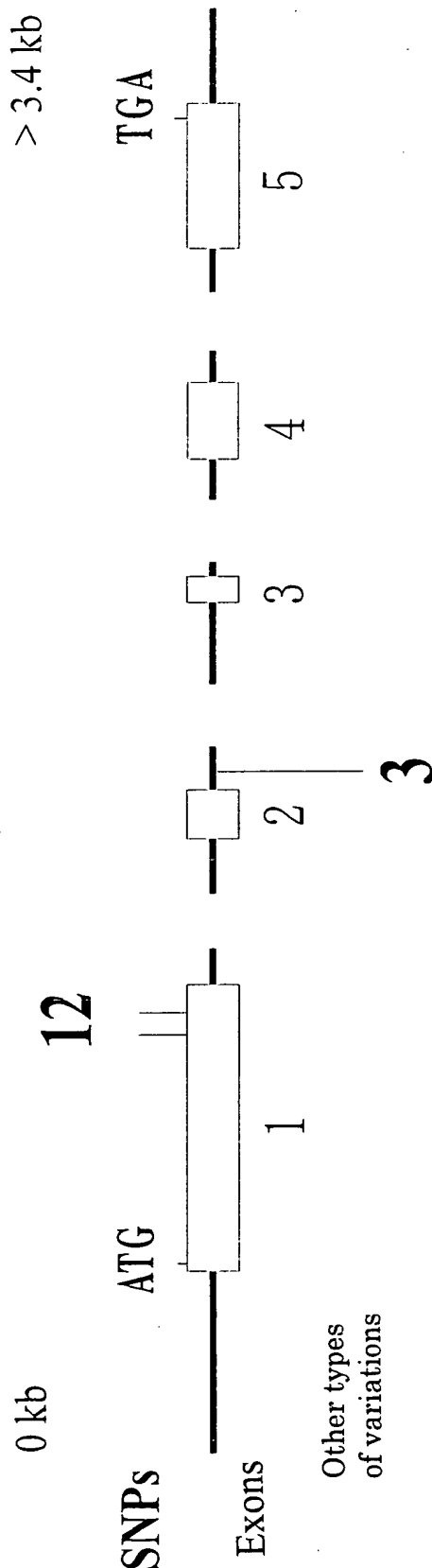


Fig.86

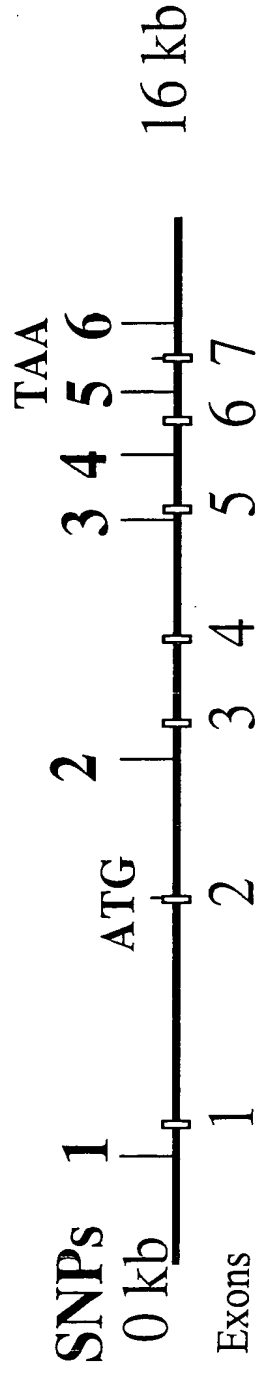


Fig.87

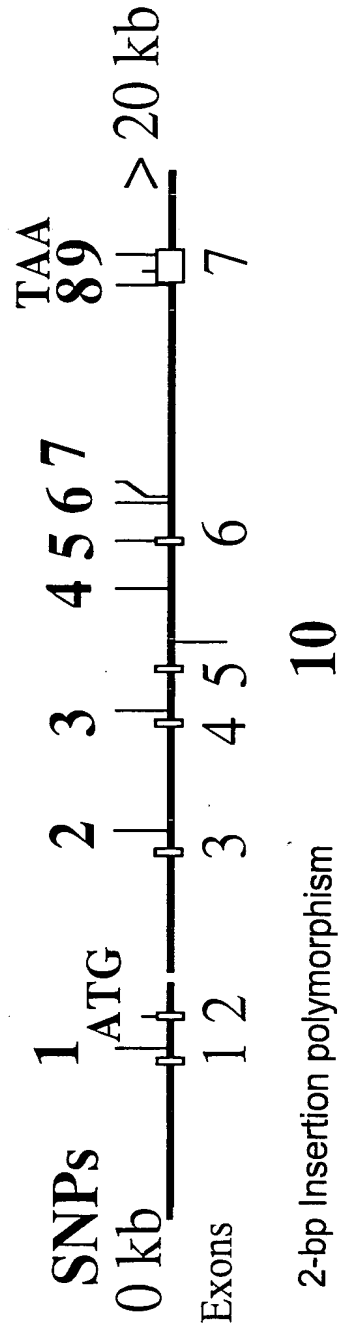


Fig.88

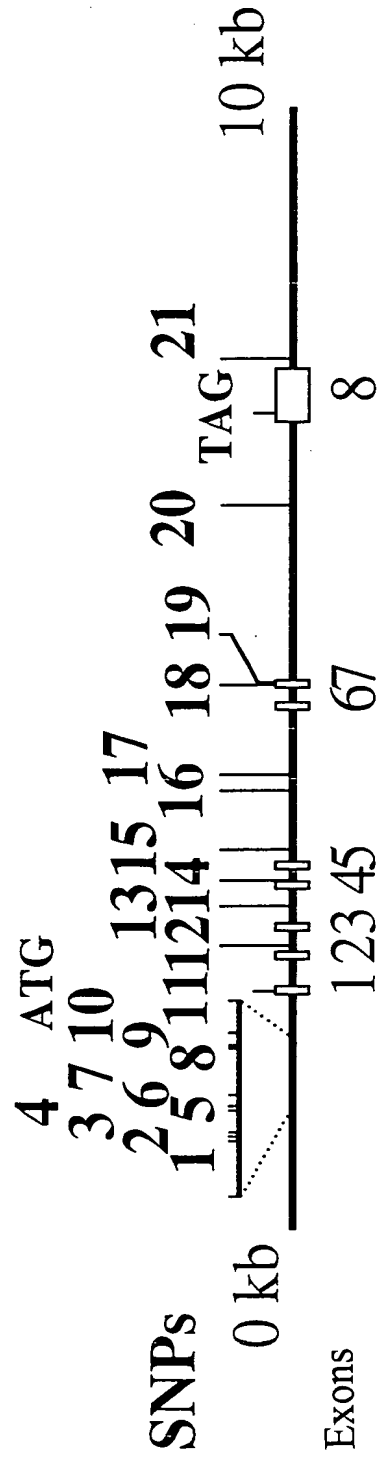


Fig.89

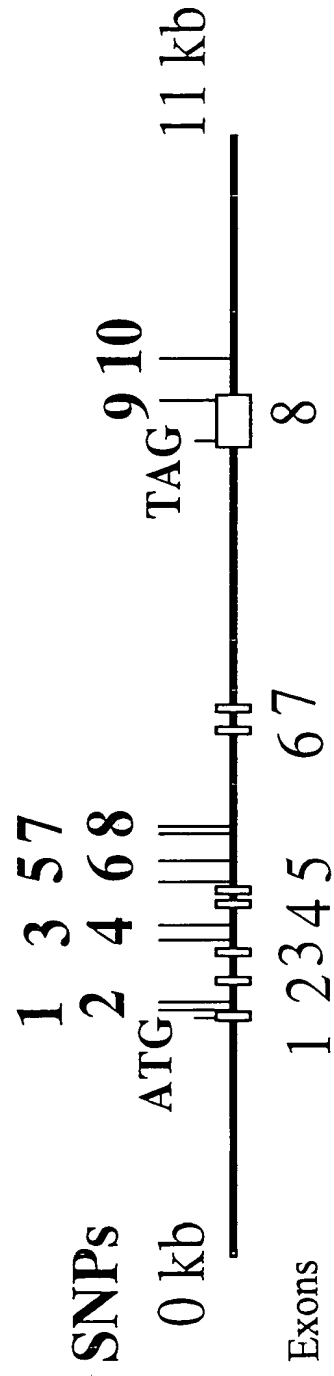


Fig.90

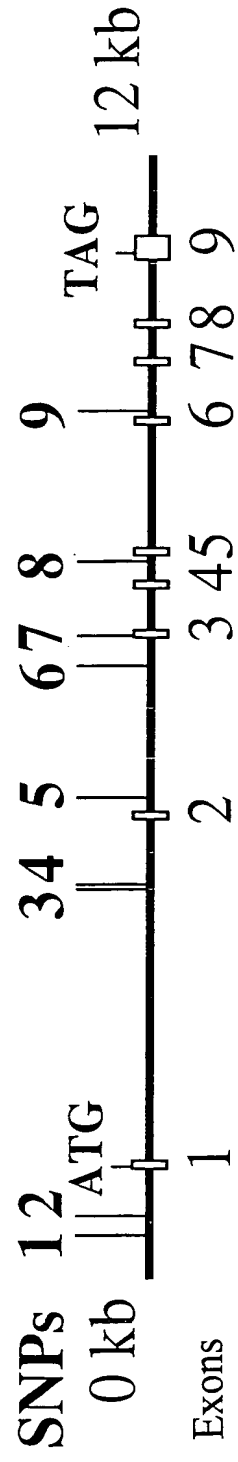


Fig.91

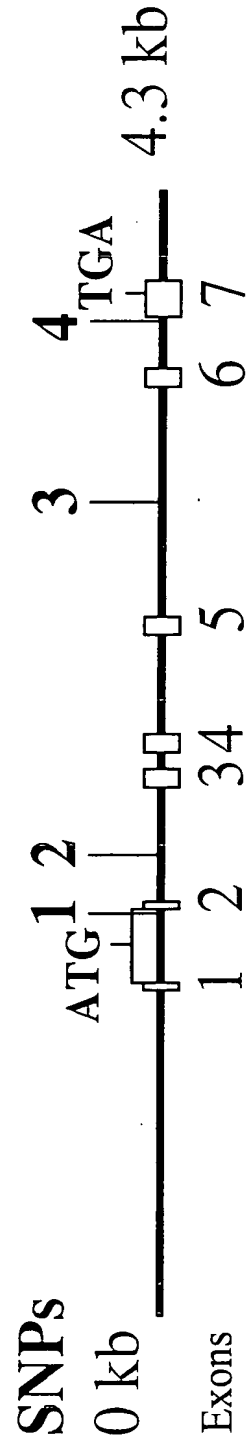


Fig.92

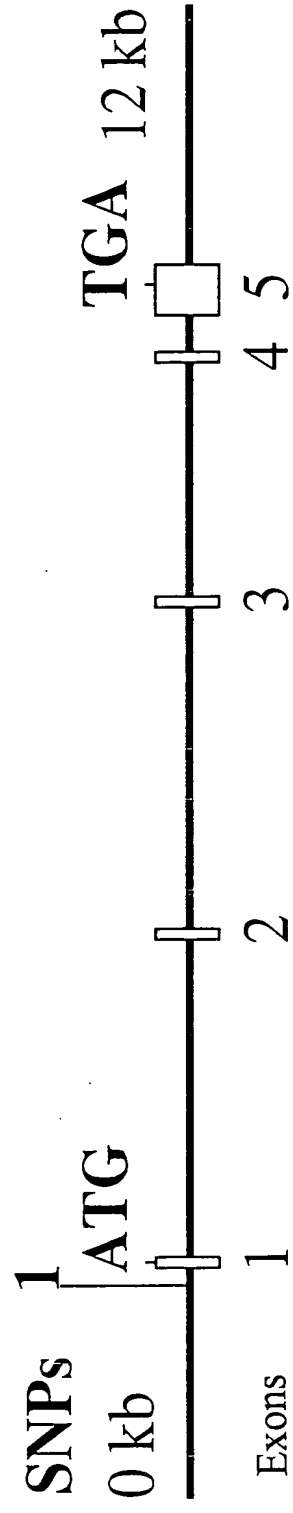


Fig. 93

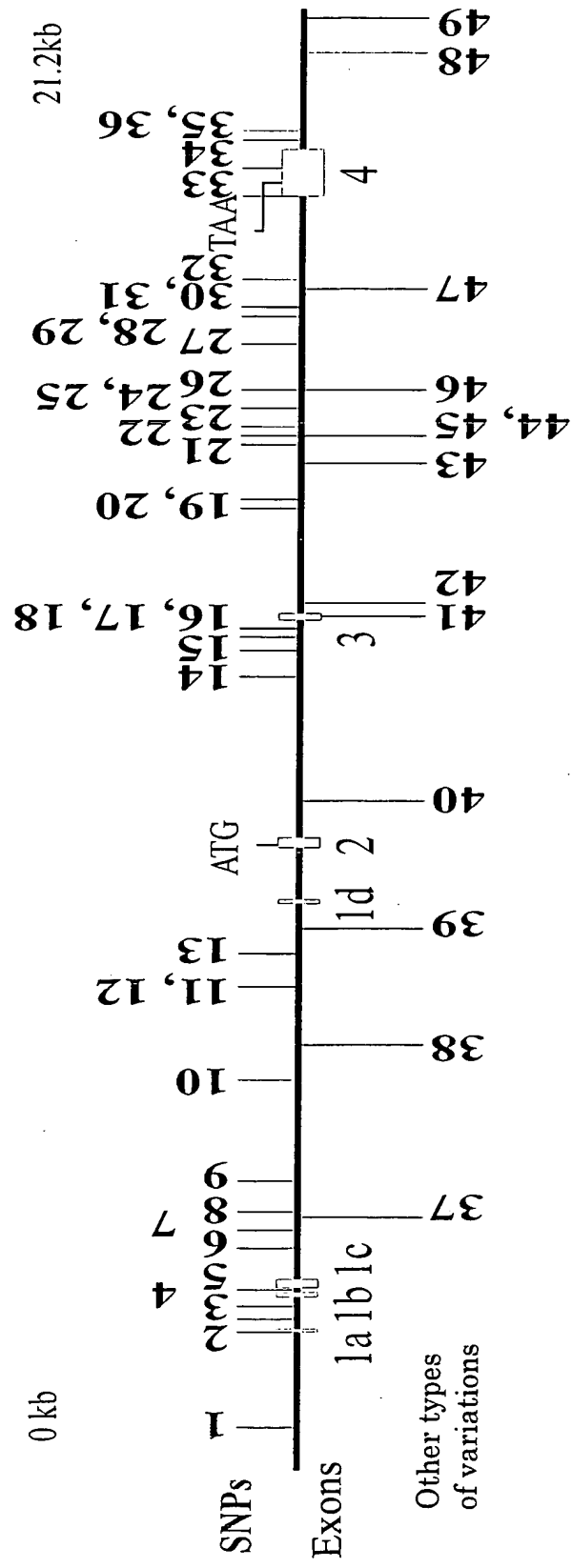


Fig.94

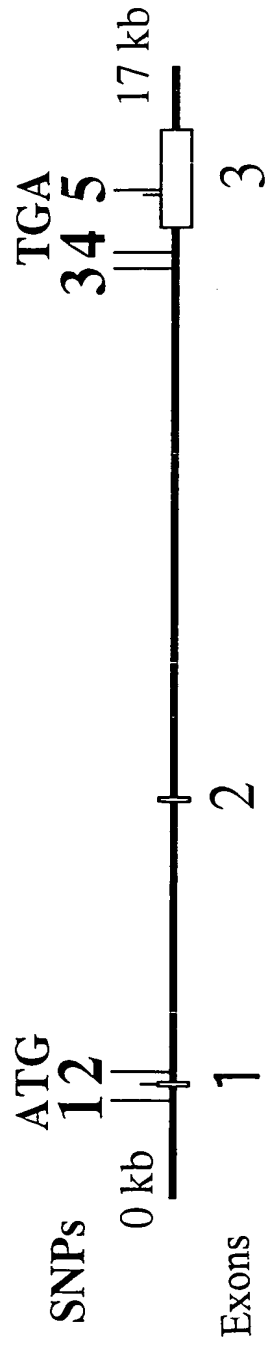


Fig.95

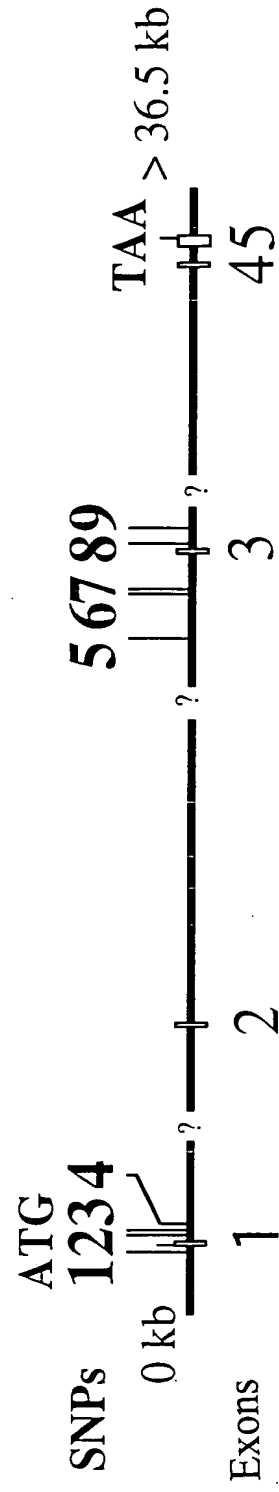


Fig.96

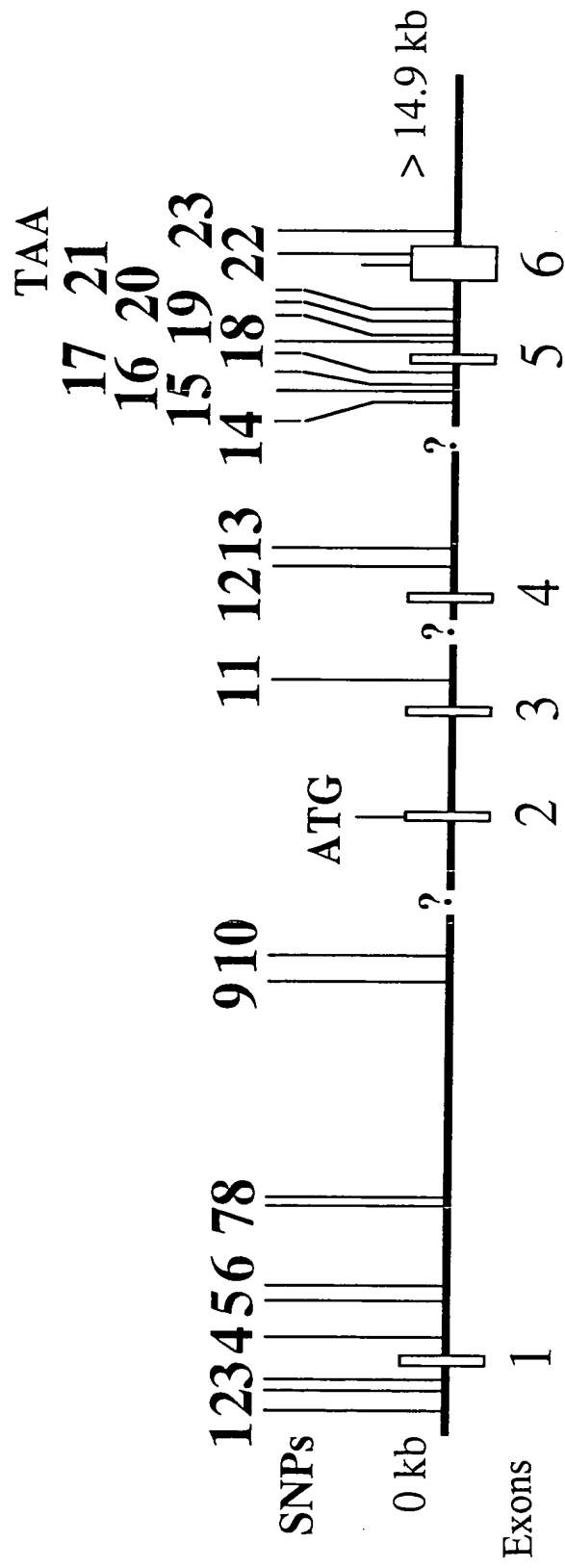


Fig.97

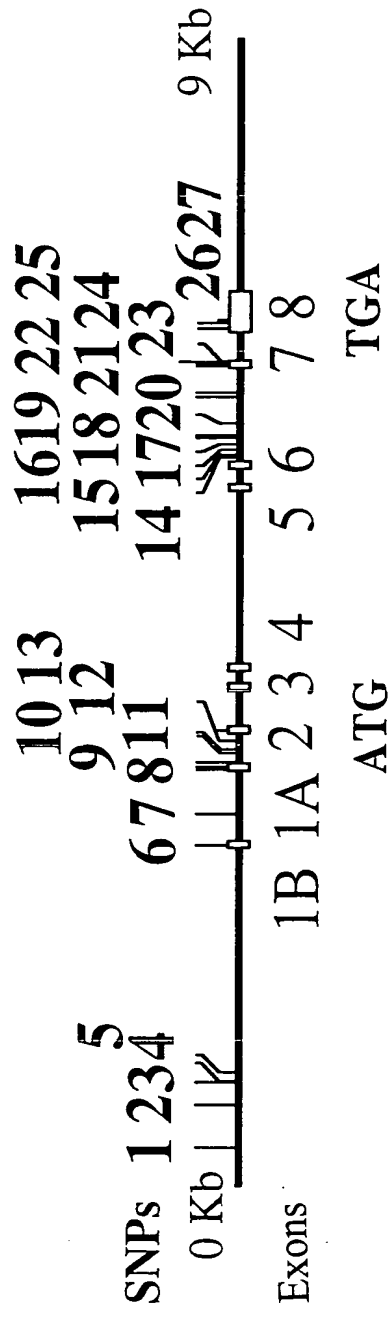


Fig.98

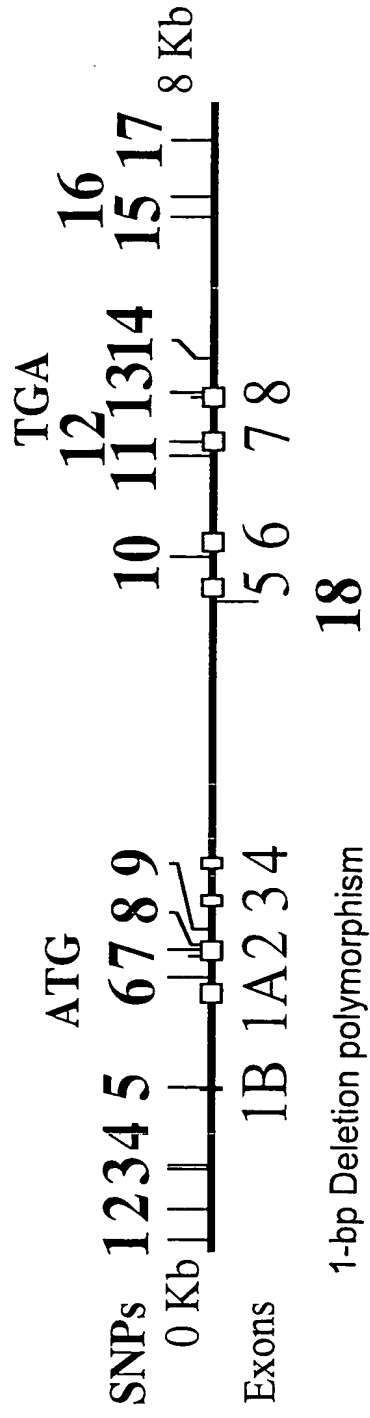


Fig.99

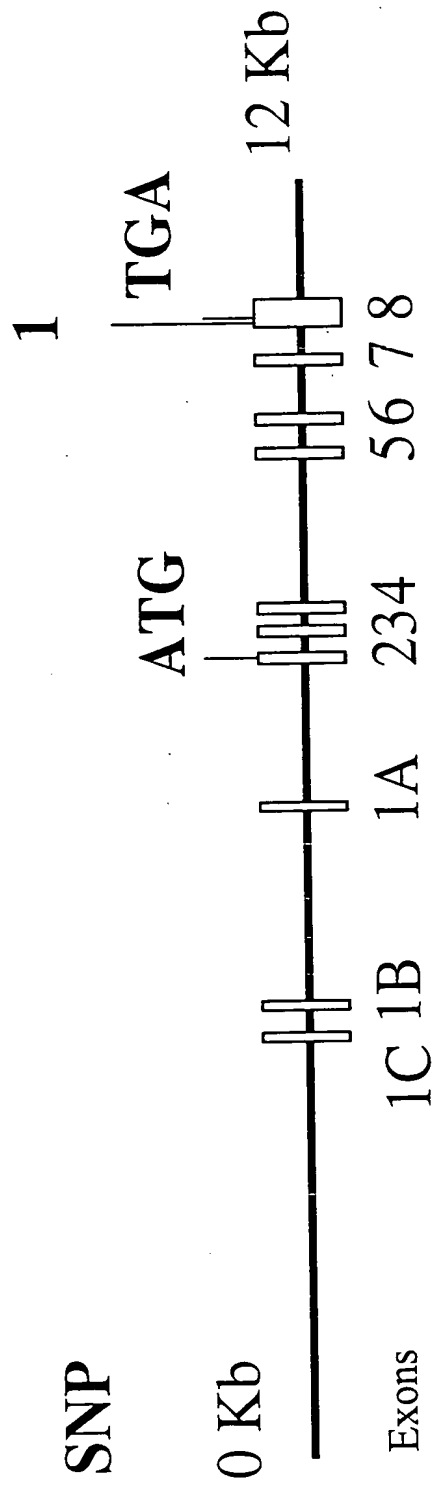


Fig.100

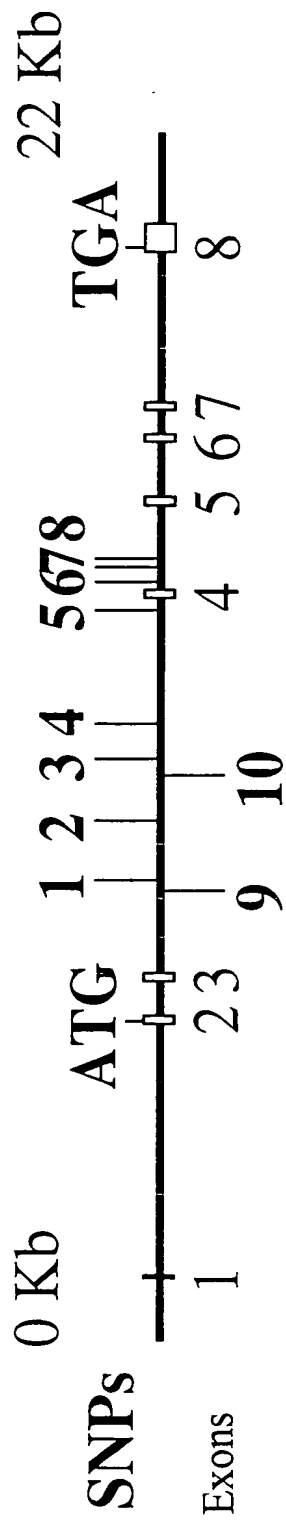


Fig.101

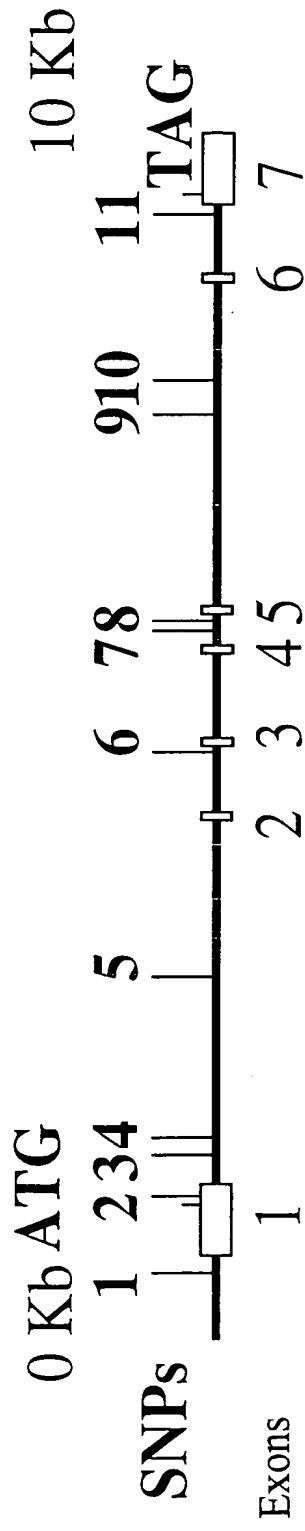


Fig.102

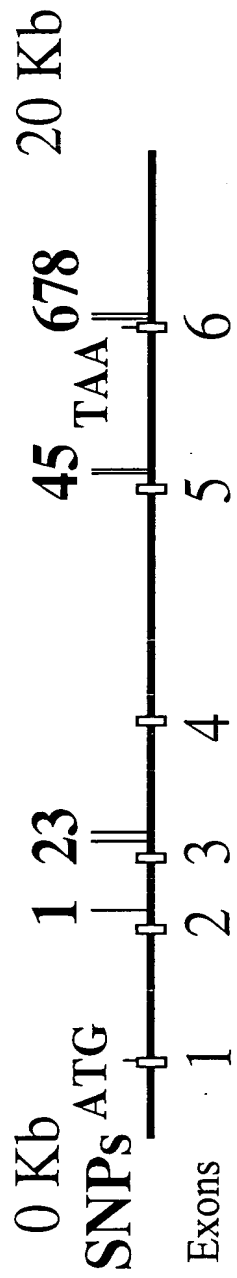


Fig.103

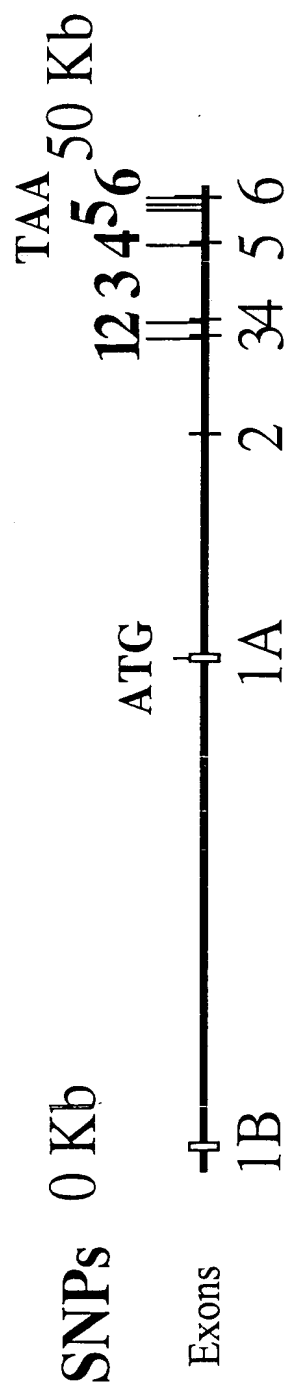


Fig.104

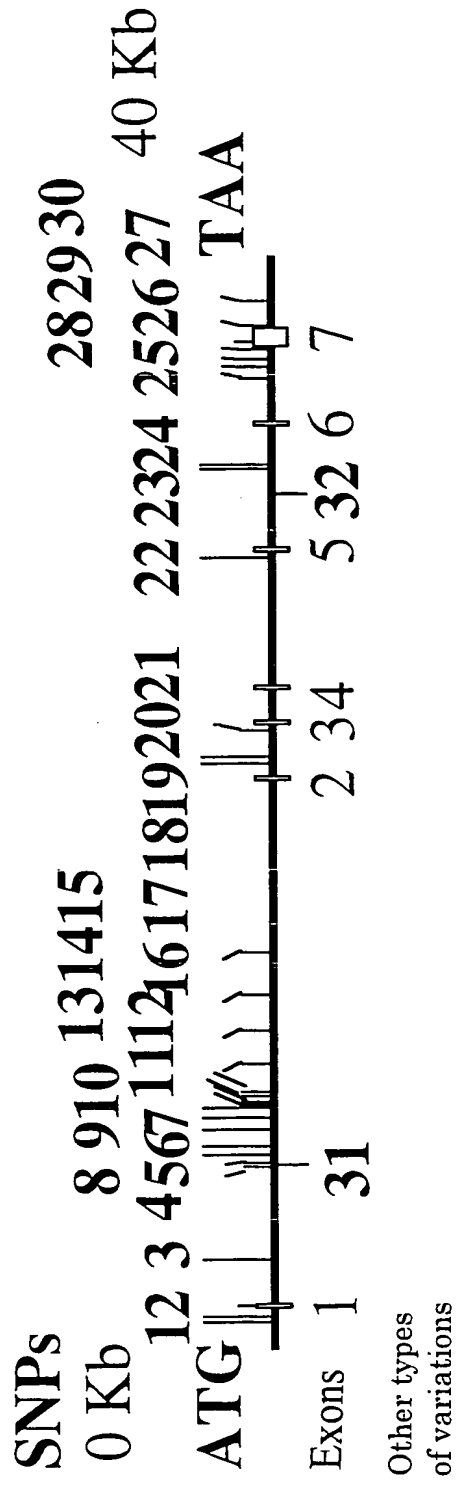


Fig.105

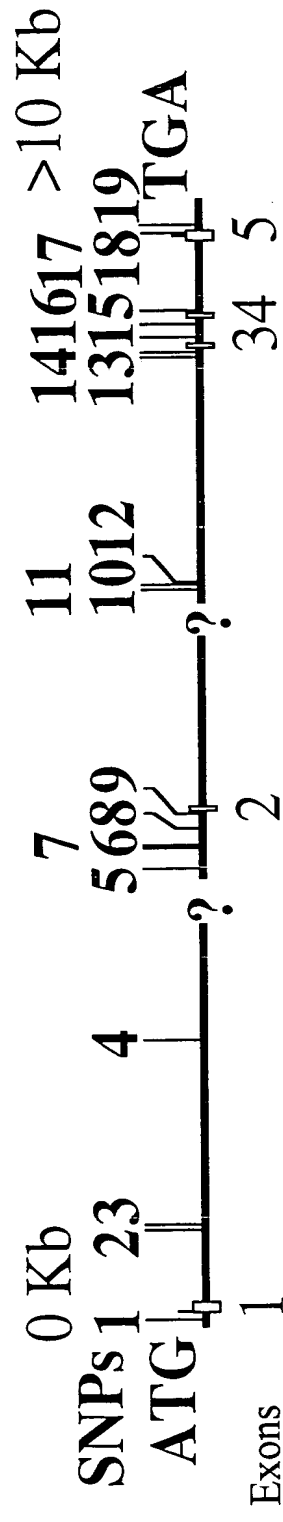


Fig.106

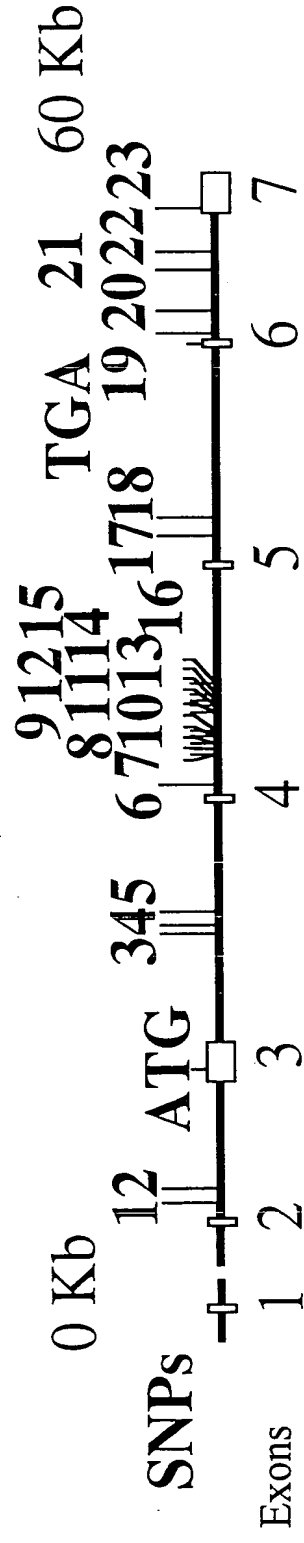


Fig.107



Fig. 108

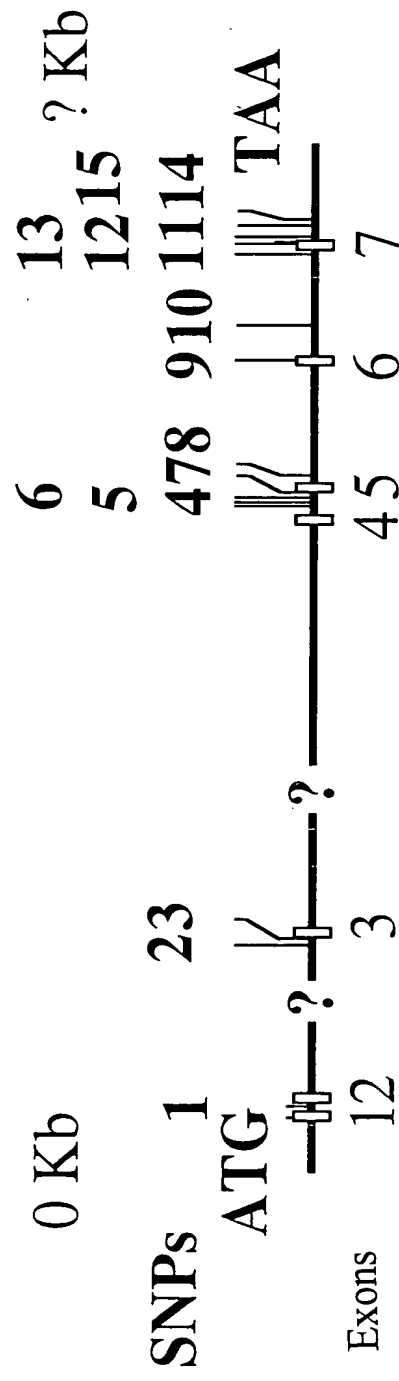


Fig. 109

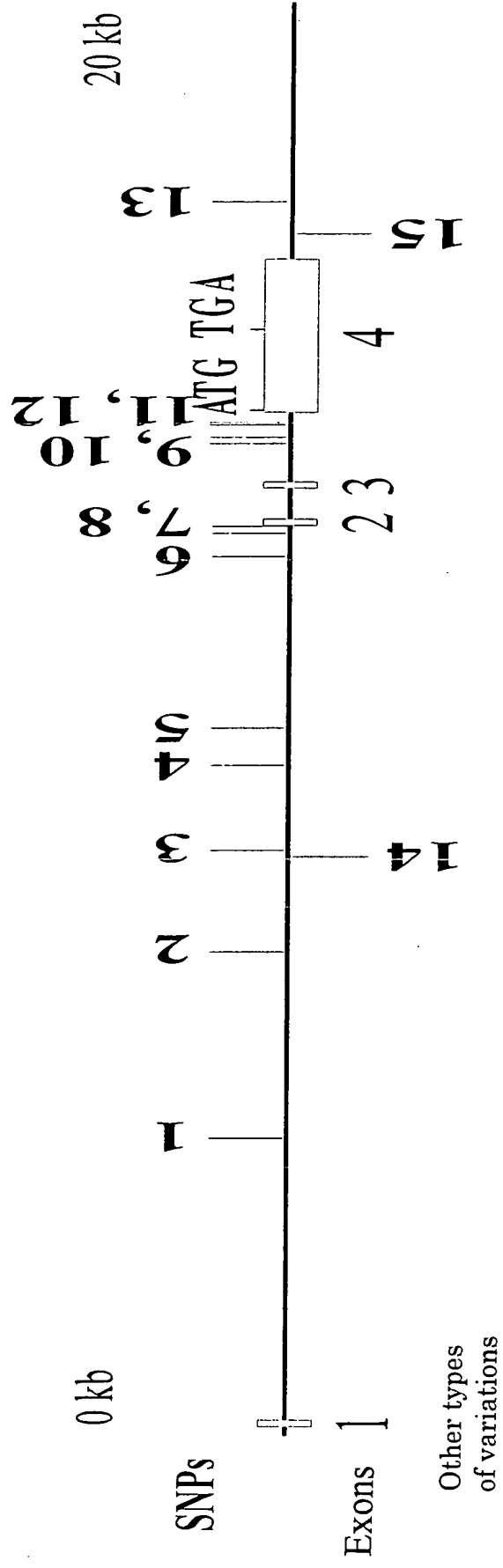


Fig.110

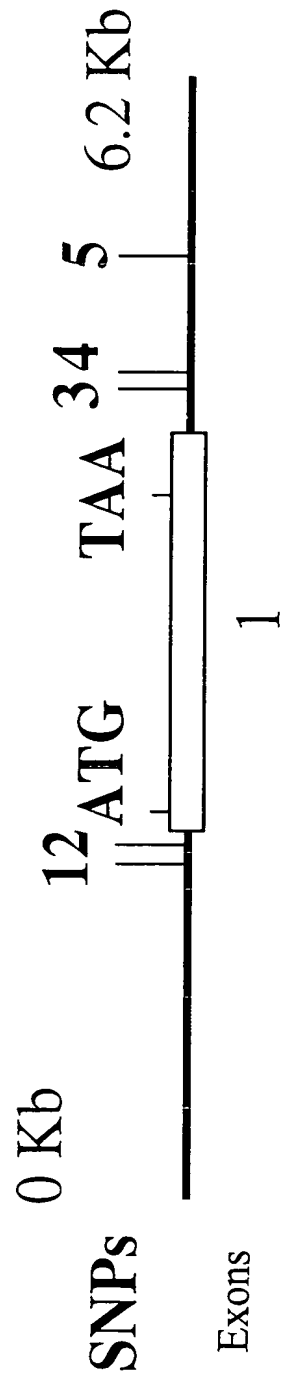


Fig. 111

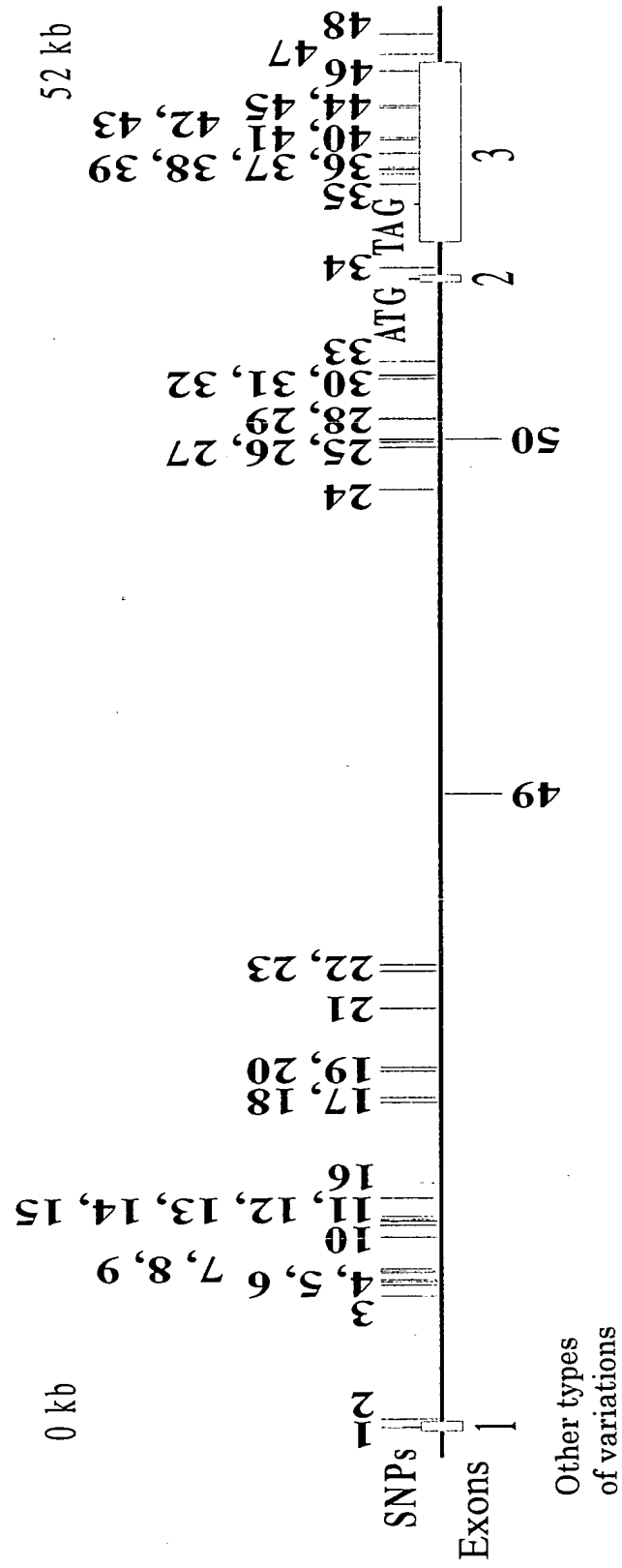


Fig.112

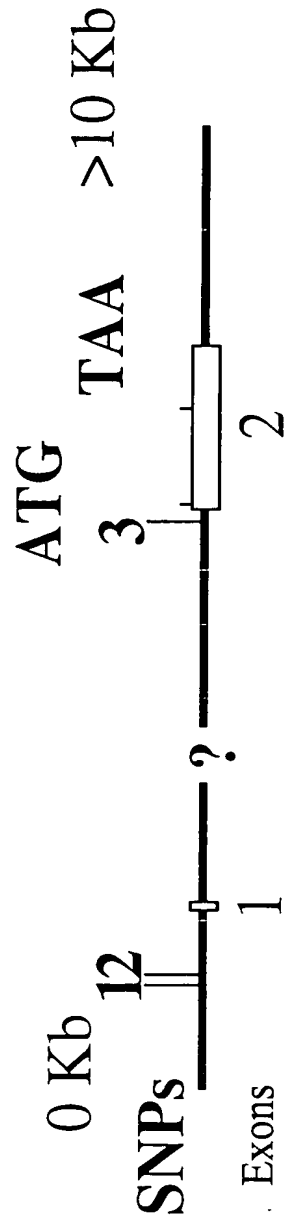


Fig.113

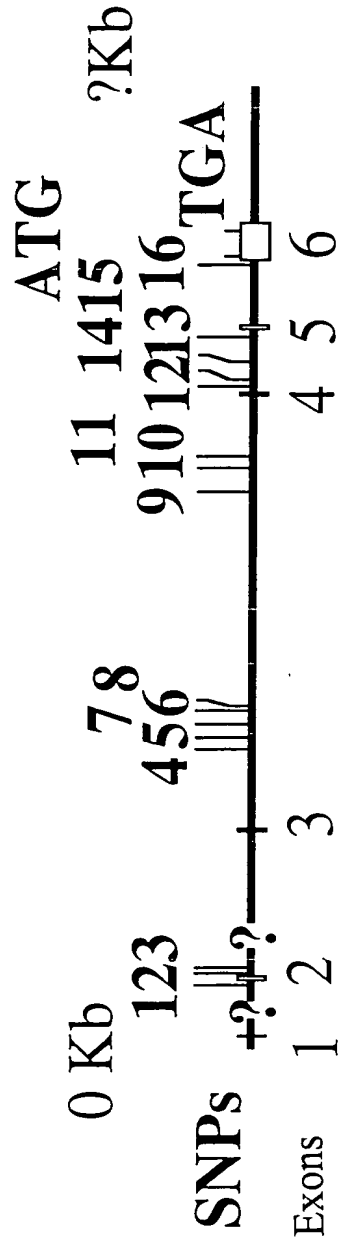


Fig. 114

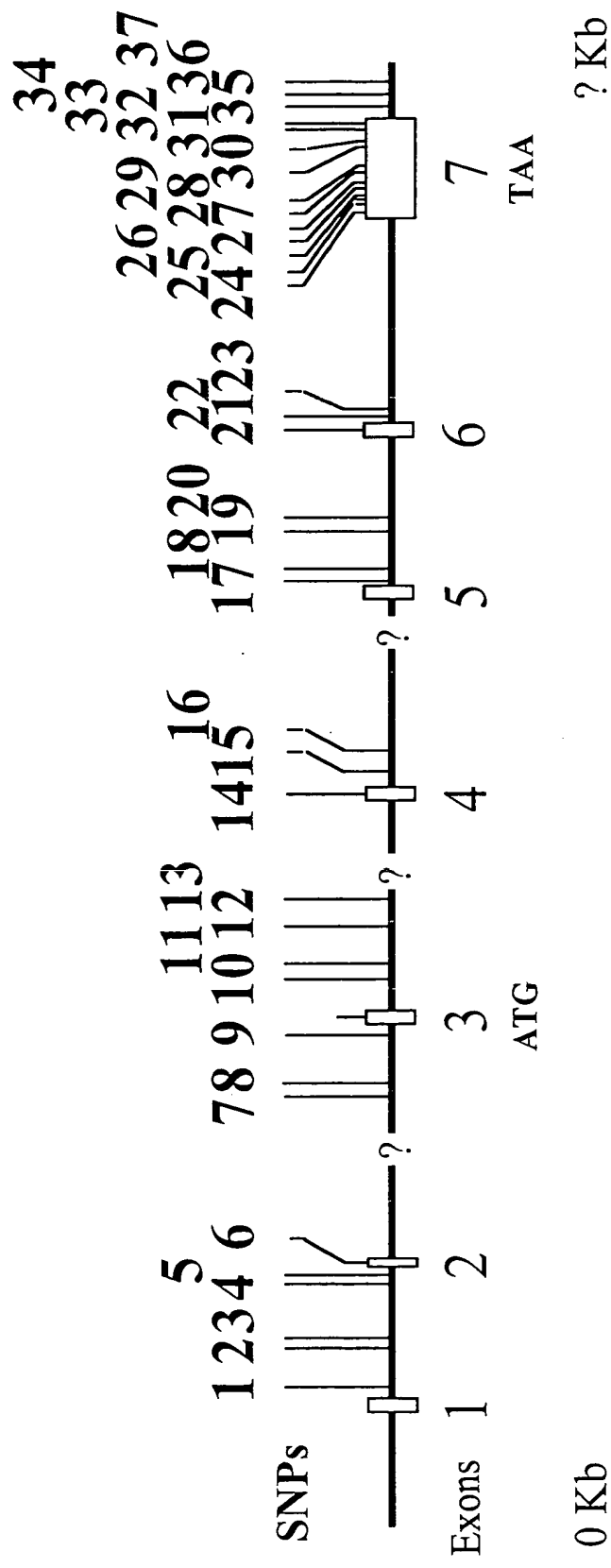


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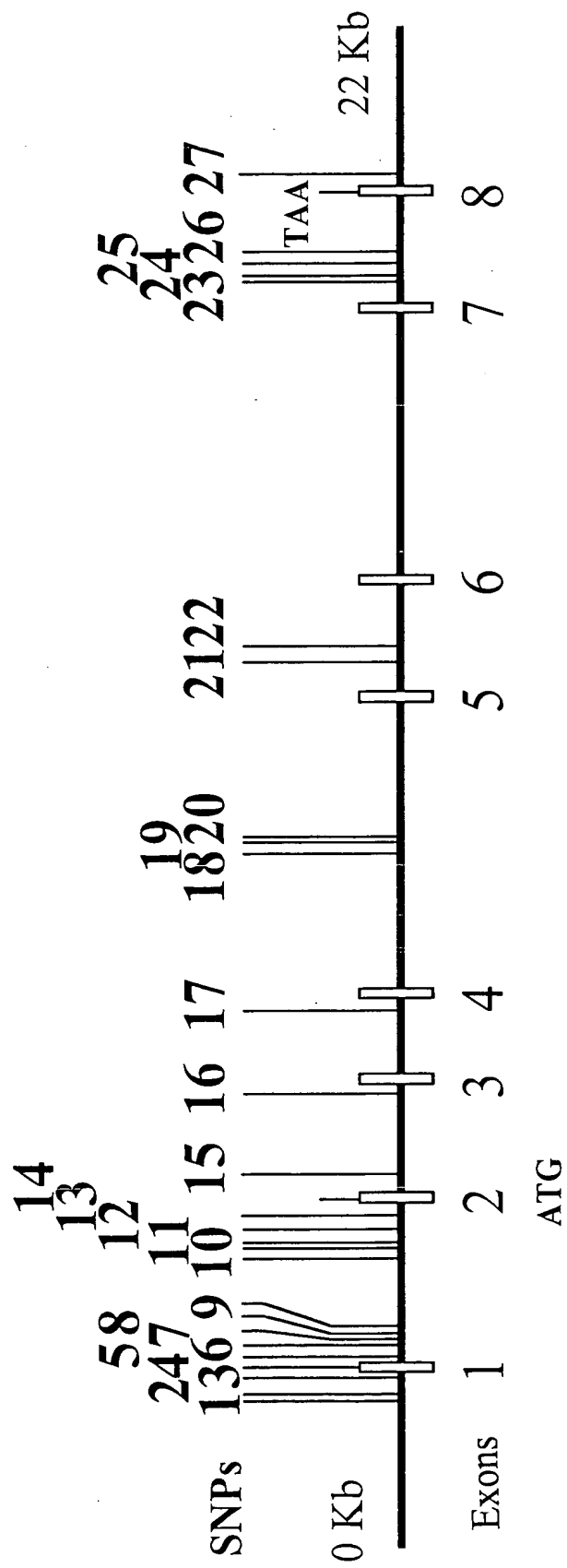


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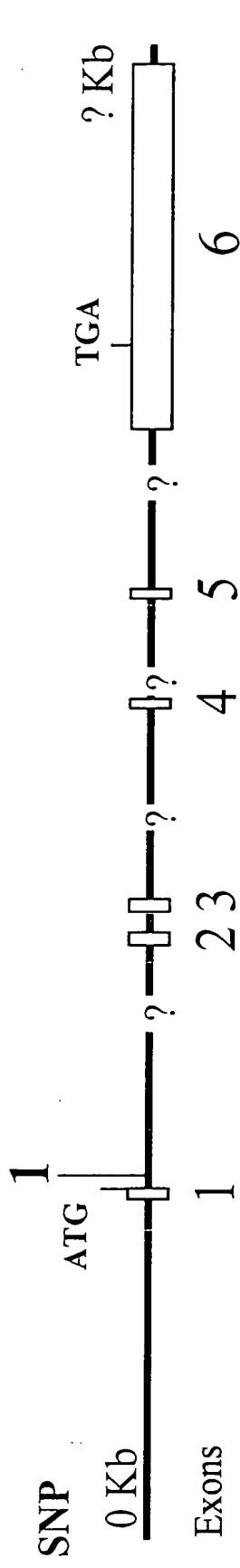


Fig. 117

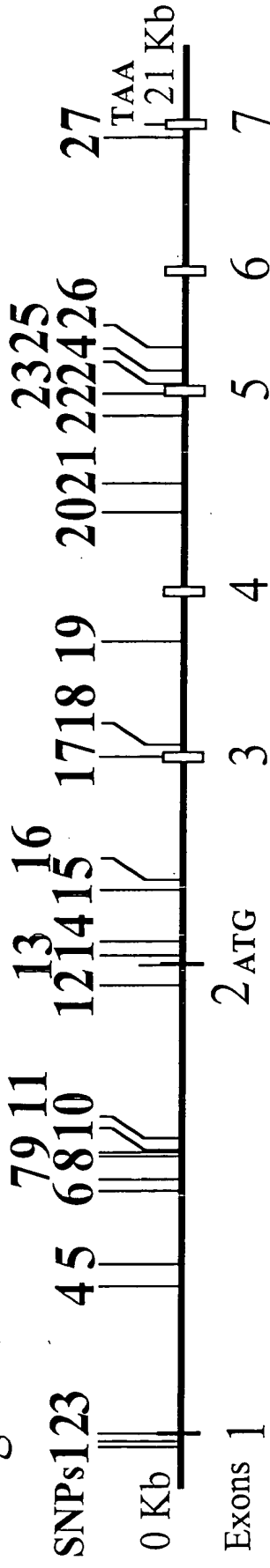


Fig. 118

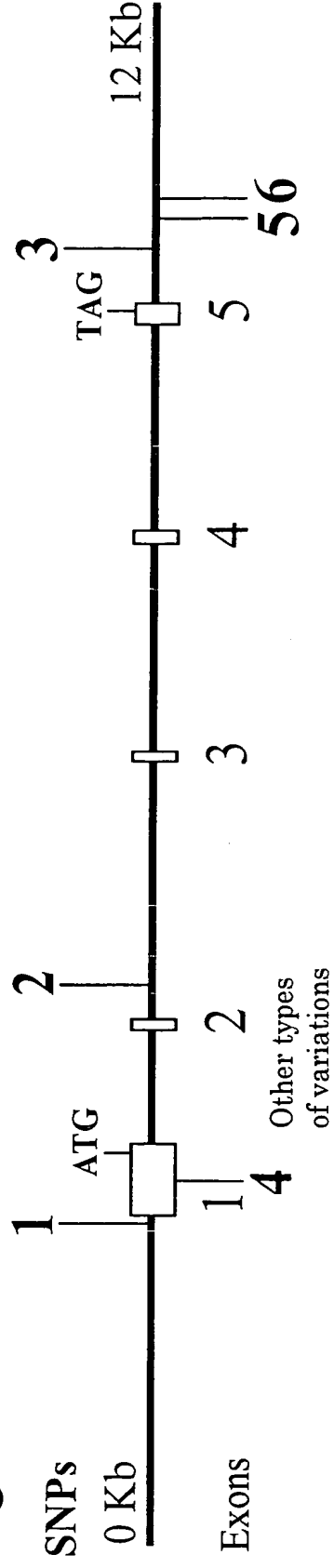


Fig. 119

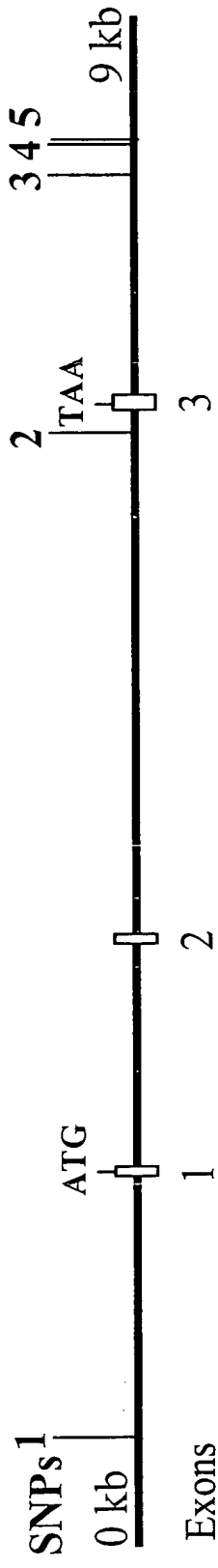


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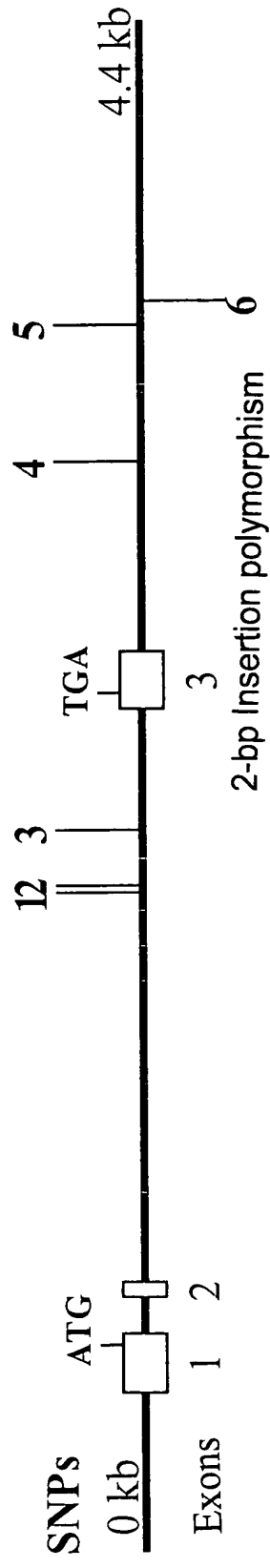


Fig. 121

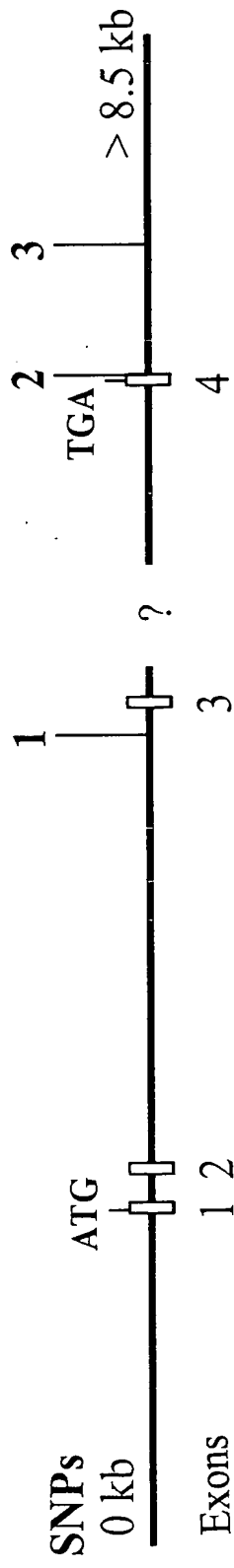


Fig. 122

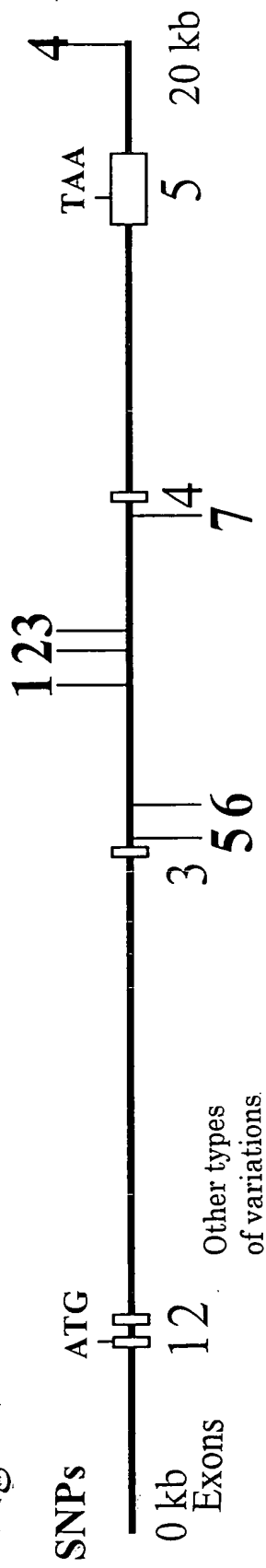


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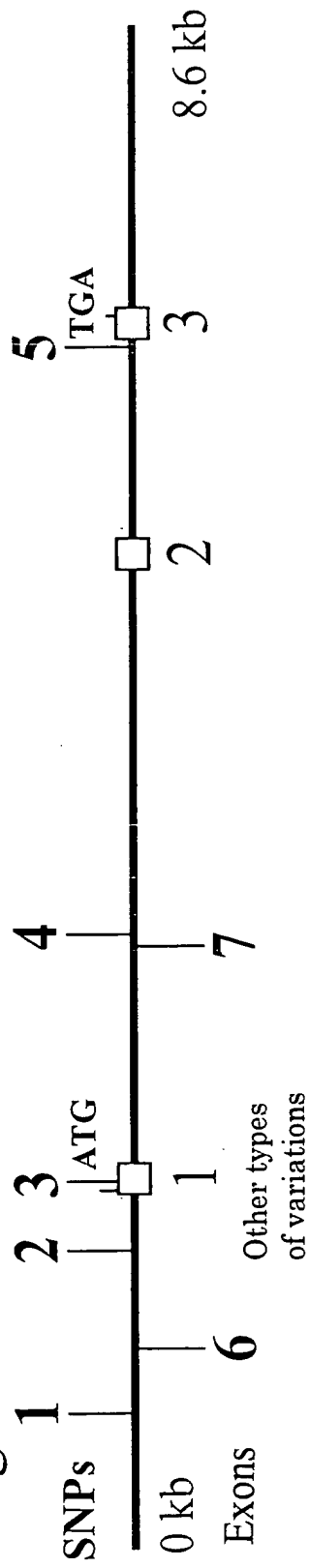


Fig. 124

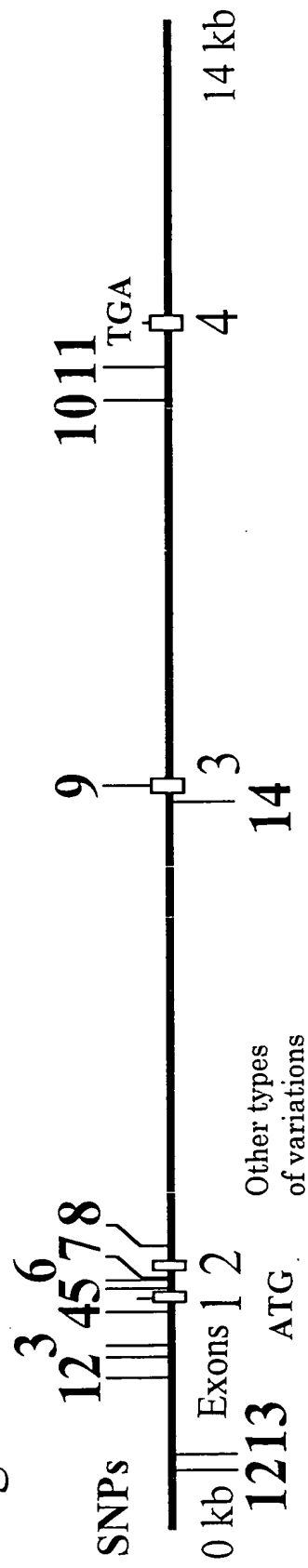


Fig. 125

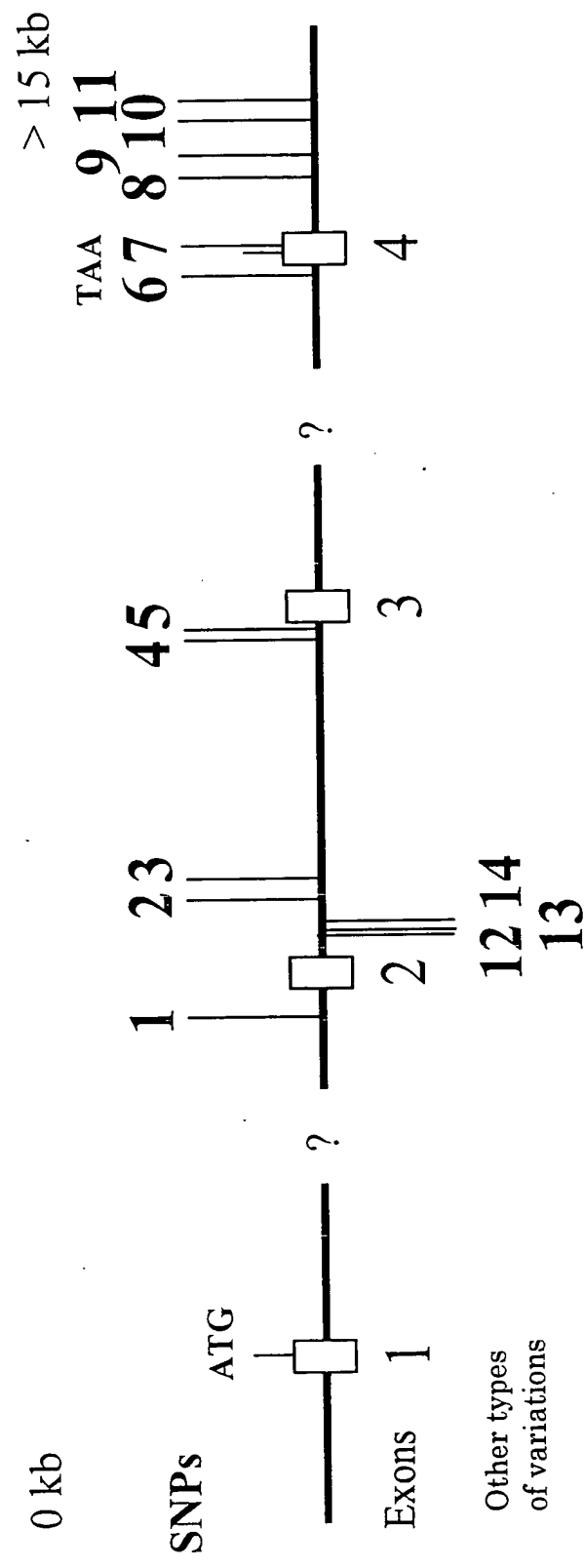


Fig. 126

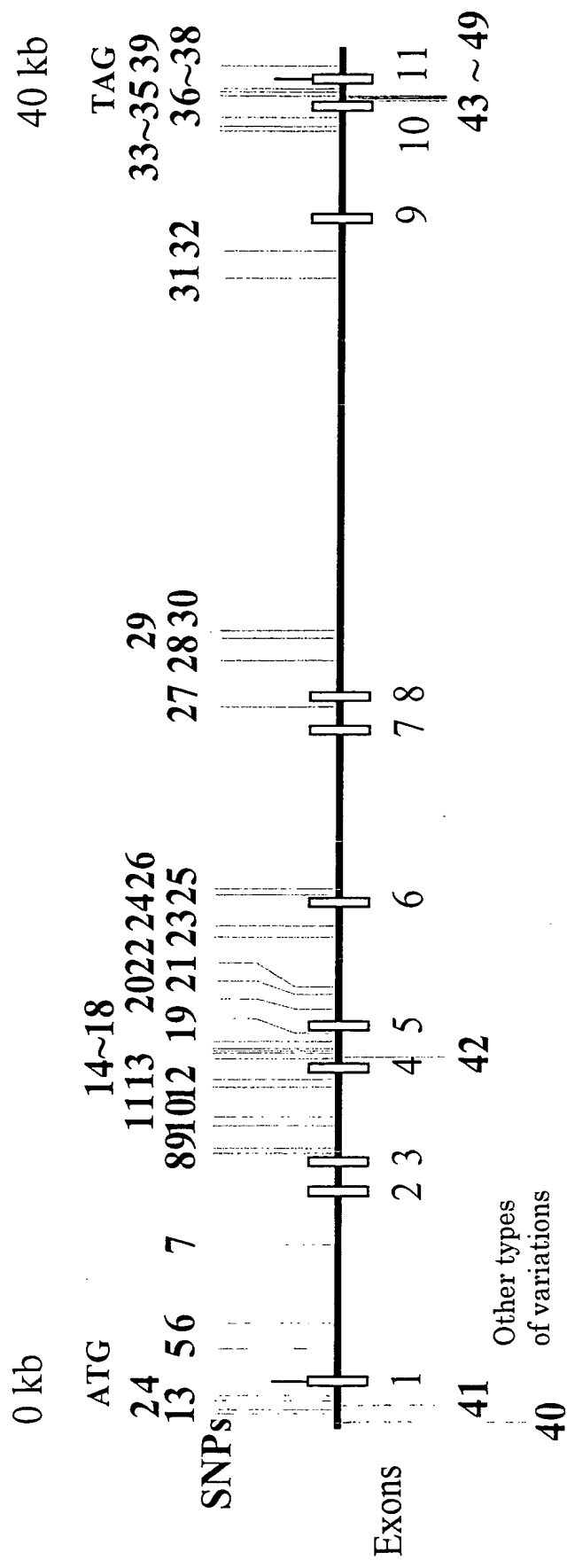


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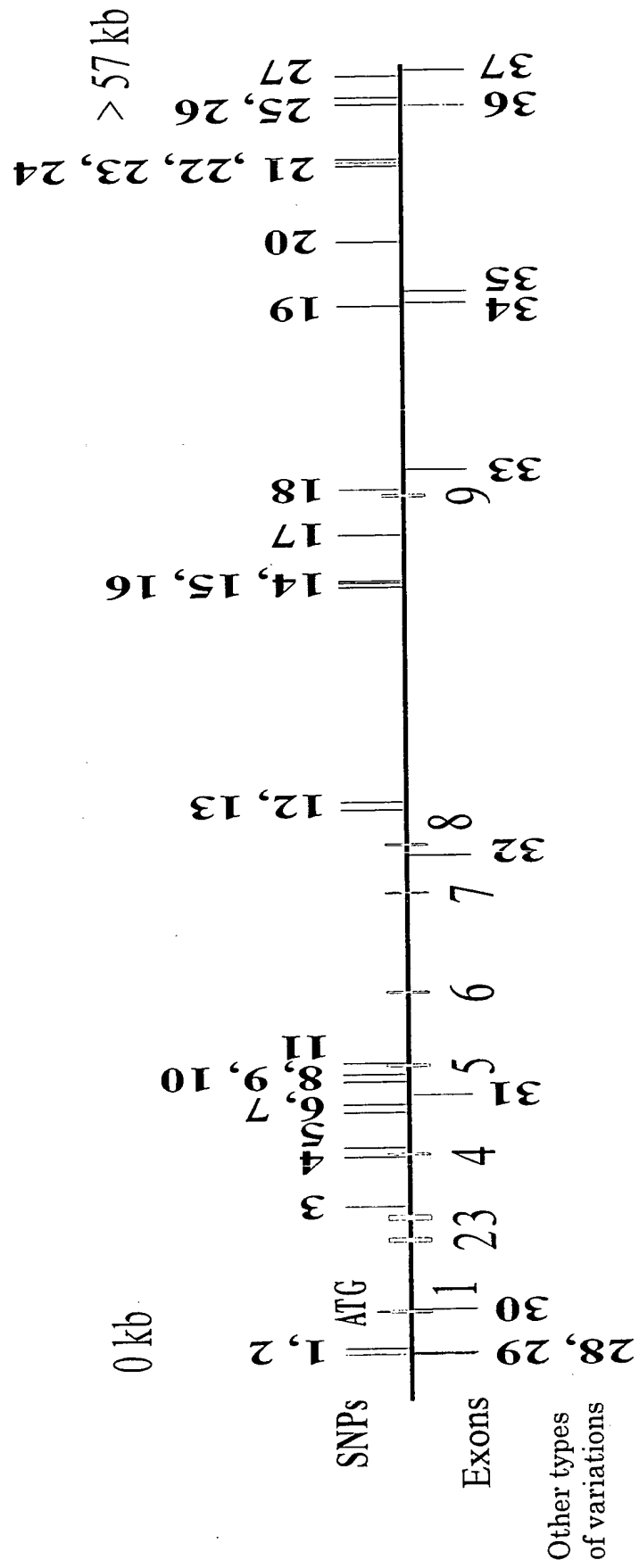


Fig. 128

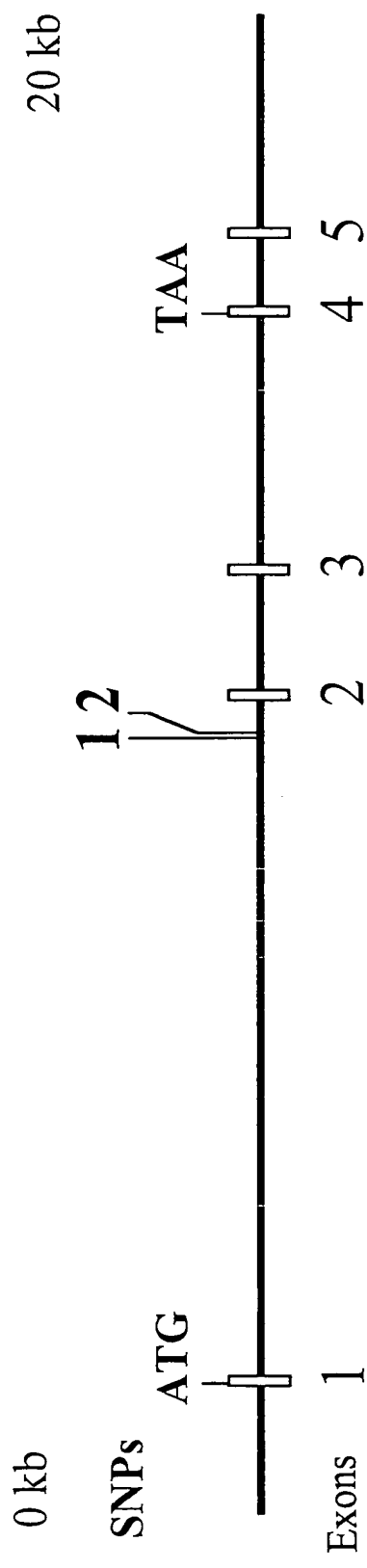


Fig. 129

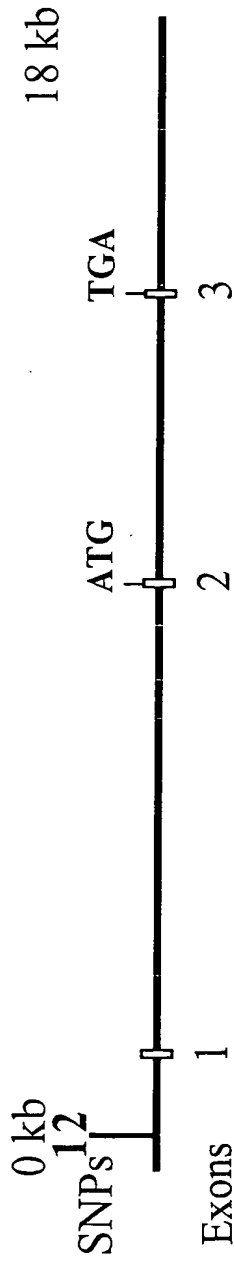


Fig. 130

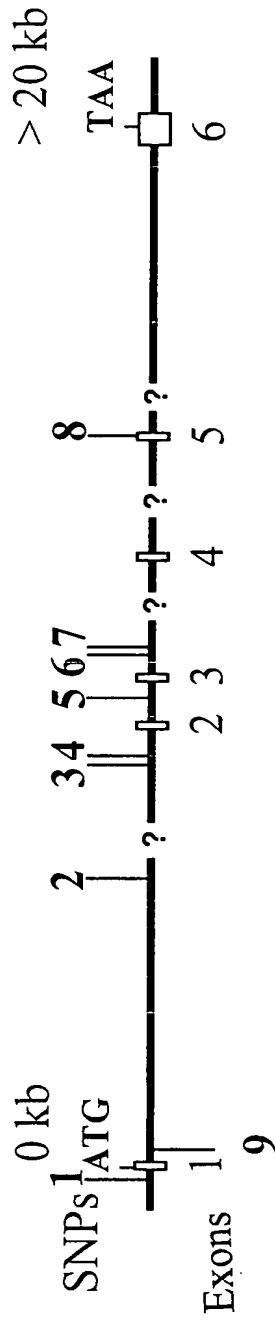
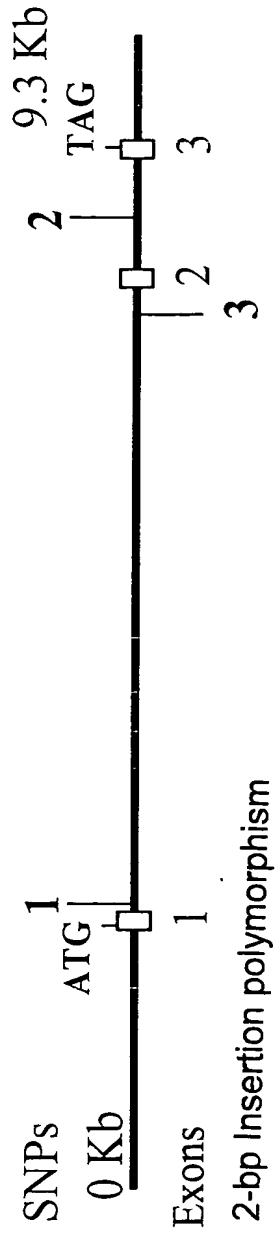


Fig. 131



2-bp Insertion polymorphism

Fig.132

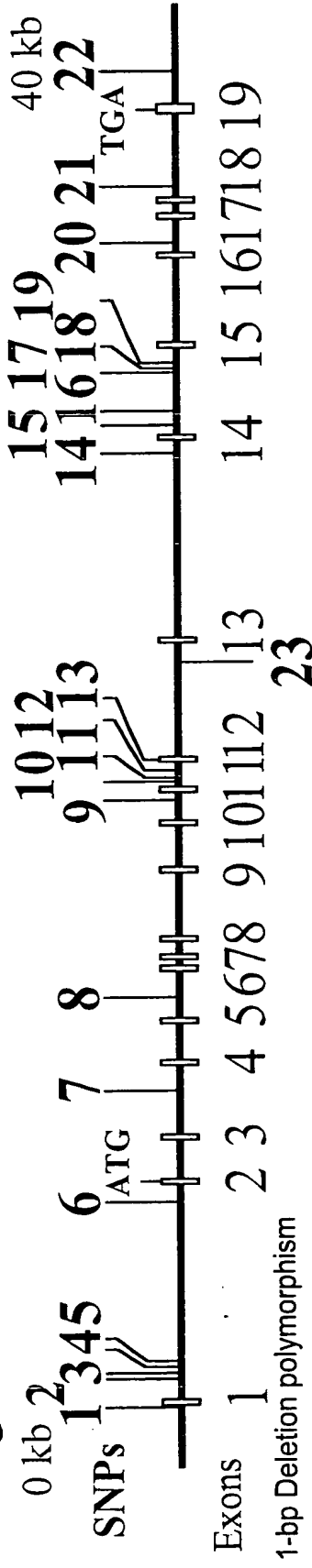


Fig.133

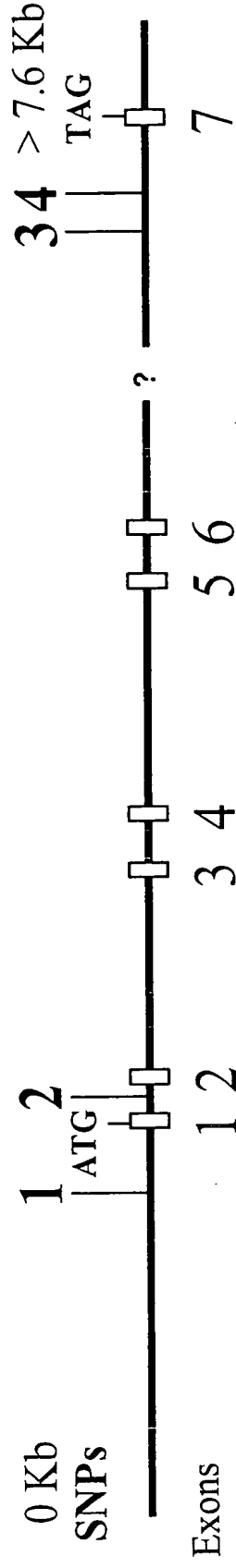


Fig.134

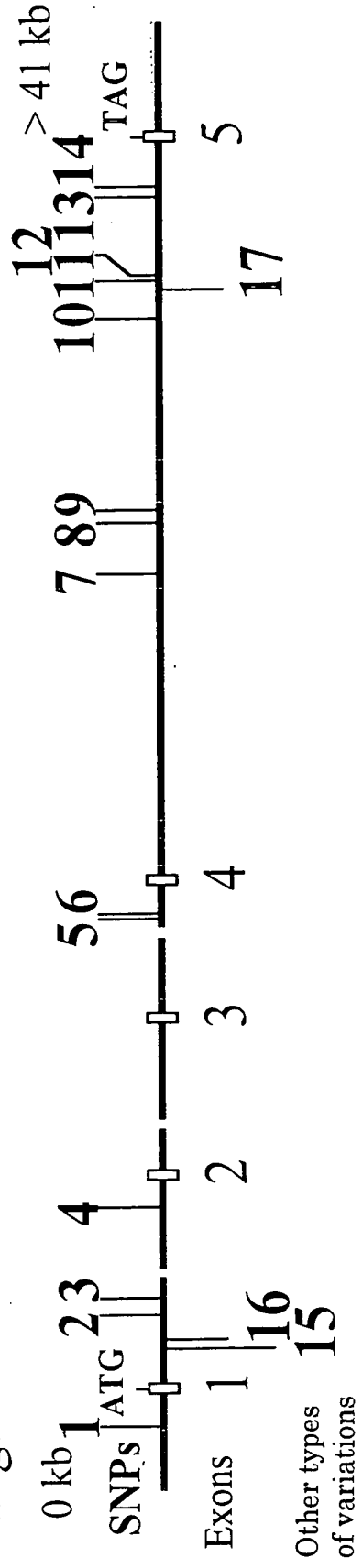


Fig.135

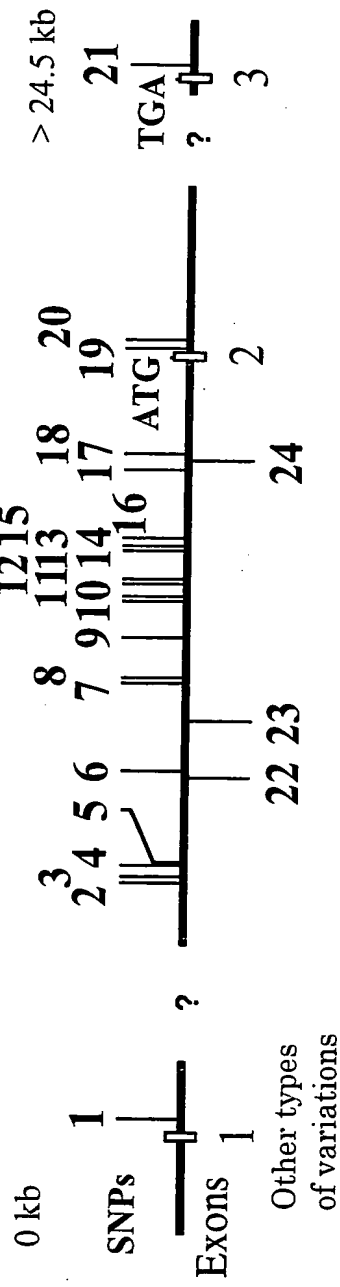


Fig.136

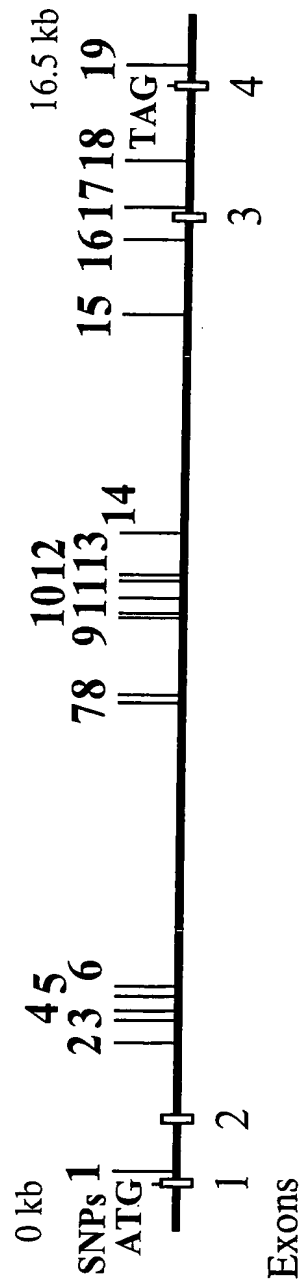


Fig.137

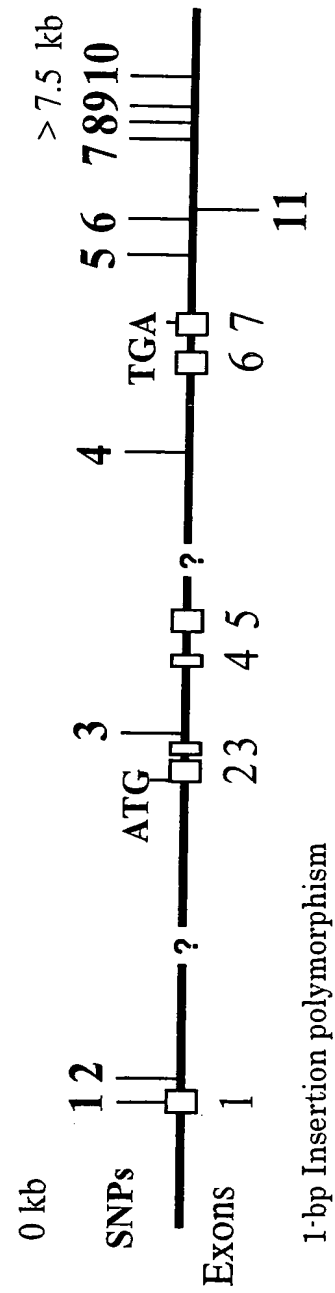


Fig. 138

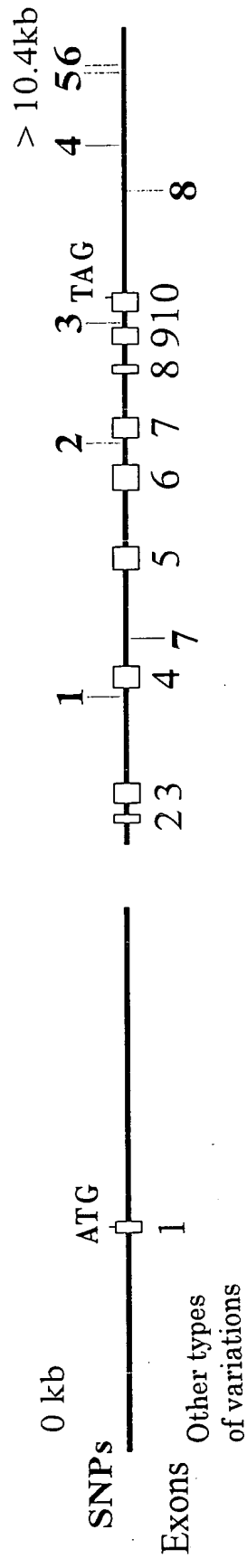


Fig. 139

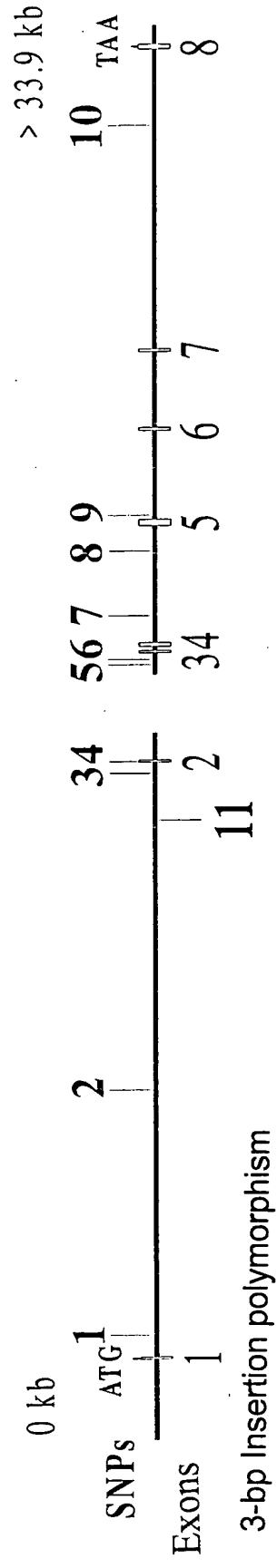


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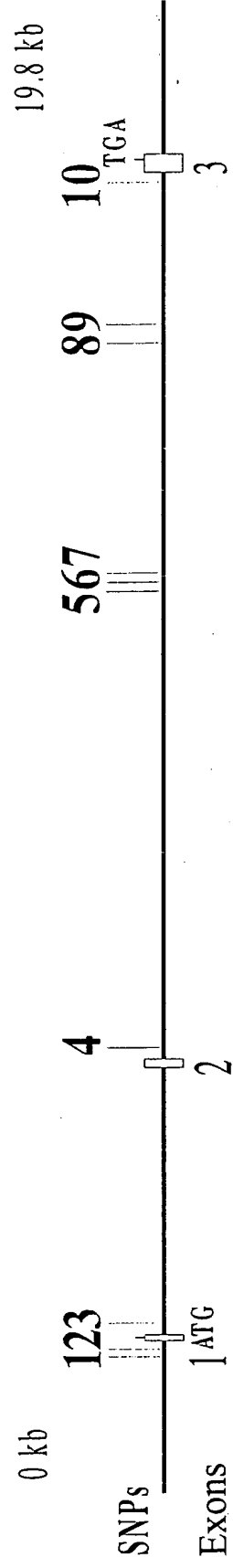


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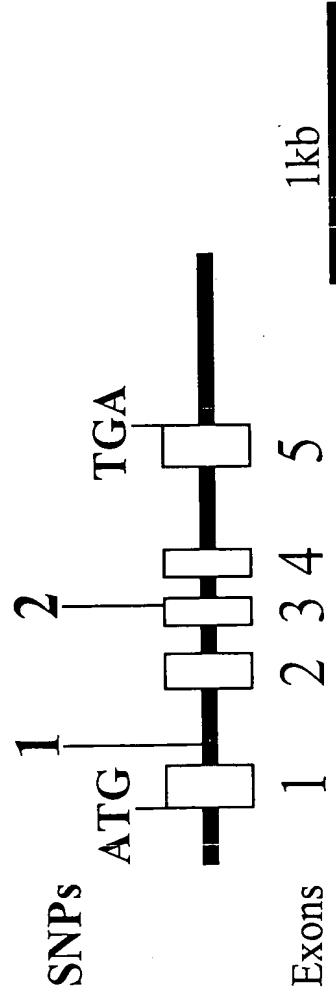


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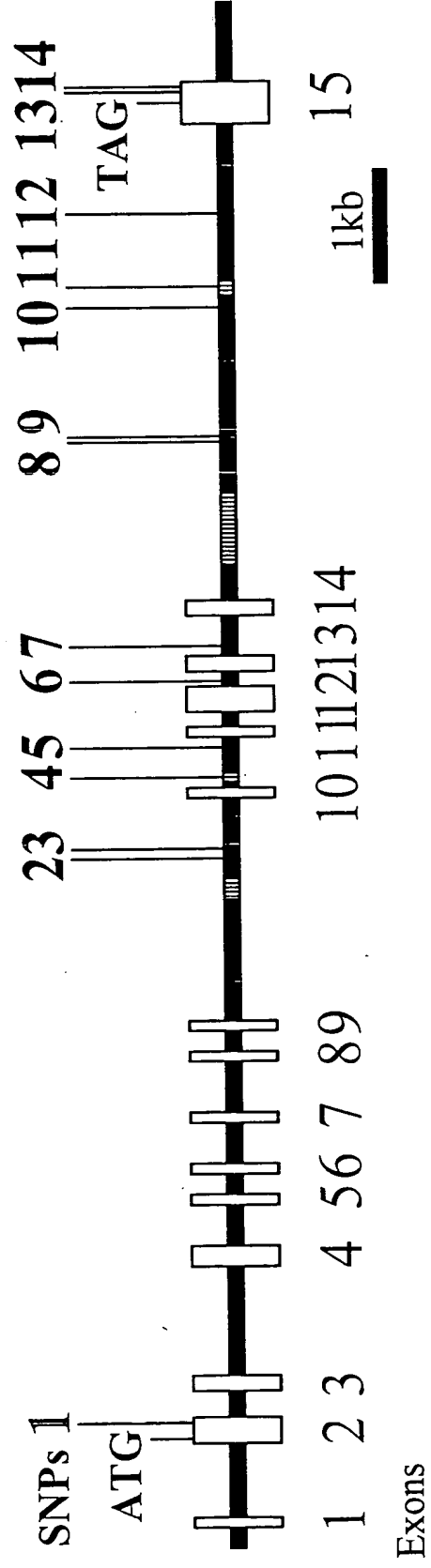


Fig. 143

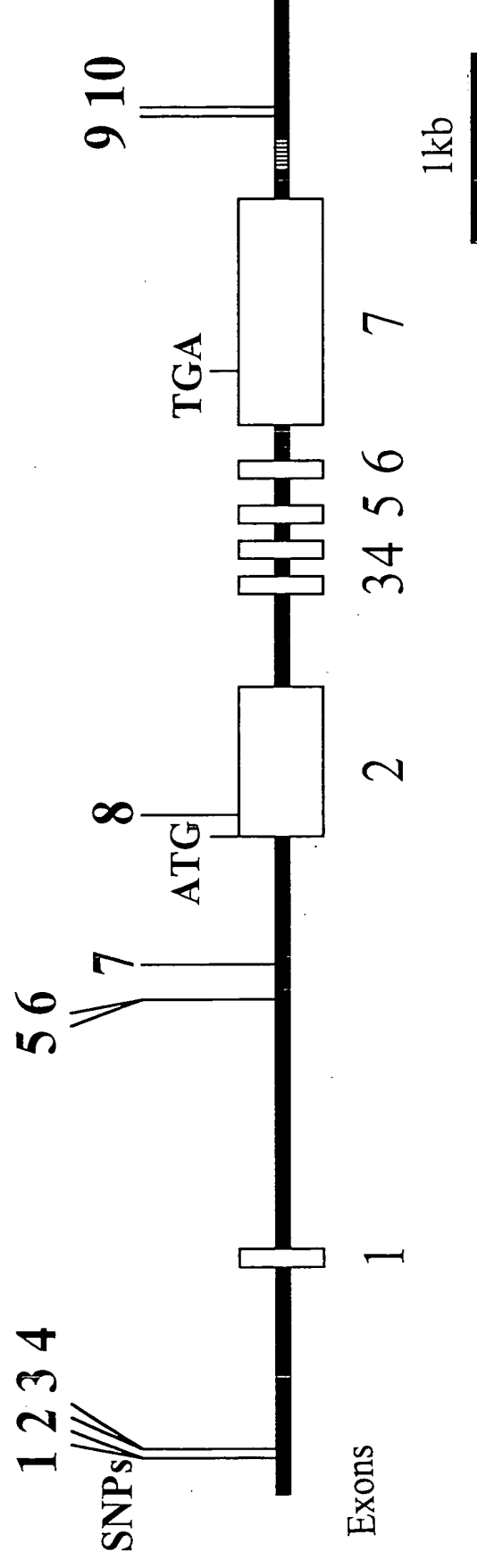


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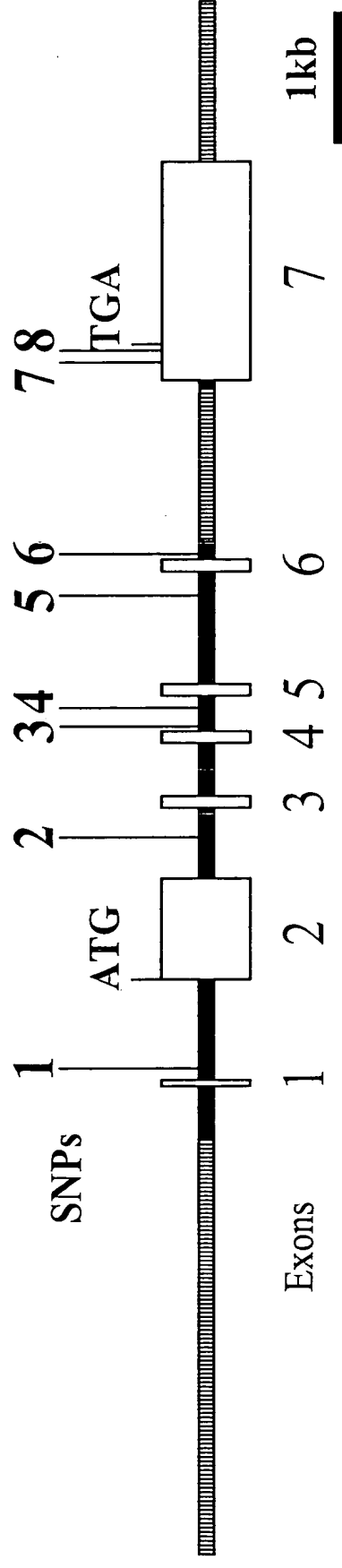


Fig. 145

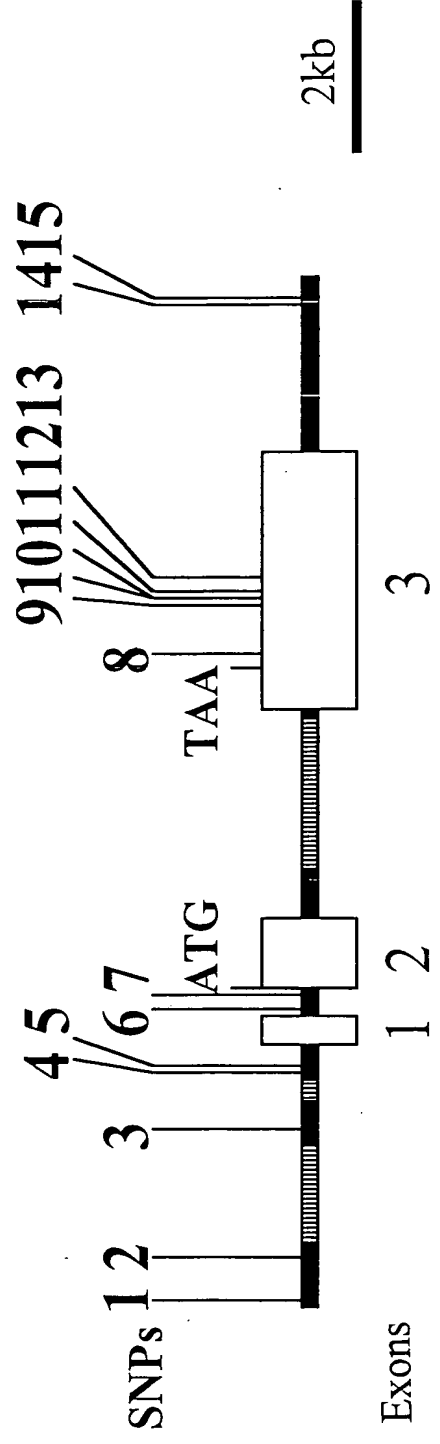


Fig. 146

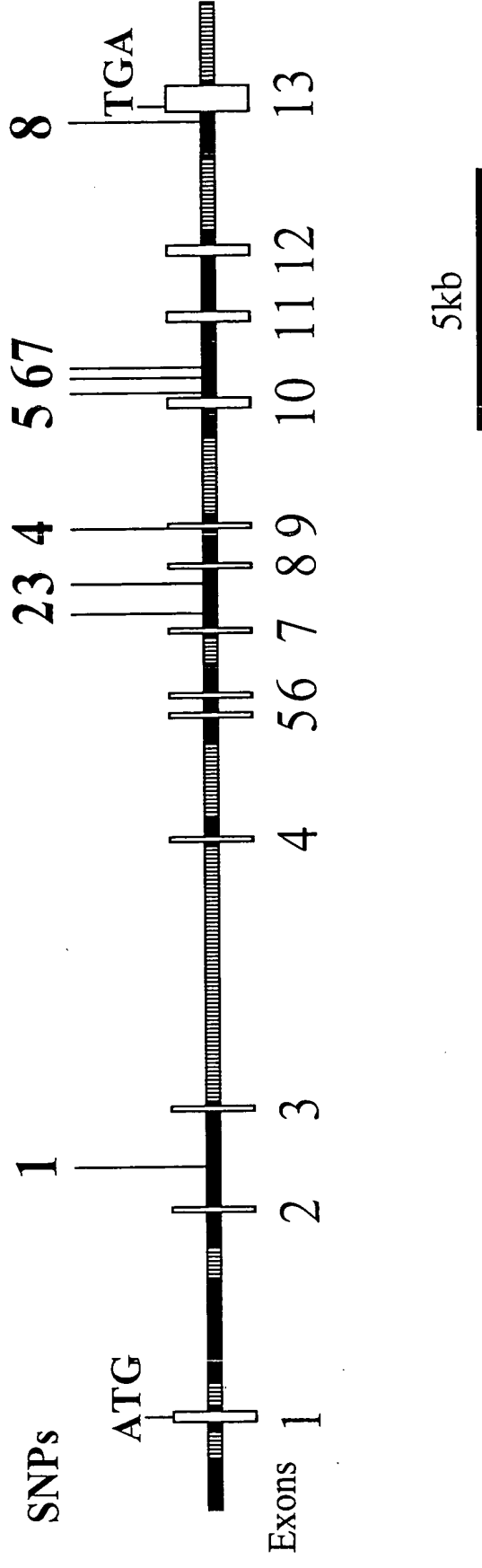


Fig. 147

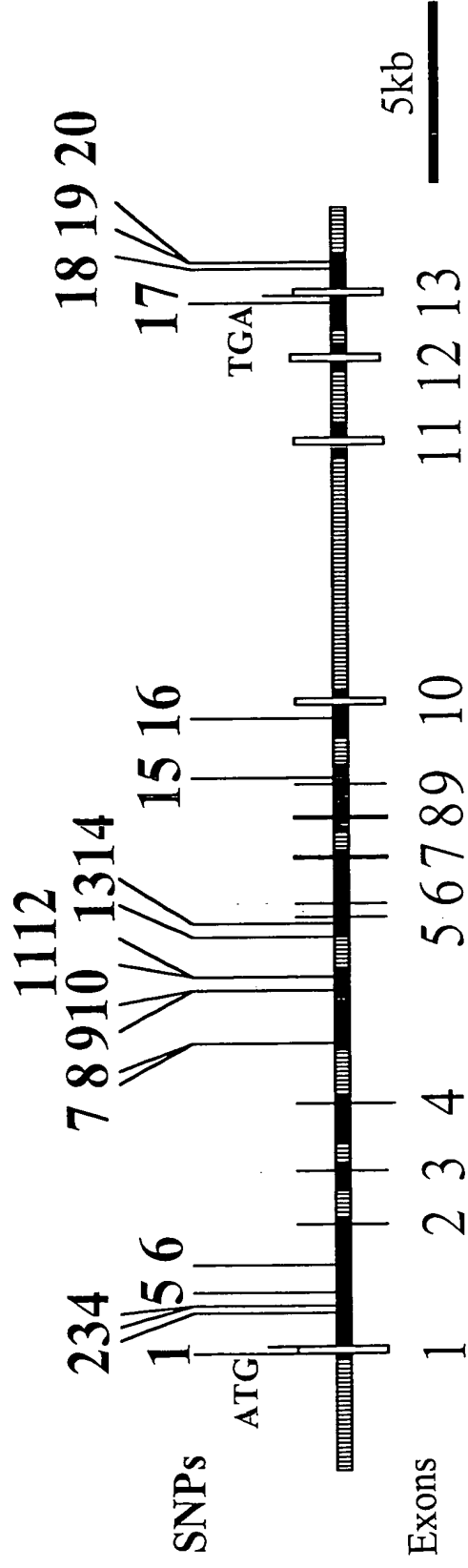


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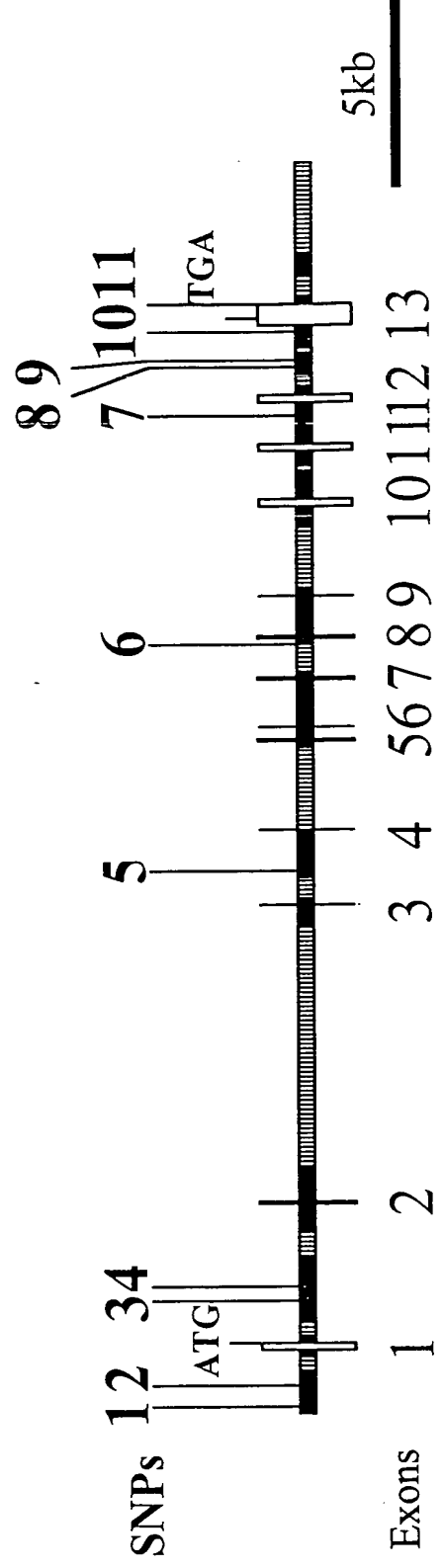


Fig. 149

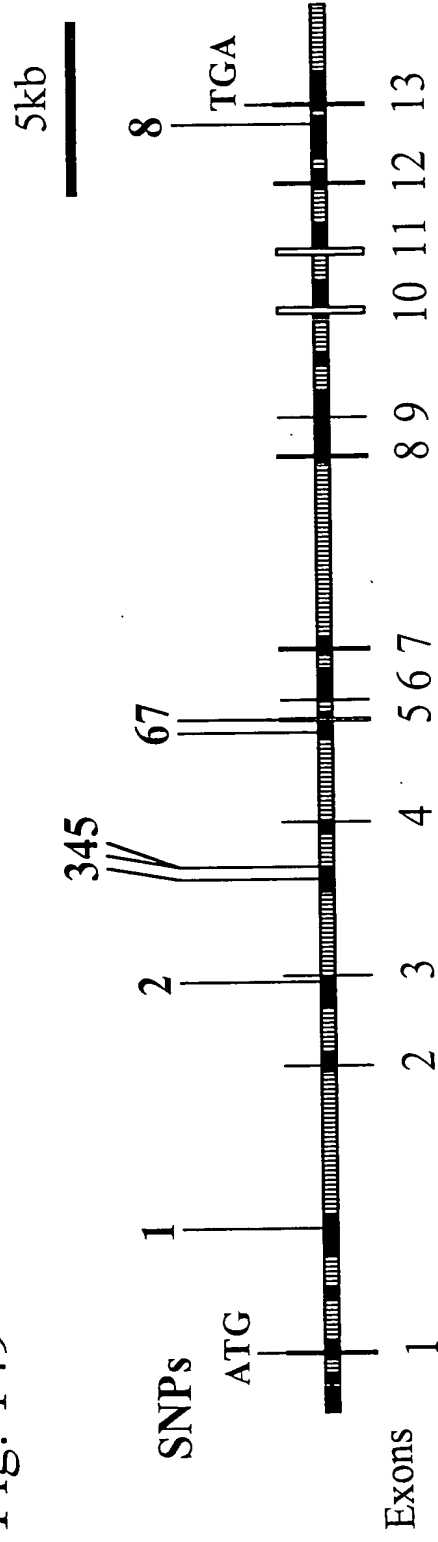


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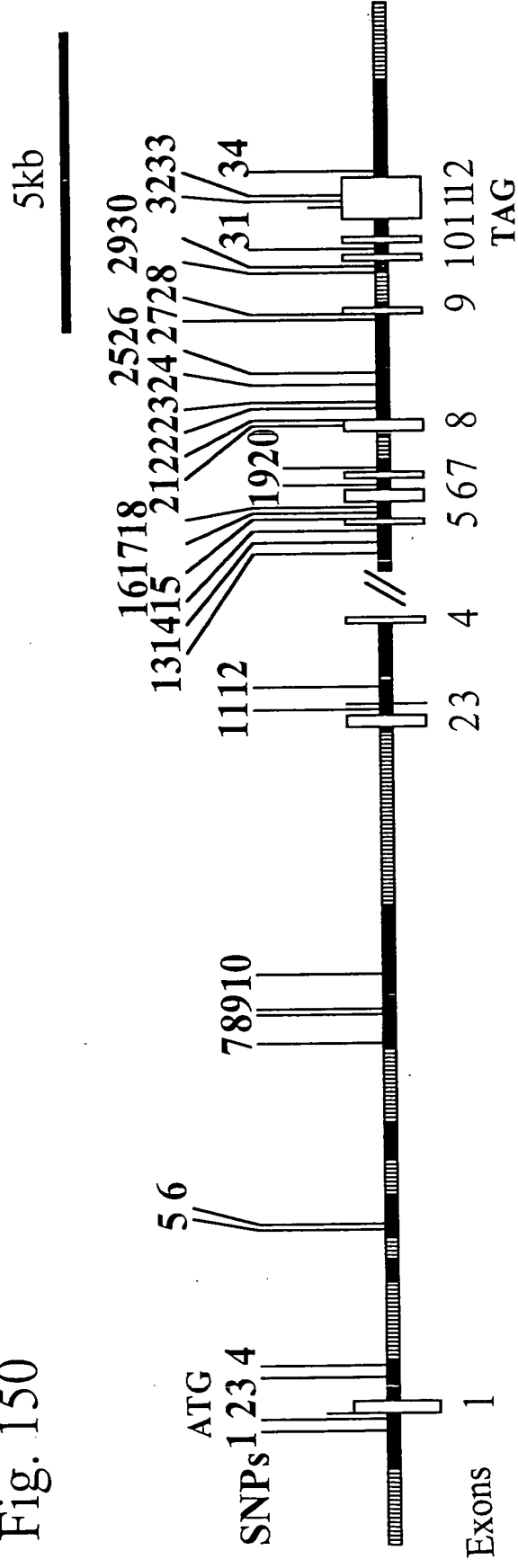


Fig. 151

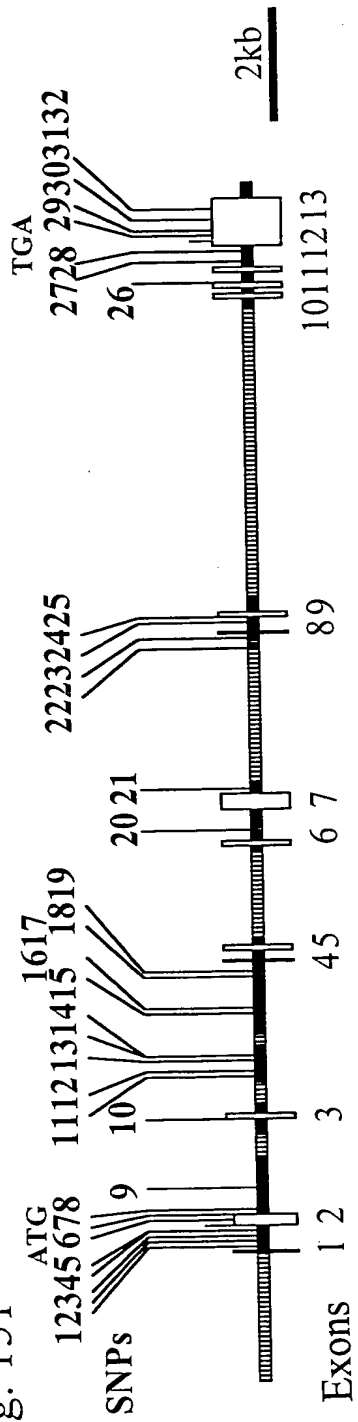


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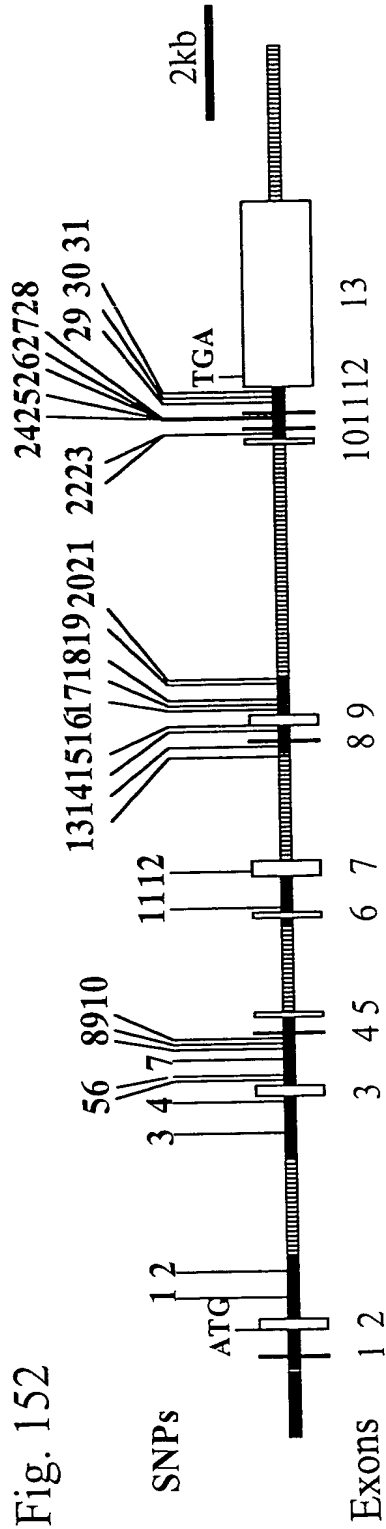


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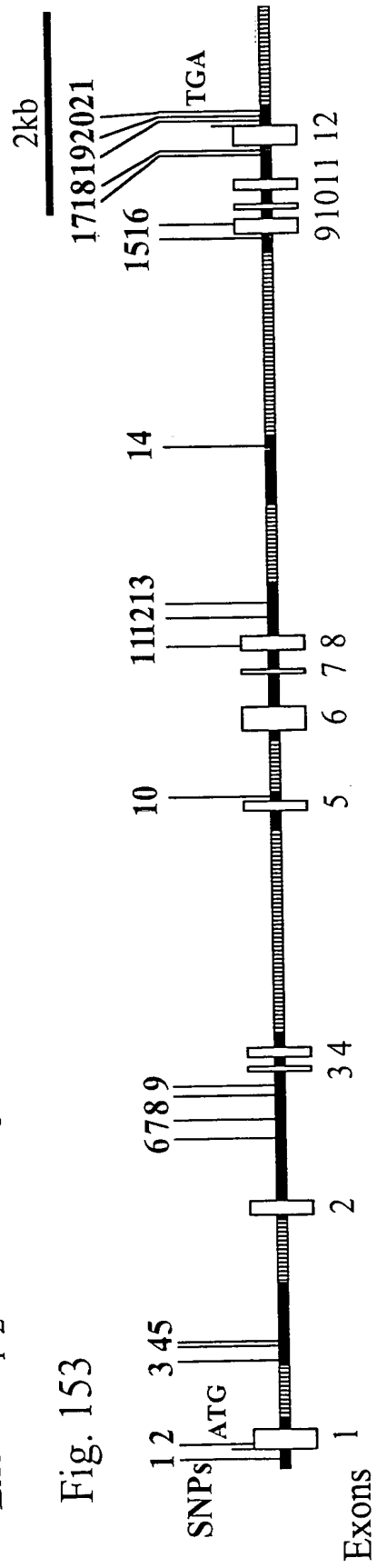


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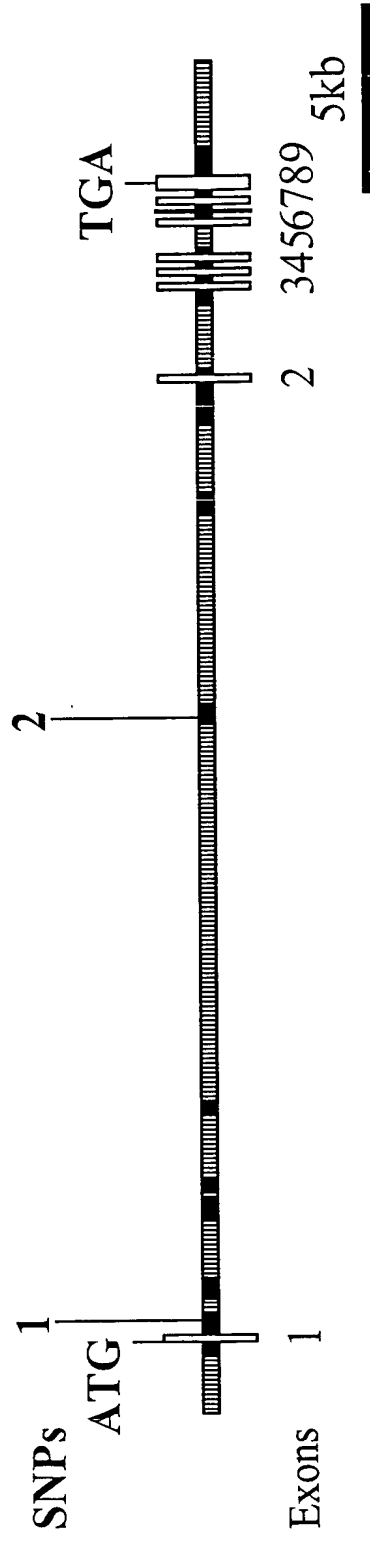


Fig. 155

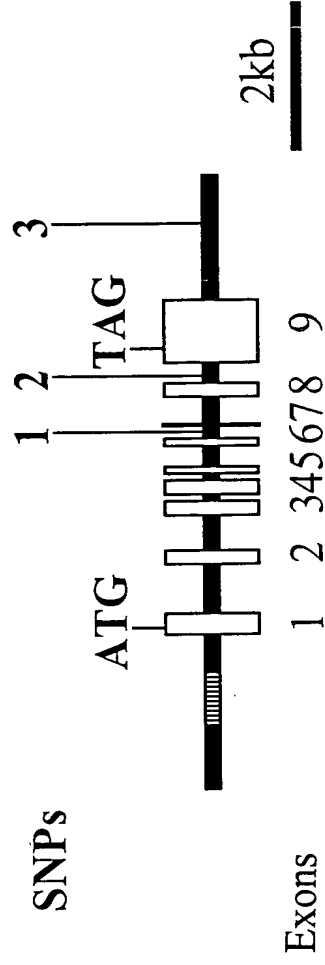


Fig.156

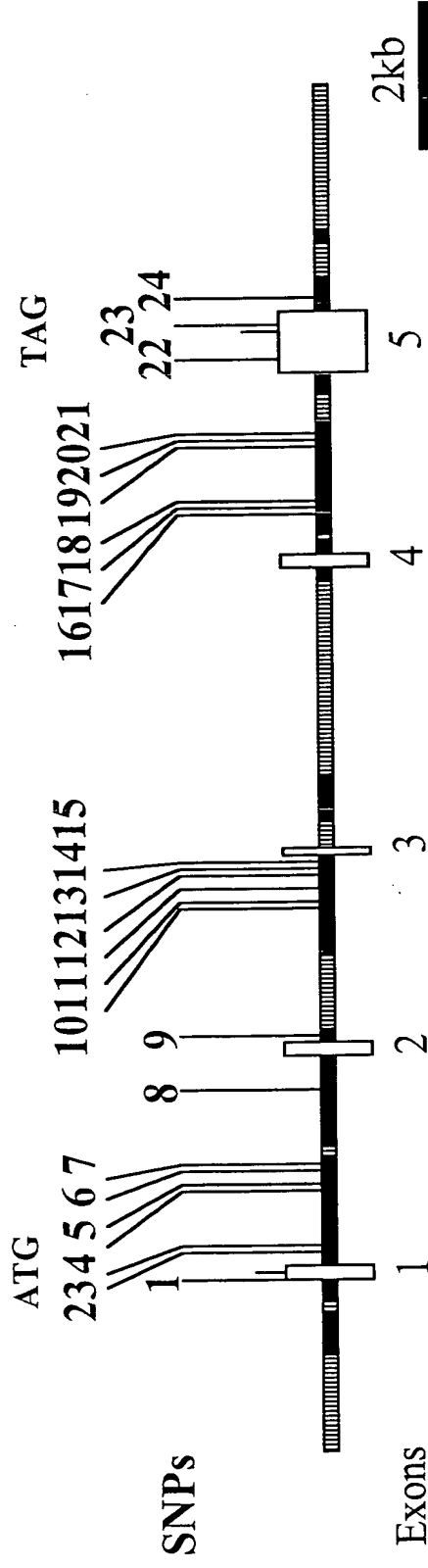


Fig. 157

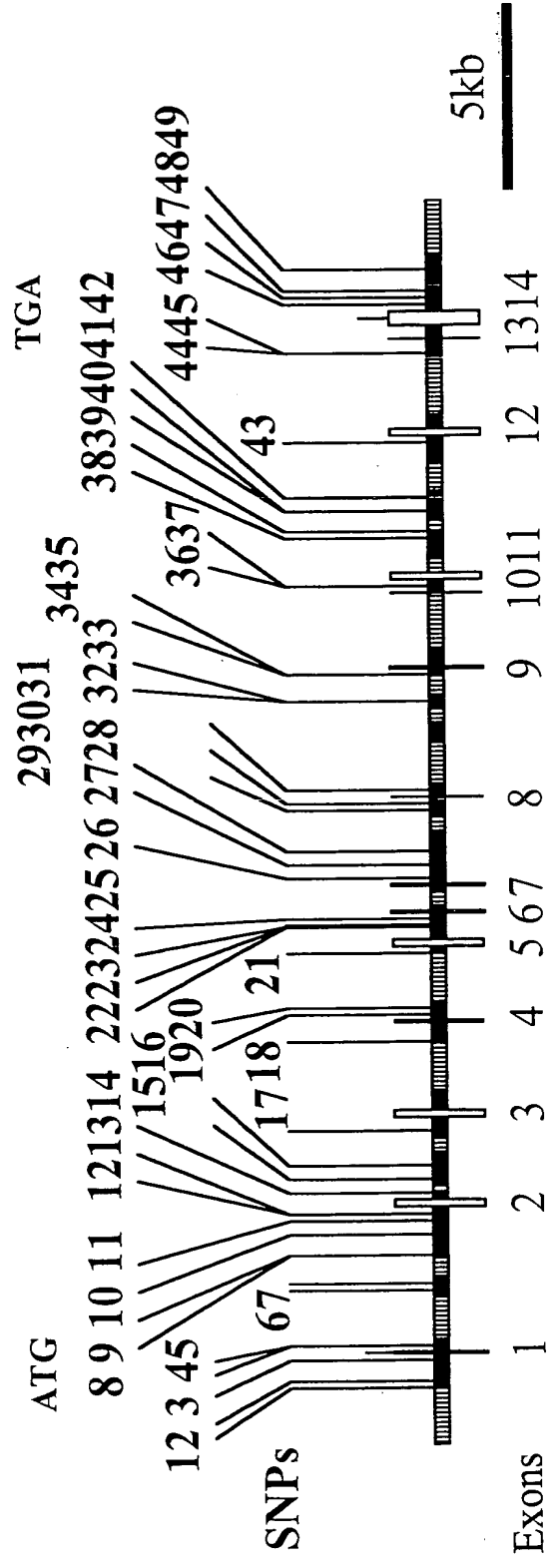


Fig. 158

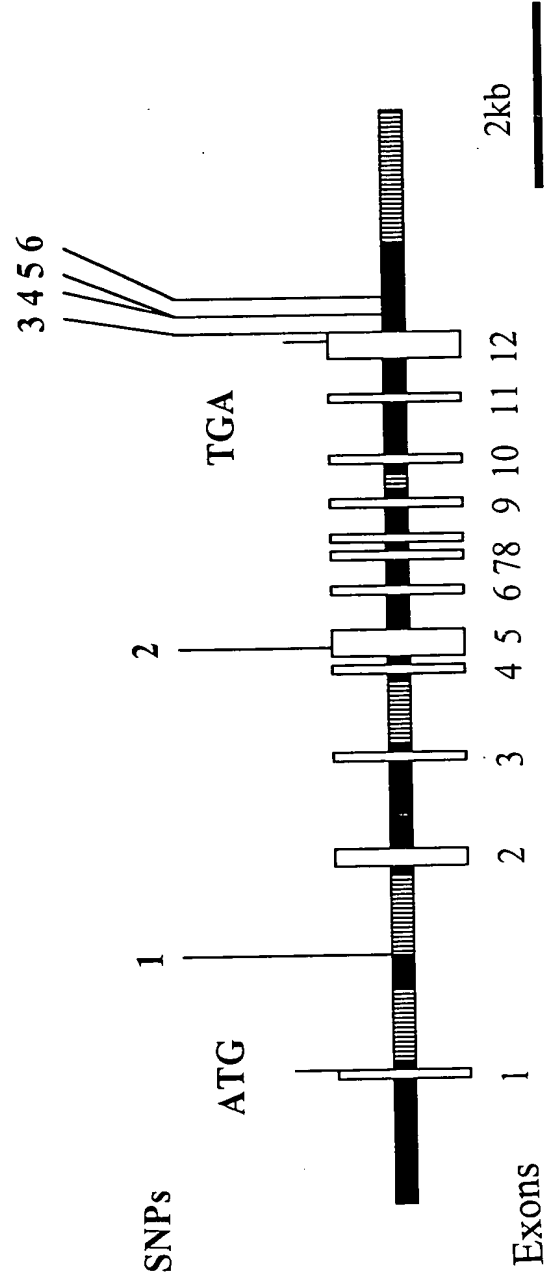


Fig. 159

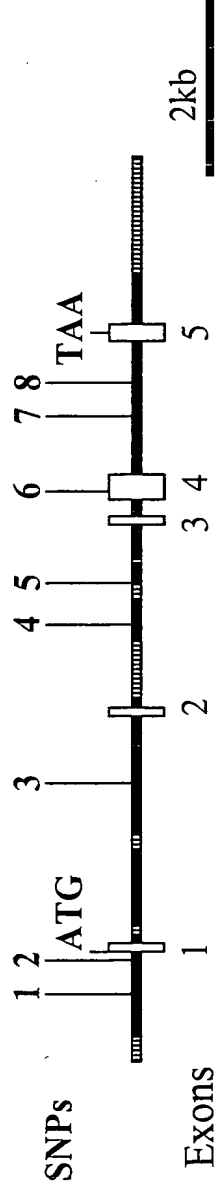


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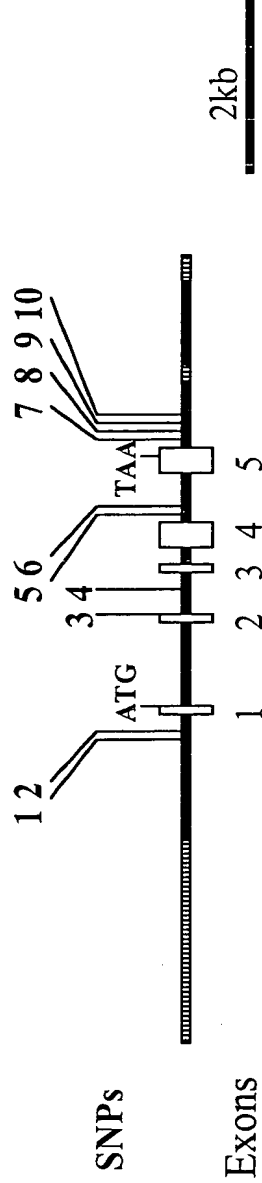


Fig. 161

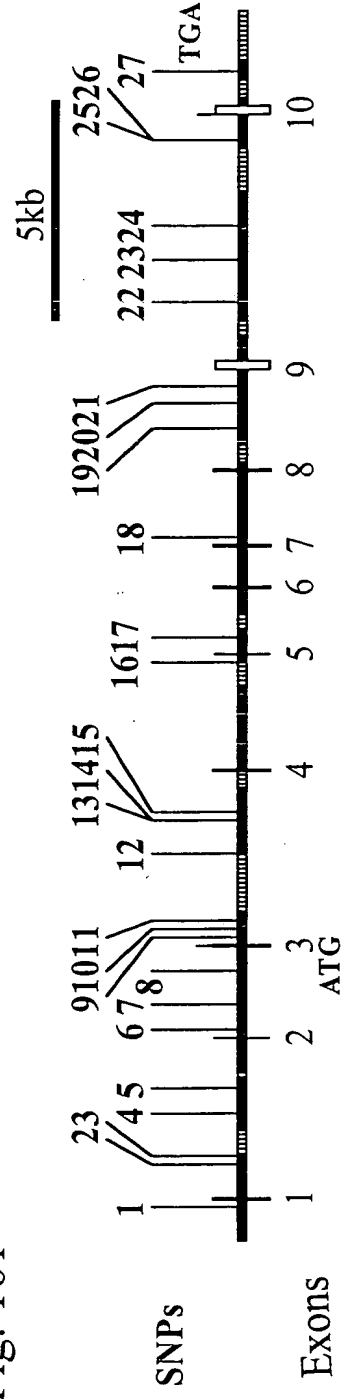


Fig. 162A

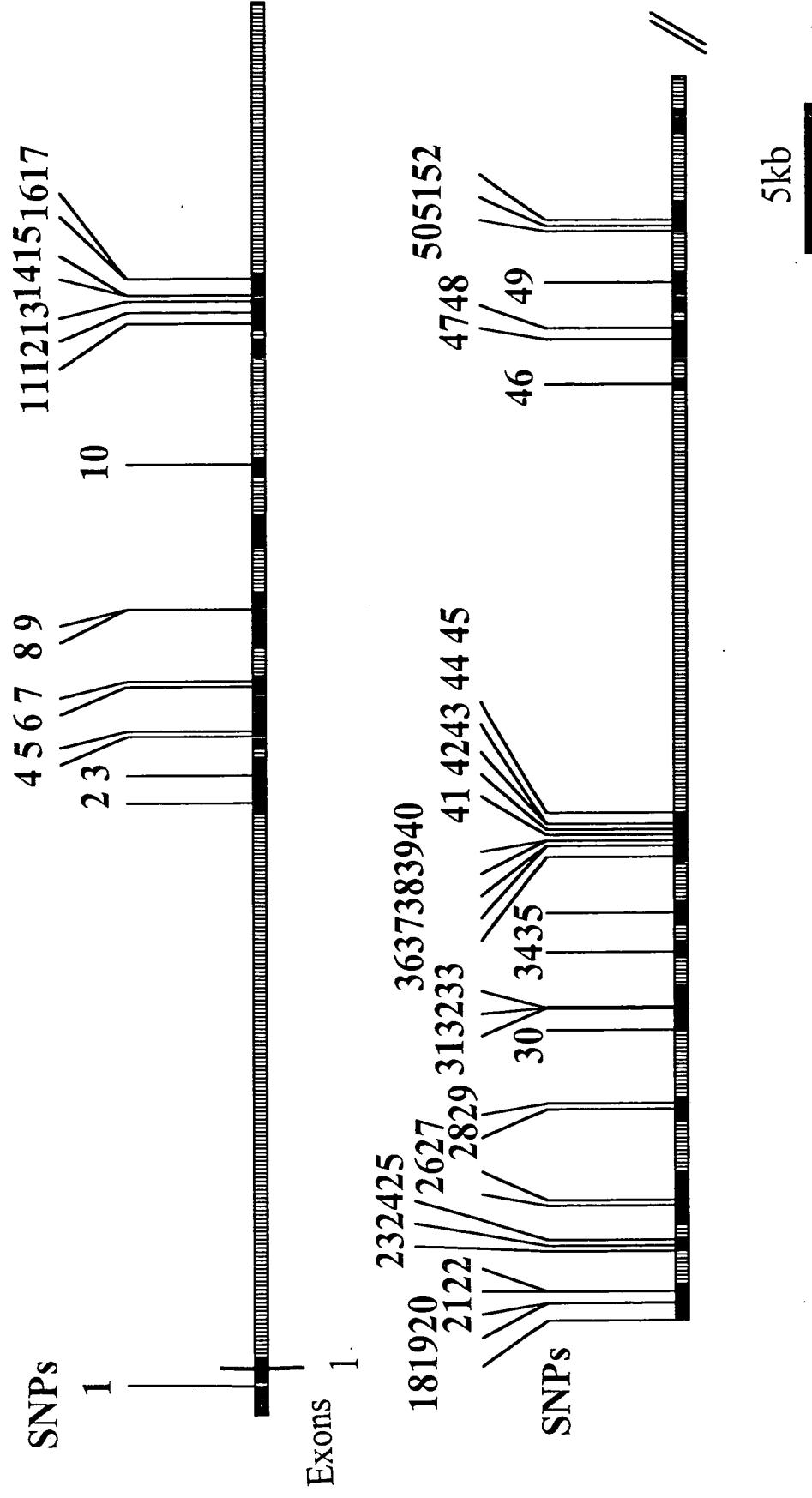


Fig. 162B

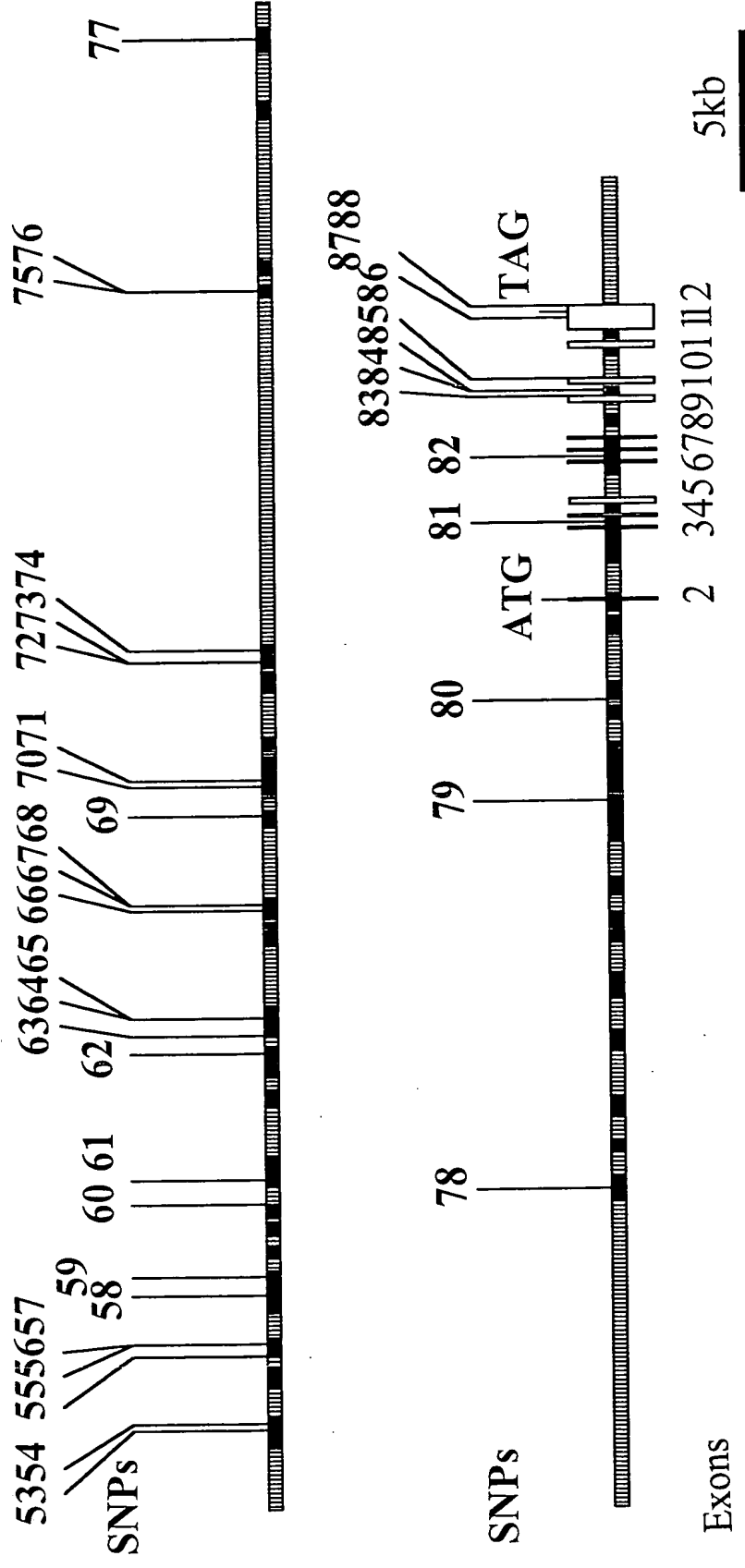


Fig. 163

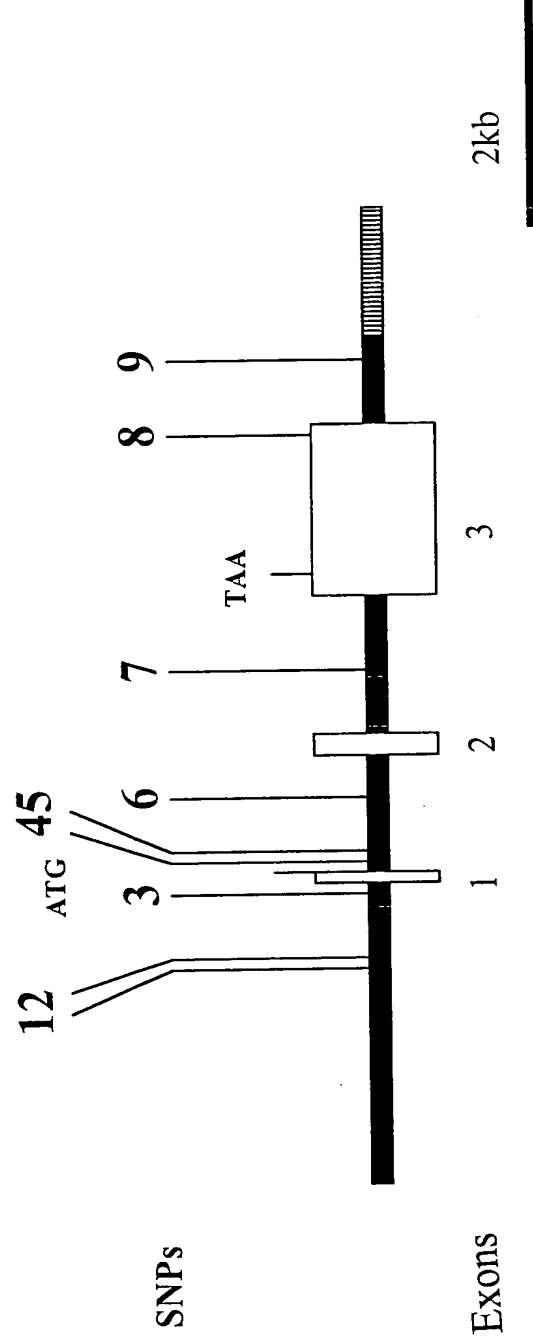


Fig. 164

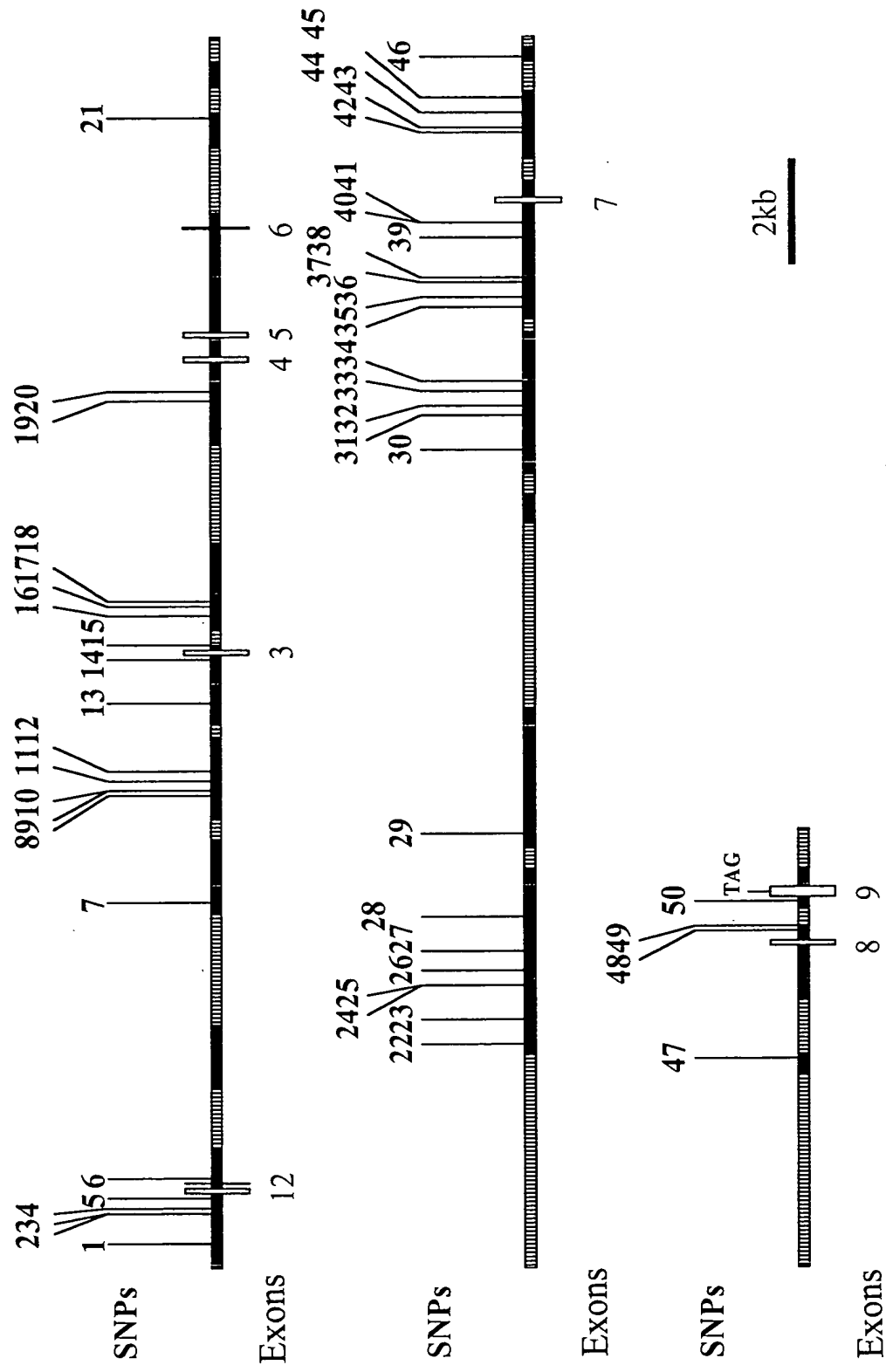


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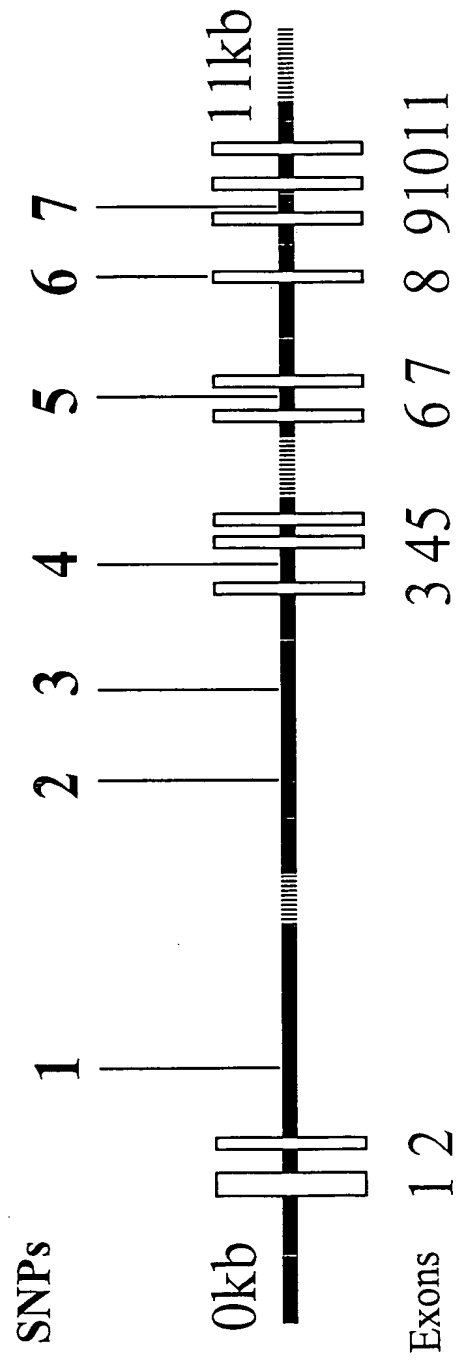


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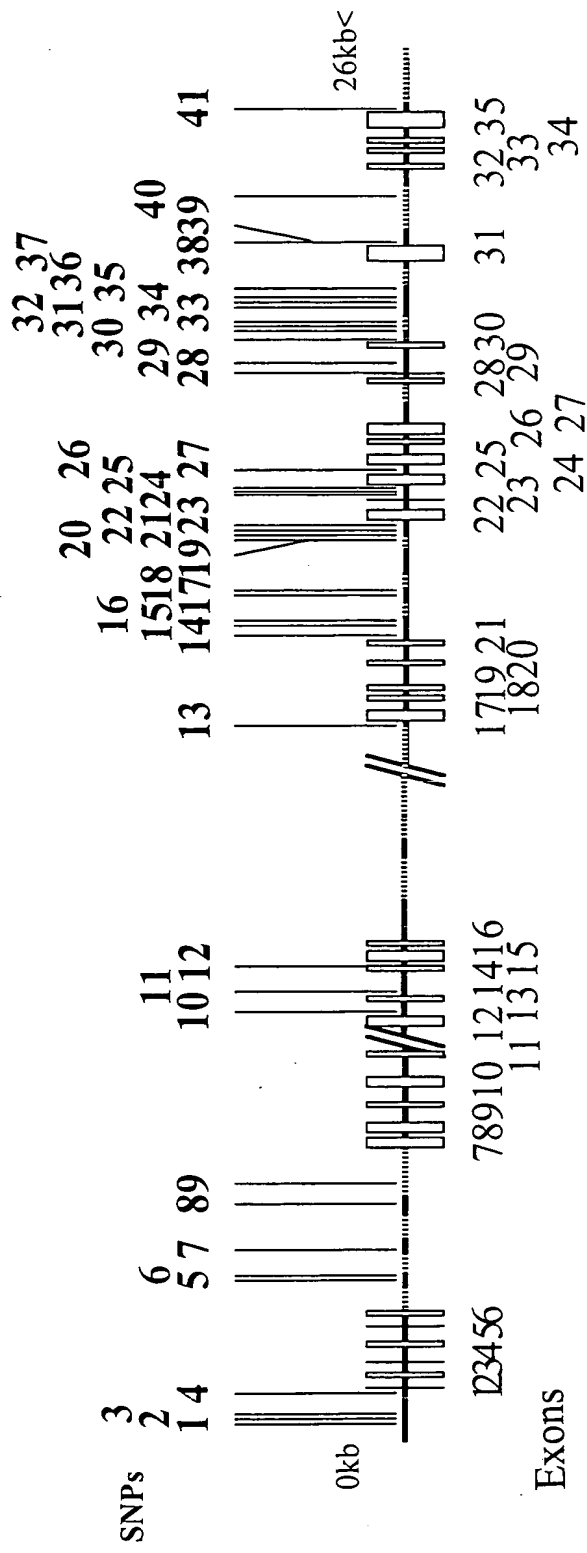


Fig. 167

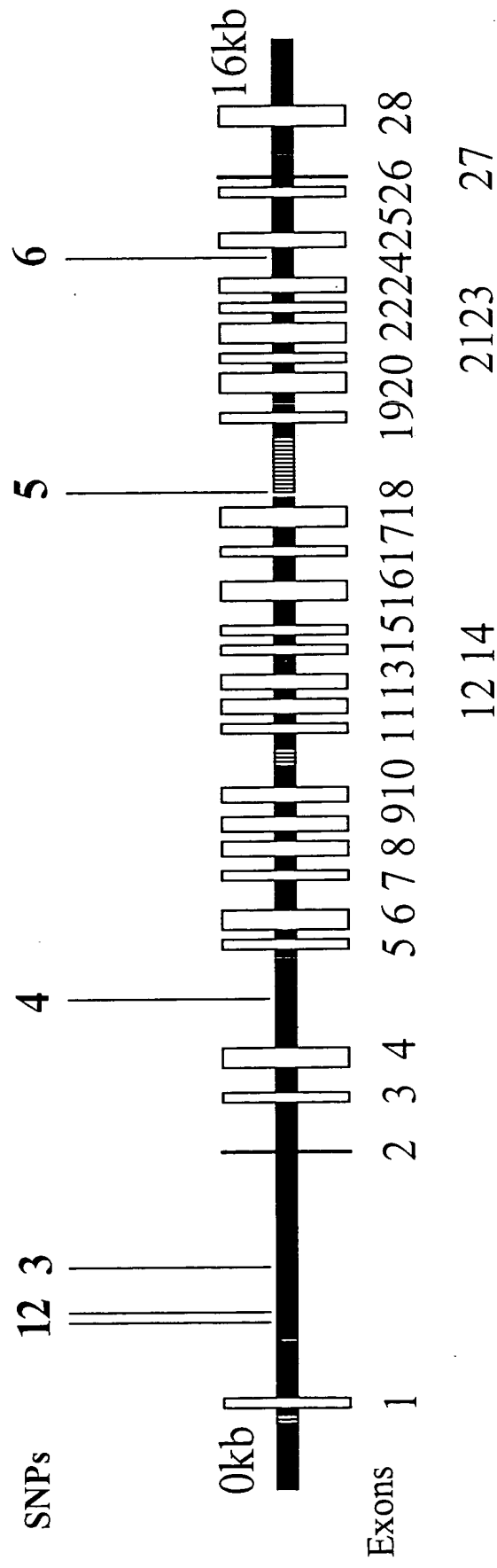


Fig. 168

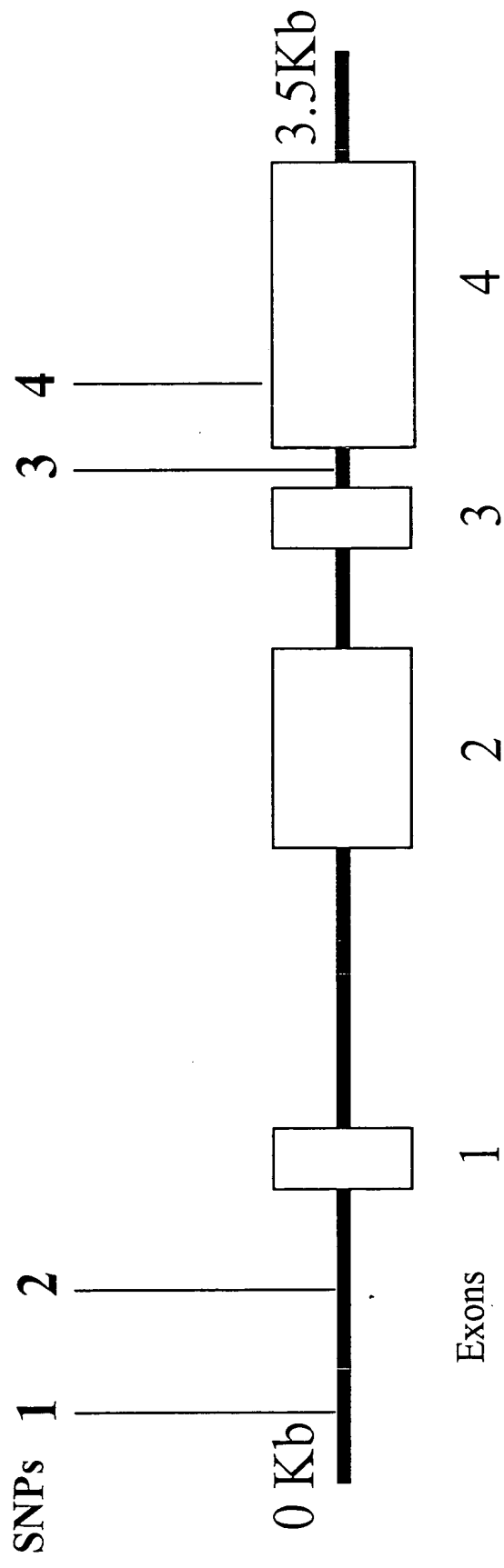


Fig. 169

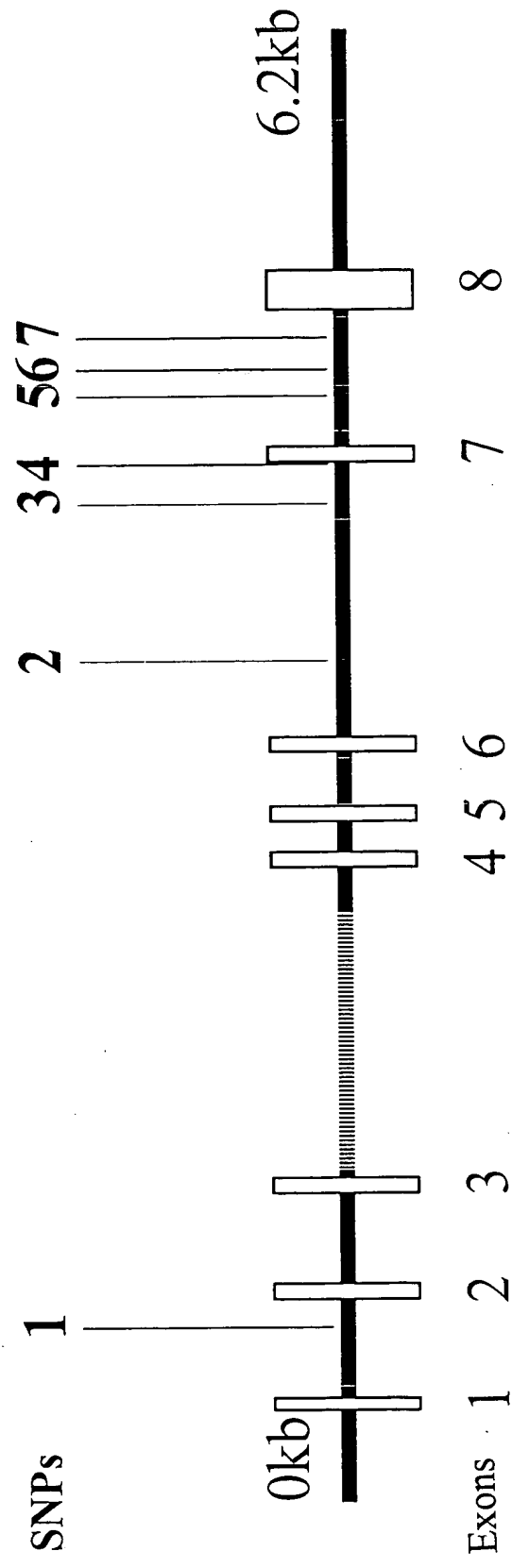


Fig. 170

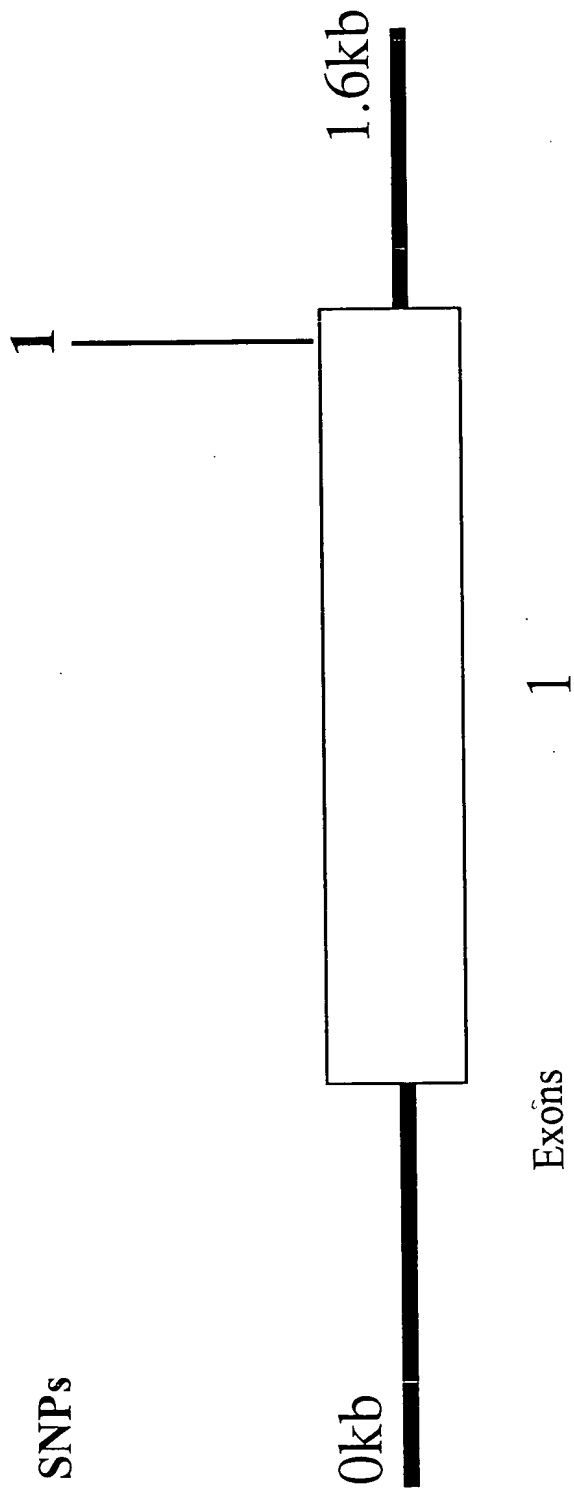


Fig. 171

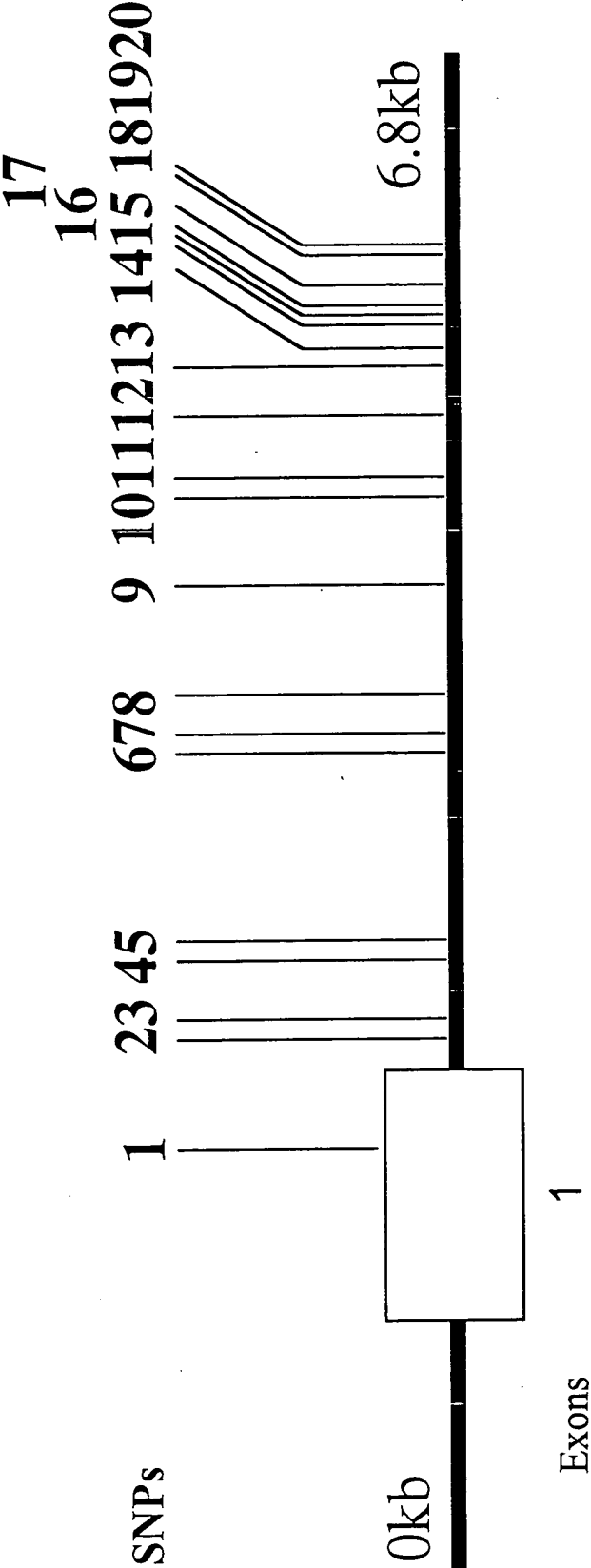


Fig. 172

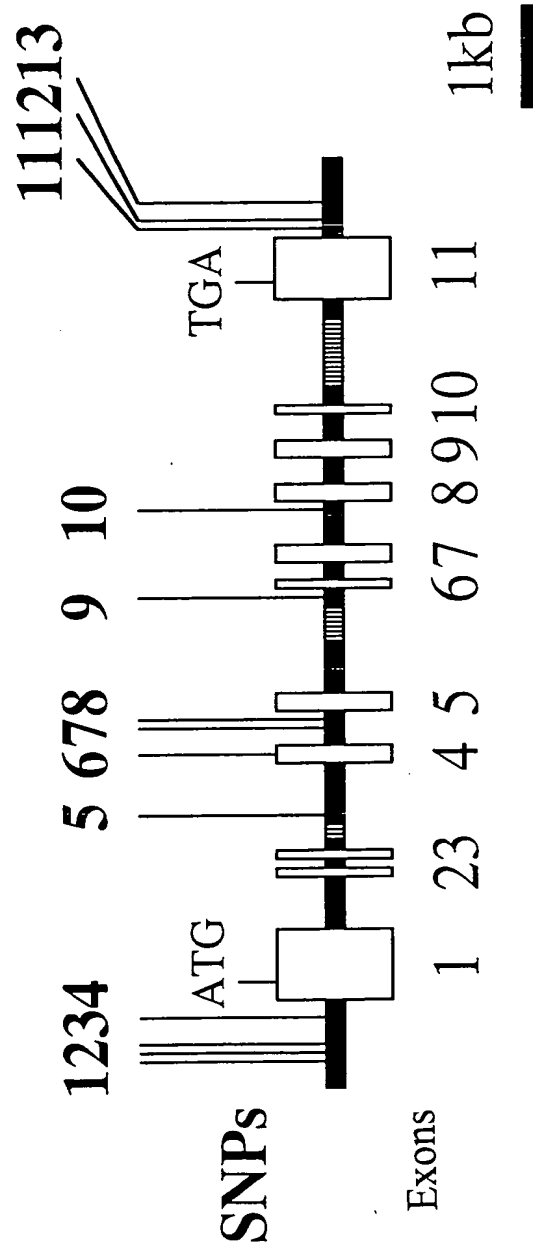


Fig. 173

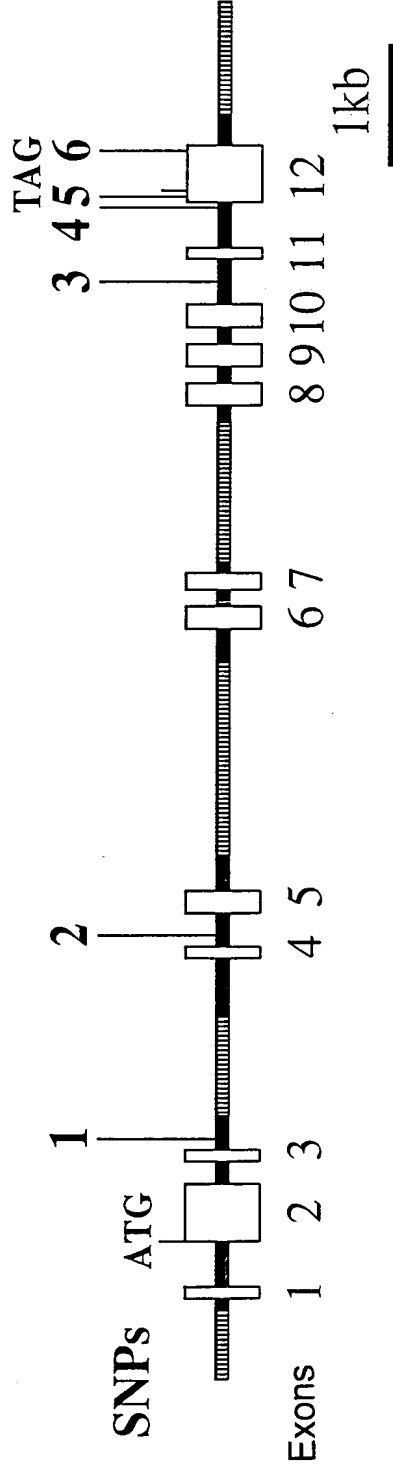


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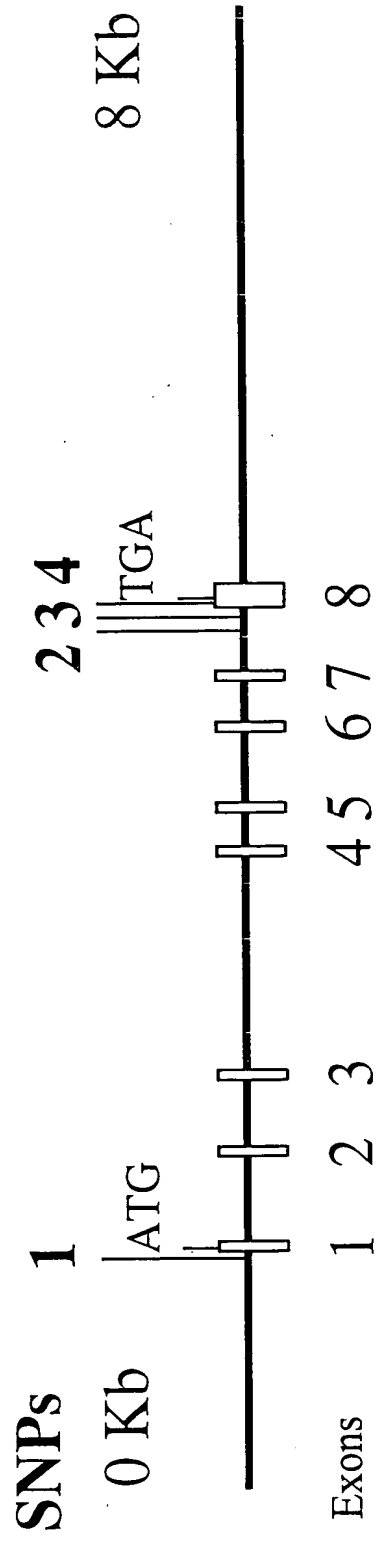


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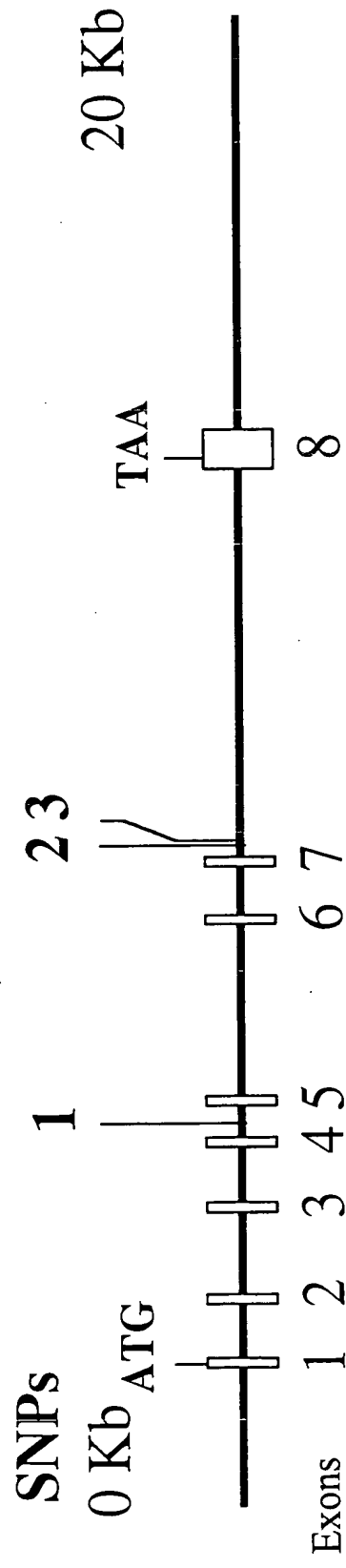


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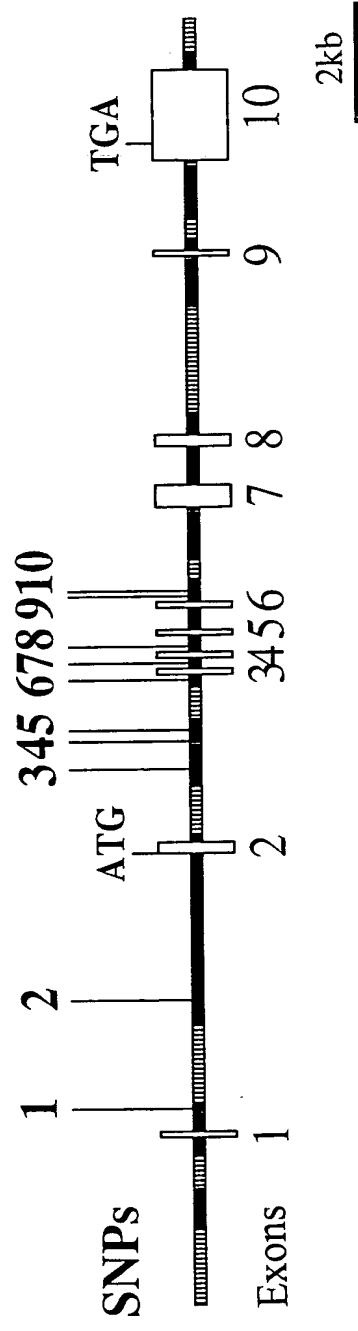


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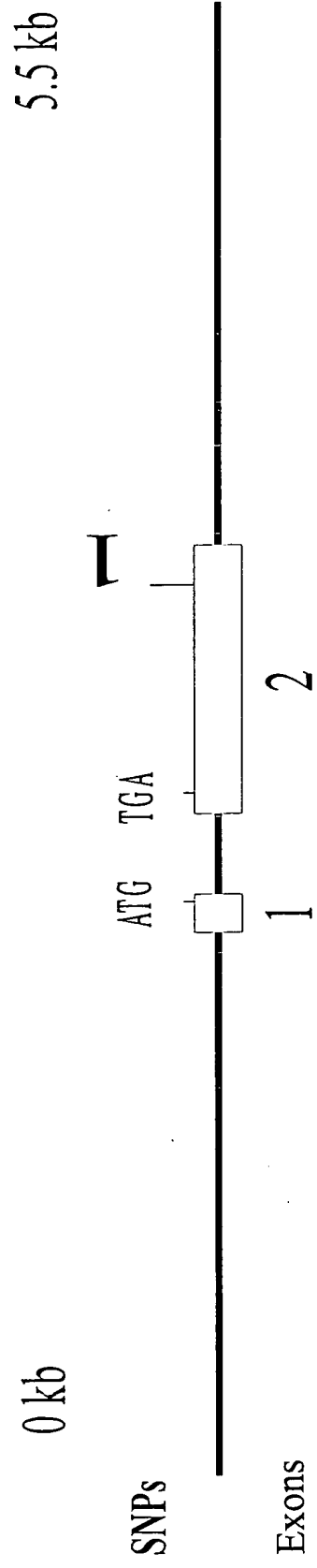
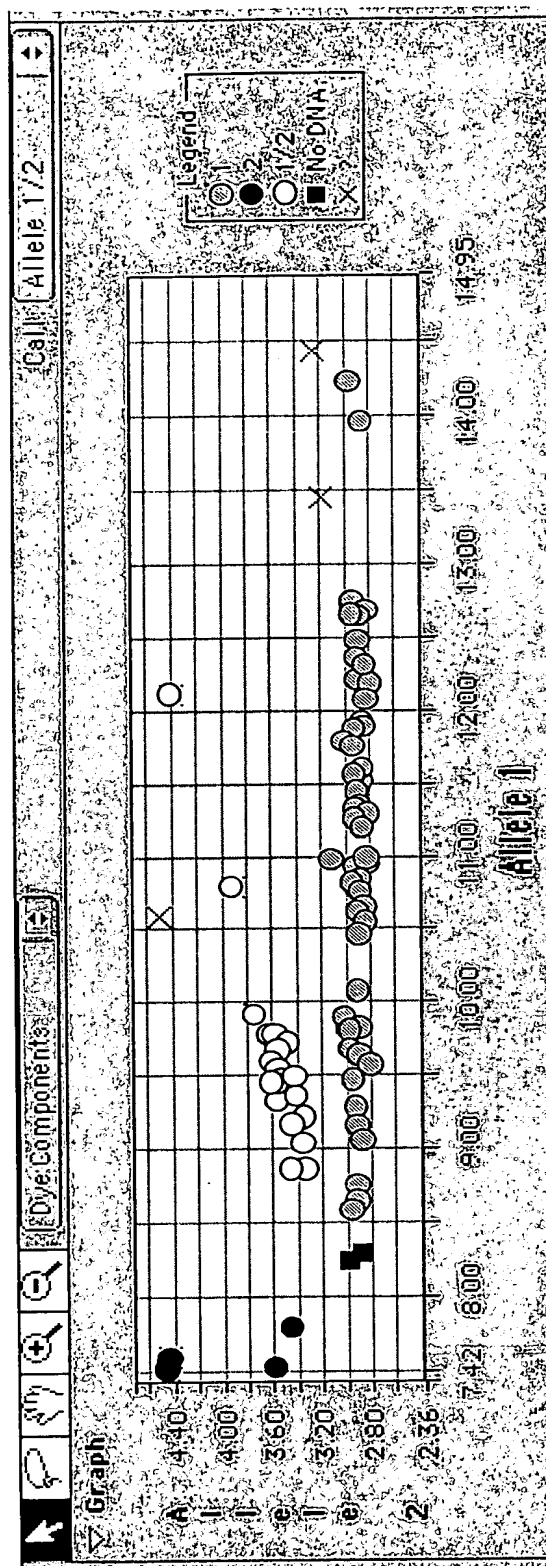
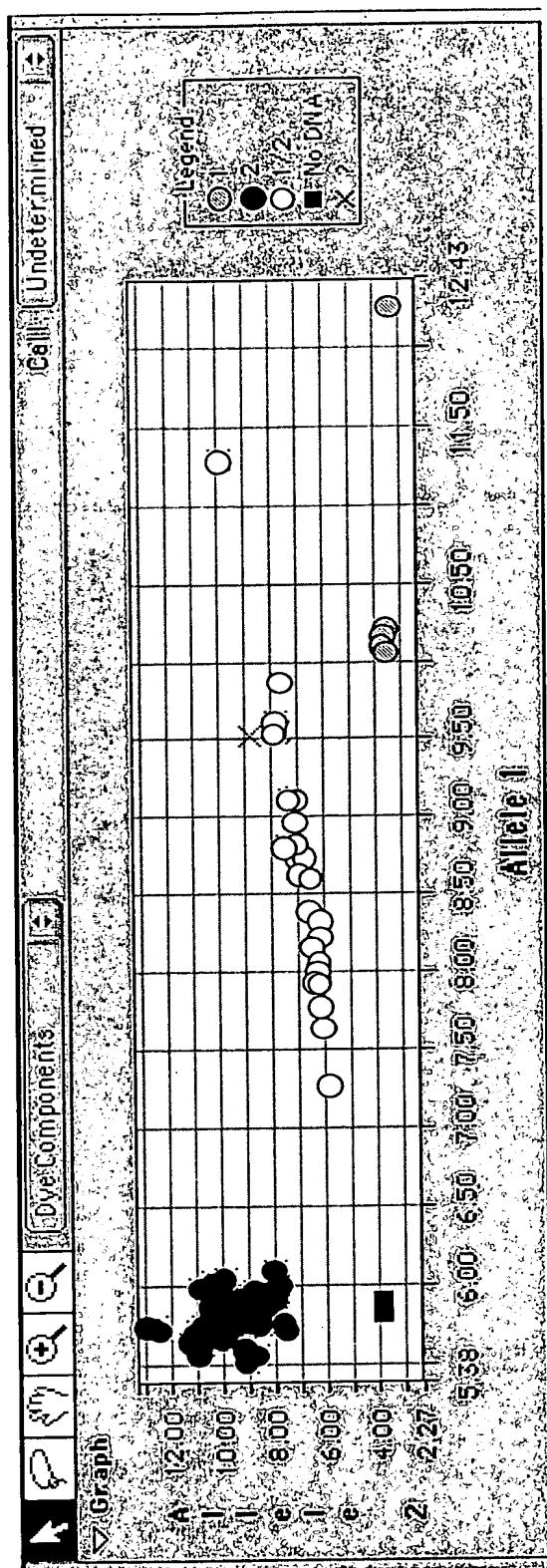


Fig. 178



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【発明の名称】 遺伝子多型の検出方法

【特許請求の範囲】

【請求項 1】 薬物代謝酵素をコードする遺伝子中に存在する遺伝子多型情報から、該遺伝子多型部位を含むように、又は薬物代謝酵素をコードする遺伝子を増幅したときの増幅断片中に前記遺伝子多型部位が含まれるように、オリゴヌクレオチドプローブ及び/又はオリゴヌクレオチドプライマーを作製し、得られるオリゴヌクレオチドプローブ及び/又はオリゴヌクレオチドプライマーを用いて、目的の薬物代謝酵素をコードする遺伝子中の少なくとも 1 個の遺伝子多型を検出することを特徴とする遺伝子多型の検出方法。

【請求項 2】 遺伝子多型部位を含むオリゴヌクレオチドプローブ及び/又はオリゴヌクレオチドプライマーが、その 5' 末端若しくは 3' 末端又は中央の塩基が当該遺伝子多型部位となるように作製されたものである請求項 1 記載の検出方法。

【請求項 3】 遺伝子多型部位を含むオリゴヌクレオチドプローブが、薬物代謝酵素をコードする遺伝子とハイブリダイズし得る断片とハイブリダイズしない断片とが結合したものであって、前記遺伝子多型部位が、当該ハイブリダイズし得る断片の 5' 末端又は 3' 末端である請求項 1 記載の検出方法。

【請求項 4】 遺伝子多型部位を含むオリゴヌクレオチドプローブ及び/又はオリゴヌクレオチドプライマーが、配列番号 1～4309 に示す塩基配列のうち第 21 番目の塩基を含む少なくとも 13 塩基の配列又はこれに相補的な配列を有するものからなる群から選択される少なくとも 1 つである請求項 1～3 のいずれかに記載の検出方法。

【請求項 5】 遺伝子多型が、一塩基多型、複数個の塩基の欠失、置換若しくは挿入による多型、又は VNTR 若しくはマイクロサテライトによる多型である請求項 1～4 のいずれかに記載の検出方法。

【請求項 6】 請求項 1～5 のいずれかの方法により得られた検出結果から、当該薬物代謝酵素によって代謝される薬物の有効性及び安全性を評価することを特徴とする薬物の評価方法。

【請求項 7】 請求項 6 記載の評価方法により得られた評価を指標として、使用すべき薬物を選択することを特徴とする薬物のスクリーニング方法。

【請求項 8】 薬物代謝酵素をコードする遺伝子中に含まれる遺伝子多型情報と、被験者から採取した当該薬物代謝酵素をコードする遺伝子の遺伝子多型情報とを比較して、当該薬物代謝酵素によって代謝される薬物の有効性及び/又は安全性を解析し、得られる解析結果から使用すべき薬物を選択することを特徴とする薬物のスクリーニング方法。

【請求項 9】 遺伝子多型情報が表 1 に示されるものである請求項 1～8 のいずれかに記載の方法。

【請求項 10】 薬物代謝酵素が、エポキシドヒドロラーゼ、メチルトランスフェラーゼ、N-アセチルトランスフェラーゼ、スルホトランスフェラーゼ、キノンオキシドレダクターゼ、グルタチオン-S-トランスフェラーゼ、UDP-グリコシルトランスフェラーゼ、アルデヒドデヒドロゲナーゼ、アルコールデヒドロゲナーゼ、エステラーゼ、NDUF、チトクローム p450 (CYP) 及び ATP-結合カセット/トランスポーターからなる群から選択される少なくとも 1 つである請求項 1～9 のいずれかに記載の方法。

【請求項 11】 配列番号 1～4309 に示される塩基配列又はこれに相補的な塩基配列からなる群から選択されるオリゴヌクレオチド。

【請求項 12】 薬物代謝酵素をコードする遺伝子中に存在する遺伝子多型情報から、該遺伝子多型部位を含むように作製されたオリゴヌクレオチド。

【請求項 13】 オリゴヌクレオチドの 5' 末端若しくは 3' 末端又は中央の塩基が、当該遺伝子多型部位となるように作製されたものである請求項 12 記載のオリゴヌクレオチド。

【請求項 14】 遺伝子多型部位を含むオリゴヌクレオチドが、薬物代謝酵素をコードする遺伝子とハイブリダイズし得る断片とハイブリダイズしない断片とが結合したものであって、前記遺伝子多型部位が、当該ハイブリダイズし得る断片の 5' 末端又は 3' 末端である請求項 12 記載のオリゴヌクレオチド。

【請求項 15】 オリゴヌクレオチドが、配列番号 1～4309 に示すいずれかの塩基配列のうち第 21 番目の塩基を含む少なくとも 13 塩基の配列又はこれに相補

的な配列を有するものである請求項12～14のいずれかに記載のオリゴヌクレオチド。

【請求項 1 6】 請求項11～15のいずれかに記載のオリゴヌクレオチドを含む遺伝子多型検出用キット。

【発明の詳細な説明】

【 0 0 0 1】

【発明の属する技術分野】

本発明は、遺伝子多型情報、遺伝子多型情報の検出方法、遺伝子多型を用いた薬物の評価方法、及び薬物のスクリーニング方法に関する。

【 0 0 0 2】

【従来の技術】

ヒトの姿形が千差万別であるように、30億からなる遺伝暗号も個人間で比較するとかなり多くの部位で異なっている。この遺伝暗号の違いを遺伝子多型（ポリモルフィズム）と呼んでおり、代表的な遺伝子多型として一塩基多型が知られている。

【 0 0 0 3】

一塩基多型（SNP:single nucleotide polymorphism）とは、個人間における1遺伝暗号の違いを意味する。ヒトの顔貌や体型が千差万別であるように、遺伝暗号である塩基配列も一人ひとりかなり多くの部位で異なっている。SNPは、その存在する位置によってcSNP(coding SNP)とgSNP(genome SNP)に分類され、cSNPには、さらにsSNP(silent SNP)、rSNP(regulatory SNP)及びiSNP(intron SNP)が含まれる。

【 0 0 0 4】

上記SNPは、多型マーカーとしての疾患の発症や増悪に関連する遺伝子を見つけるために有用であり、最終的に臨床分野において疾患のリスク診断や薬剤の使い分けなどに直接関係する。また、疾患の原因となっている物質を標的分子とした証拠に基づく薬剤開発は、世界的趨勢となっている。ある疾患に対して薬剤を投与した場合、患者の応答性は様々であり、著効を示すもの、有効性の低いもの、全く効果を示さないもののよう、薬剤に対する応答性には大きな違いがある

。これは、症状が同じで同じ診断名であっても、その背景となっている疾患を起こしている経路が異なっていたり、あるいは薬剤の代謝速度が大きく異なっている可能性があるからである。従って、SNPなど遺伝子多型を参考にしながら、目的の疾患に応じた薬物の選択、治療法の開発（いわゆるオーダーメイド医療）が望まれる。

【0005】

薬剤に対する応答性に加えて、時には致命的となるような強い副作用の問題も、医療従事者が対処していかなければならない大きな問題の一つである。これは、処方ミスなどによる過剰投与がなくても、時には思わぬ致命的な副作用に遭遇することがある。従って、薬剤の応答性に対しては、薬剤の代謝、薬剤の輸送、薬剤のレセプターなどによる薬剤応答性や副作用の強さを、SNPなどの遺伝子多型を参考にしながら決定することが望まれる。

【0006】

【発明が解決しようとする課題】

本発明は、遺伝子多型情報の検出方法とその情報に基づく薬物の有効性並びに安全性を評価するための方法、及び薬物のスクリーニング方法を提供することを目的とする。

【0007】

【課題を解決するための手段】

本発明者は、上記課題を解決するため鋭意研究を行った結果、薬物代謝酵素をコードする遺伝子中の遺伝子多型を見出し、これを用いて薬物と疾患との因果関係を評価することに成功し、本発明を完成するに至った。

【0008】

すなわち、本発明は以下の通りである。

(1) 薬物代謝酵素をコードする遺伝子中に存在する遺伝子多型情報から、該遺伝子多型部位を含むように、又は薬物代謝酵素をコードする遺伝子を増幅したときの増幅断片中に前記遺伝子多型部位が含まれるように、オリゴヌクレオチドプローブ及び/又はオリゴヌクレオチドプライマーを作製し、得られるオリゴヌクレオチドプローブ及び/又はオリゴヌクレオチドプライマーを用いて、目的の薬物

代謝酵素をコードする遺伝子中の少なくとも1個の遺伝子多型を検出することを特徴とする遺伝子多型の検出方法。

【0009】

遺伝子多型部位を含むオリゴヌクレオチドプローブ及び/又はオリゴヌクレオチドプライマーとしては、その5'末端若しくは3'末端又は中央の塩基が当該遺伝子多型部位となるように作製されたものが挙げられる。また、薬物代謝酵素をコードする遺伝子とハイブリダイズし得る断片とハイブリダイズしない断片とが結合したものであって、前記遺伝子多型部位が、当該ハイブリダイズし得る断片の5'末端又は3'末端であるものも、遺伝子多型部位を含むオリゴヌクレオチドプローブに含まれる。さらに、配列番号1～4309に示す塩基配列のうち第21番目の塩基を含む少なくとも13塩基の配列又はこれに相補的な配列を有するものからなる群から選択される少なくとも1つのヌクレオチドも、遺伝子多型部位を含むオリゴヌクレオチドプローブ及び/又はオリゴヌクレオチドプライマーに含まれる。上記遺伝子多型としては、一塩基多型、複数個の塩基の欠失、置換若しくは挿入による多型、又はVNTR若しくはマイクロサテライトによる多型が挙げられる。

【0010】

- (2) 前記検出方法により得られた検出結果から、当該薬物代謝酵素によって代謝される薬物の有効性及び安全性を評価することを特徴とする薬物の評価方法。
- (3) 前記評価方法により得られた評価を指標として、使用すべき薬物を選択することを特徴とする薬物のスクリーニング方法。
- (4) 薬物代謝酵素をコードする遺伝子中に含まれる遺伝子多型情報と、被験者から採取した当該薬物代謝酵素をコードする遺伝子の遺伝子多型情報とを比較して、当該薬物代謝酵素によって代謝される薬物の有効性及び/又は安全性を解析し、得られる解析結果から使用すべき薬物を選択することを特徴とする薬物のスクリーニング方法。

【0011】

上記検出方法、評価方法又はスクリーニング方法において、遺伝子多型情報としては、表1に示されるものを、また、薬物代謝酵素としては、エポキシドヒドロラーゼ、メチルトランスフェラーゼ、N-アセチルトランスフェラーゼ、スル

ホトランスフェラーゼ、キノンオキシドレダクターゼ、グルタチオン-S-トランスフェラーゼ、UDP-グリコシルトランスフェラーゼ、アルデヒドデヒドロゲナーゼ、アルコールデヒドロゲナーゼ、エステラーゼ、NDUF、チトクロームp450 (CYP) 及びATP-結合カセット/トランスポーターからなる群から選択される少なくとも1つを例示することができる。

(5) 配列番号1～4309に示される塩基配列又はこれに相補的な塩基配列からなる群から選択されるオリゴヌクレオチド。

(6) 薬物代謝酵素をコードする遺伝子中に存在する遺伝子多型情報から、該遺伝子多型部位を含むように作製されたオリゴヌクレオチド。

【0012】

上記オリゴヌクレオチドとしては、その5'末端若しくは3'末端又は中央の塩基が、当該遺伝子多型部位となるように作製されたものが挙げられる。また、薬物代謝酵素をコードする遺伝子とハイブリダイズし得る断片とハイブリダイズしない断片とが結合したオリゴヌクレオチドであって、前記遺伝子多型部位が、当該ハイブリダイズし得る断片の5'末端又は3'末端となるように作製されたオリゴヌクレオチドも、本発明のオリゴヌクレオチドに含まれる。さらに、配列番号1～4309に示すいずれかの塩基配列のうち第21番目の塩基を含む少なくとも13塩基の配列又はこれに相補的な配列を有するものも、本発明のオリゴヌクレオチドに含まれる。

(7) 前記オリゴヌクレオチドを含む遺伝子多型検出用キット。

以下、本発明を詳細に説明する。

【0013】

【発明の実施の形態】

本発明は、薬物代謝酵素に関する遺伝子多型情報を用いて、被検対象の遺伝子多型を検出する方法に関する。また、本発明は、薬物代謝酵素によって代謝される薬物の有効性及び安全性の有無又は強弱を解析することを特徴とし、この解析結果により、疾患と薬物との関係を評価するものである。複数人が同じ疾患に罹患している場合であっても、薬物代謝酵素遺伝子の遺伝子多型情報は個々の患者ごとに異なることが多い。従って、その異なる遺伝子多型情報から薬物代謝との

関係を導き、どのような遺伝子多型情報を有する場合に特定の薬物の有効性が認められるのか認められないのか、また、どのような遺伝子多型情報を有する場合に副作用が出やすいのか出にくいのか、その薬物の有効性及び/又は安全性を評価する。その結果、ある疾患に対してどのような薬物を使用すべきなのか、遺伝子多型情報からそれぞれの患者ごとに適した投薬（オーダーメイド医療）が可能となる。

【0014】

1. 遺伝子多型

遺伝子多型には、一塩基多型、インサージョン/デリーション型多型、及び塩基配列の繰り返し数が異なっていることにより生じる多型が含まれる。一塩基多型（SNP）とは、一般にはある遺伝子領域の特定の1個の塩基が他の塩基に置換することによる多型を意味するが、本発明においては、上記置換による多型のほか、当該1個の塩基が欠失したことによる多型、当該1個の塩基にさらに1個の塩基が挿入したことによる多型も含めることとする。また、インサージョン/デリーション型多型とは、複数の塩基（例えば2個～数十塩基）が欠失や挿入をしていることによる多型をいい、数百塩基～数千塩基が欠失や挿入されているものも存在する。さらに、塩基配列の繰り返し数が異なっていることにより生じる多型は、2～数十塩基の配列が繰り返されており、その繰り返し回数が個人間で異なっているものをいう。繰り返しの単位が数塩基から数十塩基のものをVNTR(variable number of tandem repeat)といい、2～4塩基単位程度のものをマイクロサテライト多型という。VNTRやマイクロサテライト多型においては、この繰り返し回数の違いが個々人のアレル（対立遺伝子）で異なることにより、バリエーションを獲得している。

【0015】

2. 薬物代謝酵素

「薬物代謝酵素」とは、医薬品を含む外来性異物の生体内における構造変換を触媒する酵素群の総称である。また、一部の内在性物質であっても、治療目的で投与される場合にはその代謝に関わる酵素群のことを指す。薬物代謝酵素は、薬物の吸収、代謝、排泄に関わるものであるため、その酵素の多型はその酵素の発

現量（転写や翻訳）や活性を変化させ、結果として未変化体や代謝物の血中濃度などに違いが生じる。

本発明において、遺伝子多型解析の対象となる遺伝子により発現される薬物代謝酵素としては、以下のものが挙げられる。

【0016】

エポキシドヒドロラーゼ(epoxide hydrolase)
メチルトランスフェラーゼ(methyltransferase)
N-アセチルトランスフェラーゼ(N-acetyltransferase)
スルホトランスフェラーゼ(sulfotransferase)
キノンオキシドレダクターゼ(quinone oxidoreductase)
グルタチオン-S-トランスフェラーゼ(glutathione S-transferase)
UDP-グリコシルトランスフェラーゼ(UDP-glycosyltransferase)
アルデヒドデヒドロゲナーゼ(aldehyde dehydrogenase)
アルコールデヒドロゲナーゼ(alcohol dehydrogenase)
エステラーゼ (esterase)
ユビキノンドヒドロゲナーゼ(ubiquinone dehydrogenase : NDUF)
チトクローム P450 (CYP)
ATP-結合カセット(ATP-binding cassette) / トランスポーター
その他の酵素

【0017】

(1) エポキシドヒドロラーゼは、エポキシドをトランス開裂機構で加水分解し、1,2-グリコールを生成させる酵素であり、例えばミクロソームエポキシドヒドロラーゼ1、細胞質エポキシドヒドロラーゼ2などが含まれる。

(2) メチルトランスフェラーゼは、アミノ基、水酸基、チオール基などにメチル基転移を触媒する酵素であり、例えば以下のものが挙げられる。

カテコール-O-メチルトランスフェラーゼ
ヒスタミン N-メチルトランスフェラーゼ
フェニルエタノールアミンN-メチルトランスフェラーゼ
ホスファチジルエタノールアミンN-メチルトランスフェラーゼ

ニコチンアミドN-メチルトランスフェラーゼ

グアニジノアセテートN-メチルトランスフェラーゼ

アセチルセロトニン-O-メチルトランスフェラーゼ

【0018】

(3) N-アセチルトランスフェラーゼは、アミノ基、スルホンアミド基、ヒドラジン基にアセチル基転移を触媒する酵素であり、例えば以下のものが挙げられる。

アリールアミンN-アセチルトランスフェラーゼ1、2

アリールアルキルアミン N-アセチルトランスフェラーゼ

サッカロミセス・セレビシエ(*Saccharomyces cerevisiae*)のN-アセチルトランスフェラーゼ相同体

L1 細胞接着分子

【0019】

(4) スルホトランスフェラーゼは、硫酸抱合に関与し、フェノール類、ステロイド類、アリールアミン、胆汁酸などに硫酸基転移を触媒する酵素であり、例えば以下のものが挙げられる。

スルホトランスフェラーゼ1A1、1A2、1A3、1C1、1C2、2A1、2B1

甲状腺ホルモンスルホトランスフェラーゼ

チロシルタンパク質スルホトランスフェラーゼ1、2

スルホトランスフェラーゼ-関連タンパク質3

エストロゲンスルホトランスフェラーゼ

セレブロシドスルホトランスフェラーゼ

HNK-スルホトランスフェラーゼ-1

炭水化物スルホトランスフェラーゼ2、4、5

カルボハイドレートスルホトランスフェラーゼ-1、3

【0020】

(5) キノンオキシドレダクターゼは、キノン類のo-キノンやp-キノンの還元を触媒する酵素であり、例えば以下のものが挙げられる。

NAD(P)H: キノンオキシドレダクターゼ1

NRH: キノンオキシドレダクターゼ 2

キノンオキシドレダクターゼ相同体のp53誘導遺伝子 3

(6) グルタチオン-S-トランスフェラーゼは、グルタチオンとの抱合を触媒する酵素であり、例えば以下のものが挙げられる。

グルタチオン-S-トランスフェラーゼ Mu1、Mu2、Mu3、Mu4、Mu5

グルタチオン-S-トランスフェラーゼ Z 1 (zeta)

グルタチオン-S-トランスフェラーゼ II (pi)

グルタチオン-S-トランスフェラーゼ T 1 (zeta)

グルタチオン-S-トランスフェラーゼ シータ1(theta 1)、シータ2

ミクロソームグルタチオン-S-トランスフェラーゼ1

ミクロソームグルタチオン-S-トランスフェラーゼ1-様1

ミクロソームグルタチオンSトランスフェラーゼ T 2、T 3

グルタチオン-S-トランスフェラーゼ A1、A4

グルタチオン-S-トランスフェラーゼ M1、M2、M3、M4

【0021】

(7) UDP-グリコシルトランスフェラーゼは、第I相薬物代謝経路である水酸基、カルボキシル基、アミノ基、チオール基などの官能基導入後にその官能基にグルクロン酸供与を触媒する酵素であり、例えば以下のものが挙げられる。

UDP-グリコシルトランスフェラーゼ1ファミリーポリペプチドA1

UDP-グリコシルトランスフェラーゼ2ファミリーポリペプチドA1、B7、B10、B4、B11、B15、B17

UDP-グリコシルトランスフェラーゼ8

ドリシル-ジホスホオリゴサッカライド-タンパク質グリコシルトランスフェラーゼ

【0022】

(8) アルデヒドデヒドロゲナーゼは、アルデヒドをカルボン酸に変換する酵素であり、例えば

アルデヒド デヒドロゲナーゼ1ファミリー メンバーA1、A2、A3

アルデヒド デヒドロゲナーゼ1ファミリー メンバーB1

フォルミルテトラヒドロフォレート デヒドロゲナーゼ

アルデヒドデヒドロゲナーゼ2

アルデヒド デヒドロゲナーゼ3 ファミリー メンバーA1、A2

アルデヒド デヒドロゲナーゼ3 ファミリー メンバーB1、B2

アルデヒド デヒドロゲナーゼ5 ファミリー メンバーA1

アルデヒド デヒドロゲナーゼ6 ファミリー メンバーA1

アルデヒド デヒドロゲナーゼ8 ファミリー メンバーA1

アルデヒド デヒドロゲナーゼ9 ファミリー メンバーA1

などが含まれる。

【0023】

(9) アルコールデヒドロゲナーゼは、アルコールをアルデヒド又はケトンに変換する酵素であり、例えば以下のものが挙げられる。

アルコールデヒドロゲナーゼ1~7

ヒドロキシ-CoAデヒドロゲナーゼ

短鎖アルコールデヒドロゲナーゼファミリー遺伝子

(10) エステラーゼは、エステル部分を加水分解する酵素であり、例えば以下のものが挙げられる。

アリールアセトアミドデアセチラーゼ

グランザイムA (granzyme A)

グランザイムB

インターロイキン17 (サイトトキシック Tリンパ球 アソ-シエイト セリン
エステラーゼ8)

ユビキチンカルボキシルターミナルエステラーゼL1, 3

カルボキシルエステラーゼ1

リパーゼA

エステラーゼD/ホルミルグルタチオンハイドロラーゼ

カルボキシルエステルリパーゼ (胆汁酢酸誘発リパーゼ)

ドリシル-ジホスホオリゴサッカライド-タンパク質グリコシルトランスフェラ
ーゼ

ニューロパチーターゲットエステラーゼ

【0024】

(11) NDUF (ubiquinone dehydrogenase) は、ミトコンドリアの呼吸鎖、すなわちエネルギー代謝を担う酵素であり、例えば、NADH-デハイドロゲナーゼ(ユビキノン) 1 α サブコンプレックス 1 ~ 3、5 ~ 10

NADH-デハイドロゲナーゼ(ユビキノン) 1 α / β サブコンプレックス 1

NADH-デハイドロゲナーゼ(ユビキノン) 1 β サブコンプレックス 3、5、7

NADH-デハイドロゲナーゼ(ユビキノン) Fe-S 蛋白質 1、3、4、5、6、8

NADH-デハイドロゲナーゼ(ユビキノン) フラボプロテイン 1 ~ 3

などが含まれる。

【0025】

(12) CYP (チトクローム P450) は、第I相薬物代謝を司り、薬物に酸素原子を導入する酵素であり、例えばチトクローム p450 (CYP) 1A1, CYP1A2, CYP1B1, CYP2A6, CYP2B6, CYP2C8, CYP2C18, CYP2C9, CYP2C19, CYP2E1, CYP2D6, CYP2E1, CYP2F1, CYP3A3, CYP3A4, CYP3A5, CYP3A7, CYP3A43, CYP4A11, CYP4B1, CYP4F2, CYP4F3, CYP4F8, CYP11B1, CYP17, CYP19, CYP21A2, CYP27A1, CYP27B1 などが含まれる。

【0026】

(13) ATP-結合カセット/トランスポーターは、トランスポーターで薬物の吸収や組織内濃度を調節するものであり、例えば以下のものが挙げられる。

ATP 結合カセットサブファミリー A メンバー 1、4、7、8

ATP 結合カセットサブファミリー B メンバー 1、4、7、8、9、10、11

ATP 結合カセットサブファミリー C メンバー 1、2、3、4、5、7、8、9

ATP 結合カセットサブファミリー D メンバー 1、3、4

ATP 結合カセットサブファミリー G メンバー 1、2、4、8

ATP 結合カセットサブファミリー E メンバー 1

ATP 結合カセットサブファミリー F メンバー 1

オーガニック アニオン トランスポーター 1、2、3

オーガニック アニオン トランスポーター ポリペプチド 1、2、8

トランスポーター1 ATP結合カセット サブファミリーB

トランスポーター2 ATP結合カセット サブファミリーB

SLC 2 2 A 4 ソリユート キャリア ファミリー 2 2 (オーガニック カチオン
トランスポーター)メンバー4、

SLC22A5 ソリユート キャリア ファミリー22 (オーガニック カチオン ト
ランスポーター) メンバー5

SLC22A1 ソリユート キャリア ファミリー22 (オーガニック カチオン ト
ランスポーター) メンバー1

SLC22A2 ソリユート キャリア ファミリー22 (オーガニック カチオン ト
ランスポーター) メンバー2

SLC10A2 ソリユート キャリア ファミリー10 (ナトリウム/胆汁酸 コトラ
ンスポーター ファミリー) メンバー2

SLC15A1 ソリユート キャリア ファミリー15 (オリゴペプチド トランスポ
ーター) メンバー1

【 0 0 2 7 】

(14) その他の酵素には、ガンマ-グルタミルトランスフェラーゼ1、トランス
グルタミナーゼ1などが含まれる。

3. 遺伝子多型情報

遺伝子多型情報は、一般的遺伝子多型検出法を利用して得ることができる。例
えば、PCRによる方法、アレル特異的オリゴヌクレオチドを鋳型としてハイブリ
ダイゼーションを行う方法（例えばTaqMan PCR法、インベーター法）、プライマ
ー伸長反応を利用する方法、シーケンス法、MALDI-TOF/MS法、DNAチップ法等
が採用される。PCR法やシーケンス法はいずれの遺伝子多型の検出法にも使用
することができ、他の方法は、主としてSNPの検出法に使用することができる。

【 0 0 2 8 】

TaqMan PCR法とは、蛍光標識したアレル特異的オリゴとTaq DNAポリメラーゼ
によるPCR反応とを利用した方法である (Livak, K.J. Genet. Anal. 14, 143 (1
999); Morris T. et al., J. Clin.Microbiol. 34, 2933 (1996))。インベーター
法とは、SNPのそれぞれのアレルに特異的な2種類のレポータープローブ及び1

種類のインベータープローブの鋳型DNAへのハイブリダイゼーションと、DNAの構造を認識して切断するという特殊なエンドヌクレアーゼ活性を有する酵素によるDNAの切断を組み合わせた方法である (Livak, K. J. Biomol. Eng. 14, 143-149 (1999); Morris T. et al., J. Clin. Microbiol. 34, 2933 (1996); Lyamichev, V. et al., Science, 260, 778-783 (1993)等)。

【 0 0 2 9 】

また、プライマー伸長反応を利用する方法として、例えばSniPer法を採用することもできる。SniPer法とは、RCA(rolling circle amplification)法と呼ばれる手法を基本原理とするものであり、環状の一本鎖DNAを鋳型としてDNAポリメラーゼがその上を移動しながら相補鎖DNAを連続して合成していくものである。この方法によれば、DNA増幅が起こった場合に生じる発色反応の有無を測定することによってSNPを判定する (Lizardi, P. M. et al., Nature Genet., 19, 225-232 (1998); Piat, A. S. et al., Nature Biotech., 16, 359-363 (1998))。

【 0 0 3 0 】

シーケンス法とは、遺伝子多型を含む領域をPCRにて増幅させ、Dye Terminatorなどを用いてDNA配列をシーケンスすることで遺伝子多型（特に一塩基多型）の頻度を解析する方法である。

MALDI-TOF/MS法とは、質量分析機 (mass spectrometer) を用いた方法で、基本的には異なる一塩基の質量の違いを利用してSNPジェノタイピングする方法である。PCR増幅を利用した方法とmultiplexを利用した方法がある (Haff, L. A., Smirnov, I. P., Genome Res., 7, 378- (1997) ; Little, D. P. et al. Eur. J. Clin. Chem. Clin. Biochem., 35, 545- (1997) ; Ross, P., et al. Nat Biotechnol., 16, 1347- (1998))

【 0 0 3 1 】

DNAチップ法とは、ガラスなどの基盤上に多種類のDNAプローブを整列化し、固定し、その上で標識DNAのハイブリダイゼーションを行い、プローブ上の標識（蛍光など）シグナルを検出する方法を利用して、ハイブリダイゼーションで完全マッチと一塩基ミスマッチを分別検出する方法である。

本発明の方法において使用することができる遺伝子多型情報、特にSNP情報は

遺伝子名	No.	存在位置	配列	配列番号
ABCA1	46	(intron 5 19405)	cttctcaattattatctgc t/c atataactcaatattactga	46
ABCA1	47	(intron 5 19534)	catatgacctctttagctcc g/a ggaallaactctctgctcca	47
ABCA1	48	(coding region 474 (Leu 158 Leu))	gaaccltcttggttctt g/a tatcaacacctctctctccc	48
ABCA1	49	(intron 6 210)	gaaccttggtctcatagccc a/c ccttggttaaaataaaattga	49
ABCA1	50	(intron 6 334)	acacttctgagcaataacc g/a tcttgaagggtatgatct	50
ABCA1	51	(intron 6 2288)	cctcttcaaaagcttggt g/t cactggaacagcttatgaat	51
ABCA1	52	(intron 6 2322)	atgaagataataattttagg t/c ccagaagaagcaattaaataa	52
ABCA1	53	(intron 6 2820)	gtgctttgatacttttagg t/g ttctgaagagagaccctg	53
ABCA1	54	(intron 7 416)	catataagagagacat g/a ggcctgacagatggaagcc	54
ABCA1	55	(intron 7 471)	agaccacatttttagctta c/t ttgataataacattgcaag	55
ABCA1	56	(intron 7 504)	ttagcaagaanaattccac g/a aagtttttcagcttaggaa	56
ABCA1	57	(intron 7 679)	gctctggtgaattctctc g/c ctaccacaacatcatt	57
ABCA1	58	(intron 7 1740)	acaatctcacacctttcag c/t tgaatgaattgaatttgg	58
ABCA1	59	(intron 7 2122)	tgaatgaagtgcttactacc a/g agtctttctctactatccg	59
ABCA1	60	(intron 7 7753)	tgggaattccaagctgtaga t/c tttttctgaagcctttgg	60
ABCA1	61	(intron 7 8973)	atggaatattgtttatag a/t ctacaatttgccaattat	61
ABCA1	62	(intron 7 8976)	gaattgtttattatgaat a/g cagattgccaalatattag	62
ABCA1	63	(intron 7 11327)	ctaaactcttatttccatt c/c agctcttataaagaattgg	63
ABCA1	64	(intron 7 11738)	ctgacgtttaagggagaccg c/t gtagctcctttagagactg	64
ABCA1	65	(intron 7 12295)	agtcgtaaatattgttct t/a ttttttctttagcttgcct	65
ABCA1	66	(intron 8 387)	tgcagaagccaatatttta c/g caacacacatctgtctaac	66
ABCA1	67	(intron 8 697)	ggaactctgtgtctccccc a/t gcatagaagctgagccagg	67
ABCA1	68	(intron 8 3036)	ctttatagaagaanaatt t/g tttttttagttagggaattgg	68
ABCA1	69	(intron 8 3176)	aaatggccttgctctctgc g/a cctttctgtctgtatccct	69
ABCA1	70	(intron 8 3364)	ggcagaaggcaagcttagg a/t cctagaagaatcttgaccac	70
ABCA1	71	(intron 8 3373)	caagctttaggacttagaga c/a tctggaaccagccactcac	71
ABCA1	72	(intron 8 3561)	cgagkatttattatatt c/a ttgtaaaaattttggaata	72
ABCA1	73	(intron 8 3654)	agtcgggaatattttaga t/c gtaagacagaacgctctg	73
ABCA1	74	(intron 8 4715)	ggcagaagggctcagaatc c/t gcaittccacaatgtctcc	74
ABCA1	75	(coding region 936 (Pro 312 Pro))	catatgtcttgaggcatcc c/t gagggaaggagctgaagat	75
ABCA1	76	(intron 9 2309)	cccccaagagctagattaa a/g tcttggctatgtttagtgc	76
ABCA1	77	(intron 9 2392)	atgggaaggtcttgcttcca t/c gaaaacatttttccagatca	77
ABCA1	78	(intron 10 228)	tgggaatggggaggactggc a/g caggagctgctgttatgggt	78
ABCA1	79	(intron 10 319)	ttctcgggtccctgctccc c/t acctgaactccaggtaacaa	79
ABCA1	80	(intron 11 377)	gaaagagctggggagcaaa c/g gcatgagtgatcagtagac	80
ABCA1	81	(intron 11 521)	agtccttagagacaatttg c/a ttcaaatgtggagcagctg	81
ABCA1	82	(intron 11 2850)	ctctatacaatcattatgct c/c ccaatgaaataataataca	82
ABCA1	83	(intron 11 2976)	cicccattggtagaacag a/g gcttcatcttcttctgctgaa	83
ABCA1	84	(intron 11 3056)	gtttcagctgctgttttct c/t ggcagcacatctgctcaggc	84
ABCA1	85	(intron 12 340)	ggcattttttggaactta t/c ctaaaatcaaatctggctcc	85
ABCA1	86	(intron 12 381)	aattaaatttttgaatttt a/g tattaataattatttagta	86
ABCA1	87	(intron 14 1728)	cagctcagagggcttggcc c/t atcaccctggctcacgtgtg	87
ABCA1	88	(coding region 2040 (Ile 680 Ile))	atggccttggaacaacatc c/a ctcctgttttagctgtgttca	88
ABCA1	89	(intron 15 1382)	cttttagacaganaagttac c/a tgggaatatattctccacag	89
ABCA1	90	(intron 15 1453)	tataaaggagaacacagtt c/a aaatttacctatttgaagaac	90

遺伝子名	No	存在位置	配列	配列番号
ABCA1	91	(intron 15 1567)	ttctgcgagatttgggtaa g/a tcaatatactctttagaa	91
ABCA1	92	(intron 15 1617)	caatggctcattcaaaaaa t/a gaatagcattacgctcttc	92
ABCA1	93	(intron 16 95)	agttagaacaaatgaatgaa t/a gcttttccaatggacatg	93
ABCA1	94	(intron 16 452)	tggtatttcttgagtaaa g/a ttcttgaactaagacataac	94
ABCA1	95	(intron 16 657)	ctgagctcagctcagctt t/c cataggaatcagacaccca	95
ABCA1	96	(intron 18 1730)	tgaagttcaagcagcttc c/g ctggtcttaccctcact	96
ABCA1	97	(intron 19 426)	aggacttaagtgagagaa a/g tcaagagagtcagagcttc	97
ABCA1	98	(intron 19 468)	aaagacacagcttagcttc a/g gtggtctcagcagcttc	98
ABCA1	99	(intron 20 876)	ccctctcaatcagagaa c/a aatagggtcagtgacag	99
ABCA1	100	(intron 22 118)	catggactctctctgta t/g cacagagagataaagaca	100
ABCA1	101	(intron 22 560)	aaagcttgcattctaggg g/a tcatagccatcacaggtaa	101
ABCA1	102	(intron 23 102)	acctctttgacatctgaa a/g ccacatctctctctctgt	102
ABCA1	103	(intron 23 287)	gtcaagaaagagcttgt c/a aagaggtaaagctctgtgt	103
ABCA1	104	(intron 23 1063)	acctttccctcagagagc g/a agggctttcacacccacac	104
ABCA1	105	(intron 25 321)	ctctttactaaatcacag t/g gaggacacagcgcacagaa	105
ABCA1	106	(intron 25 376)	gttaaatctcaactcttg g/c eccagctcagccctactaa	106
ABCA1	107	(intron 25 478)	catatagataaatacaaa c/t attttagagtagatagctaa	107
ABCA1	108	(intron 25 579)	tcallaatctcaaaaaa g/t algaataaaatgaacatcaa	108
ABCA1	109	(intron 27 153)	aatgttaaagacacttgt c/t ttgcacatctcgcagtgt	109
ABCA1	110	(intron 28 1058)	actatacgggaataatga c/t tatgggttccatgatgaa	110
ABCA1	111	(intron 28 1317)	caggaccagctctcagat c/t acctgaatgtgagcactat	111
ABCA1	112	(intron 30 372)	tataatgttttgggtttg t/c ttatcagctctctctctt	112
ABCA1	113	(intron 30 506)	ccctttaaagtaagcagt a/g gataataaatcagatgaag	113
ABCA1	114	(intron 30 1033)	ctggaatttgcagccctt g/c atttccacataaagcttgt	114
ABCA1	115	coding region 4261 (Thr 1427 Thr)	ctctcttttcagagagac g/a ccttcacagcagggagaa	115
ABCA1	116	(intron 33 626)	agctctctgttactatctt c/t gcttttctctctgctt	116
ABCA1	117	(intron 33 719)	taataagcctcactctaga g/a gggagccagcctctgtata	117
ABCA1	118	(intron 33 726)	cctcaactcagagagagcc g/a gggcctgtgtatagggcag	118
ABCA1	119	(intron 33 889)	ctttctcaatgtctcagt a/g tctaactctctgtgttaaca	119
ABCA1	120	(intron 33 1097)	cttgaccccccactgtctgg c/c tttaatactcagcctgtct	120
ABCA1	121	(intron 35 234)	aactatctaaactcagtt t/c cctcatctgtgaaatggaga	121
ABCA1	122	(intron 37 411)	aactctgtacatttatcag c/t agcttalcacatctgcaa	122
ABCA1	123	(intron 37 1224)	cagcgaatgagatctcaga a/g tgaaggtcaagtccttga	123
ABCA1	124	(intron 37 1720)	aaatataaattactctgact g/t ggaatccatcgttctagtaag	124
ABCA1	125	(intron 40 251)	tgaaggttaagaaataag t/g tatttctttagatccactgg	125
ABCA1	126	(intron 40 252)	gaaggttaagaaataag t/c atttctttagatccactggc	126
ABCA1	127	(intron 40 319)	accactgaagaatacaacc a/g taactttgaaatttagtga	127
ABCA1	128	(intron 40 957)	cttttactcttttcttct c/c tcatgggtatagcatttg	128
ABCA1	129	(intron 41 146)	tcatgggtatagcatttg c/t cctctcctcagcctctgaa	129
ABCA1	130	(intron 42 239)	cattggttttatatctgtac a/c ttatagtttagtttataaa	130
ABCA1	131	(intron 42 321)	aataaagtttagtttag t/a ttgattttcatagttcaaaa	131
ABCA1	132	(intron 42 322)	ataaagtttagtttag t/c tgaatttcatagttcaaaa	132
ABCA1	133	(intron 42 533)	gaatgaataatagtagal g/a ataataatagatcacgttct	133
ABCA1	134	(intron 42 546)	tatagaatgaatgaat a/g cggttctaaataaagcaggtt	134
ABCA1	135	(intron 43 739)	tacagccacacttaaatgg t/a cccattatgaatacatatt	135

遺伝子名	No.	存在位置	配列	配列番号
ABCA1	136	(intron 44 18)	tatataaataaataatgac t/c tctatttctgcaagact	136
ABCA1	137	(intron 44 264)	acaataatttcttctgtt t/c ttaagataataatttagta	137
ABCA1	138	(intron 44 279)	tggttttaagataaatt t/c agtatttttggtaaatga	138
ABCA1	139	(intron 44 508)	tttacatctatataaatt c/t cccctatgcatgacctt	139
ABCA1	140	(intron 44 1477)	gactctctctctctctt a/t cattttgacagtaacagt	140
ABCA1	141	(intron 44 1665)	tggttgaagaactgattt g/a ttggtatacttgtagggcc	141
ABCA1	142	(intron 44 1956)	gtgttctcaacacaaat t/g ctgggcttctcatttgg	142
ABCA1	143	(intron 45 58)	aatataaccttatggctt t/c ccaacgcatltagctcagg	143
ABCA1	144	(intron 46 608)	ttatactgctcantaag g/c tttagacaaaagtgttt	144
ABCA1	145	(intron 47 336)	ttcaattgtaaacacac t/c acactgaacacatctcc	145
ABCA1	146	3' untranslated region 7479	aacaaaatgtgggtctc c/t aggcacgggaacttgctt	146
ABCA1	147	3' untranslated region 8226	aggagccctcgttaacaa c/t tggggagccttttttttt	147
ABCA1	148	3' untranslated region 8697	ttcagaanttgaattat t/c actaaagggtgaagcttca	148
ABCA1	149	3' untranslated region 9097	aactatttgaagaataac a/g acattttatcacagattgaa	149
ABCA1	150	5' flanking region (-1033) (-1032)	tgacttaaatatttaacat a/t ggtgtgtagccctgcatcc	150
ABCA1	151	5' flanking region (-1033) (-1032)	tgacttaaatatttaacat ggtgtgtagccctgcatcc	151
ABCA1	152	(intron 5 6368)	tttgaagggttatgctc g/c tgaagaatcagctgggtg	152
ABCA1	153	(intron 5 9709)	catttctctgtagacccc t/c caccatcagagcagctct	153
ABCA1	154	(intron 5 13816)	ttctactctctcttttt t/c catttgcctctccacac	154
ABCA1	155	(intron 10 270 271)	ctttcaggagagagcaaa c/t cgtcattctgtctctct	155
ABCA1	156	(intron 10 270 271)	ctttcaggagagagcaaa c/t cgtcattctgtctctct	156
ABCA1	157	(intron 20 611 612)	tttagccctctctctccc c/t ggcactctcttattagac	157
ABCA1	158	(intron 20 611 612)	tttagccctctctctccc g/c acacccctctatttaggg	158
ABCA1	159	(intron 32 391 392)	gagtccttggatctctct t/c gatgggagctccatgaa	159
ABCA1	160	(intron 32 391 392)	gagtccttggatctctct ggtgtgtagccctgcatcc	160
ABCA1	161	(intron 37 847)	gcttatatttgaattctt c/d attttcaaaagcaaaccaa	161
ABCA4	1	5' flanking region -1005	tccatataacagaaact a/c tctctctctcttggagct	162
ABCA4	2	5' flanking region -819	gtcagagcttctcaagag a/t acacattctgagatttagg	163
ABCA4	3	5' flanking region -680	agcaccacccattgacagg c/a tggaaagacagtaatggcc	164
ABCA4	4	(intron 1 208)	tgccttctccaggaagat g/a ttctctgtctctcagccaca	165
ABCA4	5	(intron 1 234)	ctgtctctagccacataa a/g tcttttccctccctgctc	166
ABCA4	6	(intron 1 510)	agctacgatcaagtcacag t/c ttaactggacacattattt	167
ABCA4	7	(intron 1 1527)	gcttaaacacacagataa a/g agacacacatgggacacgt	168
ABCA4	8	(intron 1 2077)	cagagctgagctgctggc t/c aaatagagctctctctg	169
ABCA4	9	(intron 1 2174)	ccctctcaatctggccttc g/c ctggca tgggtggcgac	170
ABCA4	10	(intron 1 2246)	gctccagagatagagacc a/g ctgggctgagggcttggc	171
ABCA4	11	(intron 1 2364)	ttctgttggcagctctccc g/a atgctctccctctctacc	172
ABCA4	12	(intron 1 4243)	ctccctgggtatgctcgt g/c ggaatgaactcagagaca	173
ABCA4	13	(intron 1 4287)	atgcctctctggggagggg a/c gctgacatcttggagag	174
ABCA4	14	(intron 1 4309)	ctgagcaatgatttggagg c/t ggcagagagggctatgta	175
ABCA4	15	(intron 1 4416)	tgcagacccctcccccct c/t cgcctaaataaacacact	176
ABCA4	16	(intron 1 4996)	tttaccctggacacagcag g/a ccaagctggc t/c ggtctcc	177
ABCA4	17	(intron 1 5007)	aacaggcag g/a ccaagctggc t/c ggtctctctctctatcaca	178
ABCA4	18	(intron 1 5080)	gtatgtgctgatttcttag c/g agcaccatgggttccagtt	179
ABCA4	19	(intron 1 5152)	ggagataacactaagtaga g/a ggcagagcttacaaggttga	180

遺伝子名	No.	存在位置	配列	配列番号
ABCA4	20	(intron 1 710)	ccatggatcgtcttggg a/g tcaagagcttaagctcca	181
ABCA4	21	(intron 1 720)	gaatttgggttggcga t/a ggaacagatcattatca	182
ABCA4	22	(intron 1 7433)	tcgaacccttctctaac t/c gcaagtgatag c/t tacaga	183
ABCA4	23	(intron 1 7497)	ctaac t/c gcaagtgatag c/t tacagagaatcttactac	184
ABCA4	24	(intron 2 1067)	tcaagcagacagcaacg c/a gtagatctcttgaactaa	185
ABCA4	25	(intron 2 1243)	caccagacagagagctg c/a gtagatctcttgaactaa	186
ABCA4	26	(intron 3 26)	tggttgaacctaccatg a/g agggagaggttcacacc	187
ABCA4	27	(intron 3 101)	agcatggagctgagtt c/t ttgggttcttggagcccc	188
ABCA4	28	(intron 3 330)	tgctgggtgagtgatca t/c tgaagagaataacatgt	189
ABCA4	29	(intron 3 470)	tgaagtcagttacaaag c/g agtttacttcttggagaaa	190
ABCA4	30	(intron 3 634)	tgaacacaaatgacctt c/t ccaaaaaatggccacata	191
ABCA4	31	(intron 3 1016)	collggggagctcagatg a/g ttctccagagagagctg	192
ABCA4	32	(intron 3 1554)	aaaagttgggttctgtt t/c gcatcactatagatgaa	193
ABCA4	33	(intron 3 1686)	ctagacattctcacagac a/g agggagagagaggggctc	194
ABCA4	34	(intron 3 1823)	ttcactctctccatgac a/g gctctccctgctctcaag	195
ABCA4	35	(intron 3 1938)	caaatctcggagaaac a/g ggttaccagc t/a ttatct	196
ABCA4	36	(intron 3 1951)	acaatc g/a ggttaccagc t/g ttatctctctctccatca	197
ABCA4	37	(intron 3 2063)	ggctctcagagcttctg c/t tgaatgggtgagag g/a cagg	198
ABCA4	38	(intron 3 2079)	ctgc t/g taaatgggtgagag g/a cagatctcagagaatgggt	199
ABCA4	39	(intron 3 2188)	agacacagagagctggag c/t gaggagagagagagagctg	200
ABCA4	40	(intron 3 2214)	gagacagcttgcacaa c/t ggaactaaatagatctct	201
ABCA4	41	(intron 4 3182)	ccccccagacacagagc c/g gctctctggtggtctgt	202
ABCA4	42	(intron 4 3515)	aatataaagagagagc c/t atagcccccaactctcaga	203
ABCA4	43	(intron 4 3952)	agagacacatctgctac c/c tgggttcagacttcagagac	204
ABCA4	44	(intron 4 4637)	aatcacttccccagat c/t cttaactgttgggtgtt	205
ABCA4	45	(intron 4 5319)	accttgggtctccagag a/g cccacagacagagaccttc	206
ABCA4	46	(intron 6 2266)	caccttgcagactcagac g/a ggtcttggagcttcttct	207
ABCA4	47	(intron 6 2857)	ccagagagagagagctg c/a tag t/c cggctcagttaccca	208
ABCA4	48	(intron 6 2861)	aggagaaagctctcc g/a tag t/c cggctcagttaccca	209
ABCA4	49	(intron 6 3078)	ggagacattaaatggag c/g gctcttcttctctctg	210
ABCA4	50	(intron 6 3375)	ttaaatcacaatagtt c/g ataaacaagaagagagaa	211
ABCA4	51	(intron 6 3412)	cttctgggtgagatag c/a gtagatgcttggagagcc	212
ABCA4	52	(intron 6 4635)	gaacagaaatagatcact t/c ggaatagtagatagat	213
ABCA4	53	(intron 6 264)	gagtgagagagatagagaa c/c agccattgtactatgctc	214
ABCA4	54	(intron 7 828)	agcttcttactctcaga t/c agcaactcactatcattg	215
ABCA4	55	(intron 7 1019)	glaaacagcttggagag c/a ttllacaacaacatagct	216
ABCA4	56	(intron 8 374)	gaagacacttcttctg c/a ggtacagcctatctatg	217
ABCA4	57	(intron 8 874)	tgatgacttcttctg c/a ggtacagcctatctatg	218
ABCA4	58	(intron 9 605)	tgatgacttcttctg c/a ggtacagcctatctatg	219
ABCA4	59	(coding region 1268 Arg 423 His or His 423 His)	acttttgaagagctgagac g/a c/t gtagagaggttgcagag	220
ABCA4	60	(coding region 1269 Arg 423 Arg or His 423 His)	acttttgaagagctgagac g/a c/t gtagagaggttgcagag	221
ABCA4	61	(intron 11 5687)	atcatgaaatgactttaga c/g tcaatataaataattgt	222
ABCA4	62	(intron 11 7136)	gacttccacttacttag t/c ggaacttagttagacatagaa	223
ABCA4	63	(intron 11 7180)	agctcaaaatgcttct c/a gctctaaaggttgaattt	224
ABCA4	64	(intron 11 7701)	gltagacagagcattacc c/t gtagcttctccagatgaa	225

塩基子名	No	存在位置	配列	配列番号
ABCA4	65	(intron 11 8073)	ggatgtttccccaatcca t/g tggcattttccaaaagaac	226
ABCA4	66	(intron 11 8586)	cagctcctgctgctgagag g/a cctcaacctctccacag	227
ABCA4	67	(intron 11 11234)	cccaaatattttttttt c/a ttttgaatttaatttcag	228
ABCA4	68	(intron 11 11641)	agaaacaacattattga c/g acittttggtgagcclg	229
ABCA4	69	(intron 11 11808)	tggatttcttazagaala c/t caatccatttccittaac	230
ABCA4	70	(intron 11 11923)	agatcattattataatc a/g tcaagctgagtcacttaag	231
ABCA4	71	(intron 12 305)	tcacccgtggttccggaggt g/a tgaatagctatccaagccc	232
ABCA4	72	(intron 13 1461)	ttgggtttcagctgacat g/a tagctgtactcagatccc	233
ABCA4	73	(intron 14 1268)	ggactgagcccttttctt c/a atctagctttccctgttct	234
ABCA4	74	(intron 17 23)	gggtcttttaaacacaat c/g ttaagtittgaatacaact	235
ABCA4	75	(intron 17 715)	ggactctccctagacgaa g/a tacttccatcgttctgtt	236
ABCA4	76	(intron 18 1282)	ggaatagaagaactaac c/t gcttcagaaattctaggg	237
ABCA4	77	(intron 20 -195)	acagatttctcatgtatg c/a algaactatgaagccatcc	238
ABCA4	78	(intron 23 755)	ctggctcctcctgggtt c/t taltccatccacggggagg	239
ABCA4	79	(intron 26 702)	tataaatacaactcagag t/g cagctctcagccctttga	240
ABCA4	80	(intron 27 155)	ctgttttcaaaccttat c/t ttgattcttgaatcagaa	241
ABCA4	81	(intron 27 385)	tttaagaacagtgagctac c/a tgaactctcttgaatgc	242
ABCA4	82	(intron 28 299)	gacatgactcagaccatg c/t agatctcagcagcttacc	243
ABCA4	83	(intron 29 168)	ctcttccactttgtgc a/g gggacatctcacttacctta	244
ABCA4	84	(intron 29 487)	gctgtaataagaacaaa c/t agactaatctcaattcttc	245
ABCA4	85	(intron 29 567)	agctctagaataaaga g/a agacaaac g/a atccacaagc	246
ABCA4	86	(intron 29 577)	aataaaaag g/a agacaaac c/a atccacaactaagatgt	247
ABCA4	87	(intron 30 -2494)	aatcaactctatctctgc a/g tcataggaatcccaagaa	248
ABCA4	88	(intron 30 -2169)	aagtacaacacagctct a/g gaaaaagcagccagcttc	249
ABCA4	89	(intron 31 535)	ctaacctgacttatactt t/g tgaatcagcttcttgaat	250
ABCA4	90	(intron 35 209)	tcctcccaattttaggg c/a aagtatttactatttgggt	251
ABCA4	91	(intron 37 525)	ttaatttaaagaaatc a/g tcaatcagccctcagtttc	252
ABCA4	92	(intron 37 768)	tggttcagcctggaaacc t/g cctatgaattgtacaggtct	253
ABCA4	93	(intron 37 856)	aaacccctagaagtgctc a/g ggcagcactatctatctca	254
ABCA4	94	(intron 38 62)	tatagaatagttgtgtc c/a agcagagcagggcagca	255
ABCA4	95	(intron 38 761)	tccttggcaggttaattt c/a atgaagacttgggttct	256
ABCA4	96	(intron 38 1315)	caagctcagacttggaaag c/t c/a gggggaataaagacagc	257
ABCA4	97	(intron 38 1316)	agagtcagacttggaaag g/t c/a gggggaataaagacagc	258
ABCA4	98	(intron 38 1561)	gtattttatataatc c/a g/a atacacagctcgtcagaa	259
ABCA4	99	(intron 38 1562)	tattttcagtaattat c/a c/a atacacagctcgtcagaa	260
ABCA4	100	(intron 38 2874)	ctagacaagagg g/c agctcc c/t gccacacagaacttcagc	261
ABCA4	101	(intron 40 1904)	gacactacagcagccca a/c tcttaccctcttcttcat	262
ABCA4	102	(coding region 5814 (Leu 1938 Leu))	ggaaataaacagacattt a/g agcctacatgaactaacaa	263
ABCA4	103	(intron 41 122)	atttgattccagttttatg t/g agggctcatctctgtgt	264
ABCA4	104	(intron 41 411)	ctcttctctctctctct c/a accctctcagttctcag	265
ABCA4	105	(intron 41 443)	gttcagctcaggtttct c/a tctctcagatttacc a/g g	266
ABCA4	106	(coding region 5944 (Pro 1948 Pro))	c g/a tctctcagatttacc a/g ggcacctcagccagcag	267
ABCA4	107	(intron 43 328)	ttttagcctatctctaa a/g aatgcacattgttc c/g cat	268
ABCA4	108	(intron 43 345)	taa a/g aatgcacattgttc c/g cttacctctctccacat	269
ABCA4	109	(intron 43 370)	acctctctccacatttt a/g caaaa c/t gtttcaggagttt	270

遺伝子名	No	存在位置	配列	配列番号
ABCA4	110	(intron 43 376)	caccacatttt a/g caaaa C/I attcaggagtttactag	271
ABCA4	111	(intron 43 670)	ttaacagacttgctccctia T/C aggcagagacagagagatga	272
ABCA4	112	(intron 43 822)	gttaggtctgtctacatct G/A tccagacttctgttactagg	273
ABCA4	113	(intron 43 915)	ggcagagacagctctagaca C/I gcttacttgcttcagacag	274
ABCA4	114	(intron 43 1242)	actgagcttgagcctagaaa G/I aaactatagctttaagacac	275
ABCA4	115	(intron 43 1671)	tagaagaatttcttctcact G/A ggcacacatcatcttctia	276
ABCA4	116	(intron 43 2036)	ttagaggaatcagatatt C/A cttttttcttgcagatttt	277
ABCA4	117	(intron 45 176)	gttttggttctacacac C/I ggcagaaaacacagica C/I agc	278
ABCA4	118	(intron 45 193)	ctc c/t ggcagaaaacacagica C/I ggcagaccttacttggga	279
ABCA4	119	(intron 47 238)	ccaagctcttgatggggc A/G tctgacagagatgcatgacag	280
ABCA4	120	(intron 47 269)	atcagtcagaccttgactg C/A gataagagagggctctacc	281
ABCA4	121	(intron 47 326)	accatttatctcaacagatc C/G gggaccttggccctatitac	282
ABCA4	122	(intron 47 715)	aagtctactagcttggttgg C/A ggcagacacacataac C/I c	283
ABCA4	123	(intron 47 734)	t g/a ggcagacacacataac C/I cacttctatctctgaggt	284
ABCA4	124	(intron 47 931)	ggacactcatatatacta T/C agaatagcagcatgctcagg	285
ABCA4	125	(intron 47 1260)	accctctctgtggacacatc A/C ccatccagagagaggtaac	286
ABCA4	126	(intron 48 1663)	tctctctctcttacttctc T/C aggtttttgaaatttgc	287
ABCA4	127	(intron 49 127)	ggagagcccccacacaccca C/I ggtccctacacagctccac	288
ABCA4	128	(5' flanking region (-1441) (-1400))	gtaaattctagttgaatcag TCA 14-16 attttcagcttgcttctg	289
ABCA4	129	(intron 1 4712 7304)	ggagggcgggagctataggg (A) 8-10 cagcctaattcaagatag	290
ABCA4	130	(intron 1 7295 7304)	ttatggcttggcaa t/a gcat CACAGTCA/Δ ttattctcatcattcac	291
ABCA4	131	(intron 2 951 952)	ccctgcatcagctctctt T/Δ acctctccggagggccca	292
ABCA4	132	(intron 3 2642 2653)	cttgggtaagagcagat (A) 10-12 tagcatgatatattact	293
ABCA4	133	(intron 4 5202)	cacaaagcatctacacccc C/Δ atccacccggctaacctt	294
ABCA4	134	(intron 6 3029 3044)	caataaaacaaattttac (A) 16-18 ctgaagaagatgcaggca	295
ABCA4	135	(intron 6 5138 5139)	ttcatagacatcagatgt (G) cttttatggatttacaaga	296
ABCA4	135	(intron 6 5138 5139)	ttcatagacatcagatgt cttttatggatttacaaga	297
ABCA4	136	(intron 6 5985)	tttcccttcaaacacccc C/Δ agactagagagaggtctgtc	298
ABCA4	137	(intron 6 6094)	ggacagacagaaaagacc T/Δ agttctgtttagcccaaga	299
ABCA4	138	(intron 6 -161)	tatttttcaattatataaa A/Δ agtttttlltlltctaaag	300
ABCA4	139	(intron 7 809 810)	gggcccagatagacacctga (G) 10-13 ggtcttctatggagtaagg	301
ABCA4	139	(intron 7 809 810)	atcttcccaccttctctca (T) 10-13 ggtcttctatggagtaagg	302
ABCA4	140	(intron 8 472 484)	gtaccctggaccttccagaa (G) 11-13 gagagaaatgaccttccg	303
ABCA4	141	(intron 9 48 71)	ataggagcagaagagacaca A/Δ ccaaaatctctctacit	304
ABCA4	142	(intron 9 554)	catgactagatgaaggagg C/Δ ttgagagatgggggggggg	305
ABCA4	143	(intron 10 11)	ggagagaaatgattgattg C/Δ cctcttgaataataggccag	306
ABCA4	144	(intron 11 4242)	tactcttttgggggtaagg (T) 9-11 cctcttccagagagagaaa	307
ABCA4	145	(intron 11 13743 13753)	cegggtggaggggttggggagg (C) cttatttctattatagatg	308
ABCA4	146	(intron 13 636 637)	cegggtggaggggttggggagg cttatttctattatagatg	309
ABCA4	146	(intron 13 636 637)	tctggcttcatctctctc T/Δ aaactagttctgtattctc	310
ABCA4	147	(intron 18 569 570)	tataacctgaactttttttc (A) 7-9 ggaatgcttttttaacala	311
ABCA4	148	(intron 20 (-304) (-297))	gcgaattggttcttctggg (T) 9-11 aaatacctctgattttac	312
ABCA4	149	(intron 22 1236 1246)	gataatcaatgctctaaagg (A) 9-10 tggcattagagatccagacc	313
ABCA4	150	(intron 26 4626 4635)	taaaacgcttctgtttgttt GT/Δ ttacatggttttttagggccc	314
ABCA4	151	(intron 33 115 116)		315

遺伝子名	No.	存在位置	配列	配列番号
ABCA4	152	(intron 36 1078)	taagcagctatcactaaca A/A taacaaaccagagattatca	316
ABCA4	153	(intron 37 290 291)	ctttagcacaagcctggggg (T) tagcattcccca a/g cccctc	317
ABCA4	153	(intron 37 290 291)	ctttagcacaagcctggggg cagcattcccca a/g cccctc	318
ABCA4	154	(intron 38 896)	atataaaggaggagaaaaa A/A gaaggcagctcgtccagggc	319
ABCA4	155	(intron 38 1209 1210)	gtgaccccttagagctact C/T Δ ttcagatctttagaggtt	320
ABCA4	156	(intron 38 1322)	agacttgaag g/ c/a ggggg C/A atagacacaccccagca	321
ABCA4	157	(intron 38 3107)	ggggccacacitcgaagg A/A ggggggggggggttggccc	322
ABCA4	158	(intron 40 152)	ttttctcattatcaagt A/A gaggatcgggttaataagg	323
ABCA4	159	(intron 43 330)	ttagcctattctataa a/g a A/Δ tgcacattgttc c/g calla	324
ABCA4	160	(intron 43 1354)	tttaattggccagccatgc C/Δ ttgggtgttttgtatg	325
ABCA4	161	(intron 47 1305 1308)	caactctgaaggagaag AAG/Δ caccatggcccaagcccta	326
ABCA7	1	5' flanking region -1596	gaaatttttggccctccc C/T t c/ ctcacatcctcagagag	327
ABCA7	2	5' flanking region -1594	aatttggccctccc c/t t C/T ctgactctcgaagcc	328
ABCA7	3	5' flanking region -1180	ggcagtgagtcagggcag C/A tgcaccaalagcacagctgc	329
ABCA7	4	5' flanking region -460	agagctgggtctgtctcc A/G gctggcactcgtctctc	330
ABCA7	5	5' untranslated region -9	ctctccctcctccc A/G gttccacatggctttctg	331
ABCA7	6	(intron 5 91)	ccccggcgaagagctccc G/A ttccagcatccagcgtgc	332
ABCA7	7	(coding region 563 (Glu 188 Gly))	cagctgttggagccctc A/G ggaactggccaggggtac	333
ABCA7	8	(intron 8 103)	ggcggaggctcaggaact A/G tttaagaagtagaggtta	334
ABCA7	9	(intron 8 166)	tgcggagga tcaagagaca C/T gcaagacaaagcagagggg	335
ABCA7	10	(coding region 955 (Thr 319 Ala))	accggacttcagagctc A/G cctcgtcgaaggatctcgg	336
ABCA7	11	(intron 9 421)	ttttttttttttttt T/A taagagatggagatctcac	337
ABCA7	12	(intron 9 463)	gttgcagagctggagctca G/A tgg c/t gaaatctggctact	338
ABCA7	13	(intron 9 467)	ccagcctggagctca g/a tgg C/ t gaaatctggctactca	339
ABCA7	14	(intron 9 488)	gaaatctggagctca C/ t cccgcctcctggatcca	340
ABCA7	15	(coding region 1184 (His 395 Arg))	cgcacagctga tctggggc A/G cctgtggcagcctgggccc	341
ABCA7	16	(intron 10 10)	gagtcaggggtggggccc T/C gtcacctggcgggtctgtt	342
ABCA7	17	(coding region 1388 (Arg 463 His))	cttggggccggccagctgc G/A catcaaatcccaaggaca	343
ABCA7	18	(intron 12 115)	cagcttgcgaacttgcacc T/G ttaacacatccacataacc	344
ABCA7	19	(coding region 1824 (Ala 608 Ala))	cccttctctcagggccc A/G ctcctgttctgtgtctcaa	345
ABCA7	20	(intron 13 55)	ggctcctcaggggtgacag A/G cagggggggcccccagctgg	346
ABCA7	21	(intron 13 78)	ggggcggccctcagctgggtg C/A gggcccccagcccaatccag	347
ABCA7	22	(coding region 1851 (Gly 617 Gly))	cglttctctcacacagctggg A/G gacatcttccctcacagcca	348
ABCA7	23	(coding region 2153 (Asn 718 Thr))	cgaaggccacagctggcaca A/C cgtggcagcccgccctacgg	349
ABCA7	24	(intron 15 34)	ggcggggctcggggccgggt C/G gcacactgtttgcgggggc	350
ABCA7	25	(intron 16 8)	ctggaccacaaggctgagcc A/C ctacagagcttaatagctgg	351
ABCA7	26	(intron 16 161)	ttccgcagctttatagccc C/T cggccagcagggctccggat	352
ABCA7	27	(coding region 2385 (Leu 795 Leu))	caccatctctcagact G/A glagaaagagccacacccgg	353
ABCA7	28	(coding region 2421 (Val 807 Val))	ccggccttgaactctggact C/A tcccttgcagcagctggaaaa	354
ABCA7	29	(intron 20 166)	cgaacacatagagtttgggg A/G tgaacagaagtttcccttgg	355
ABCA7	30	(coding region 3027 (Ala 1009 Ala))	ctctggagagacgtatggc C/T gttggagcaggtggccgctt	356
ABCA7	31	(intron 22 1386)	gggtggggctggagccgggg C/T tccctgaagcaccctttgt	357
ABCA7	32	(coding region 3417 (Leu 1139 Leu))	ggaaatctcagacacagcct C/G gaggagagtttgaagccttgg	358
ABCA7	33	(intron 23 147)	ggagctctggggctcagat C/A tcccttgggaagggcctgggg	359
ABCA7	34	(coding region 3528 (Leu 1176 Leu))	gctggccttagacgttaacct A/G cggctcagatggcccccaca	360

遺伝子名	No	存在位置	配列	配列番号
ABCA7	35	(coding region 4046 (Arg 1349 Gln))	ccccgctggcagtgatgccc G/A gccctgtcccggcgcttgc	361
ABCA7	36	(intron 30 81)	ccccctggagctctccgg G/A cccccggcctcagctccc	362
ABCA7	37	(intron 32 1)	caaggacacgtgtctgggg G/C tgcactgttgatctctccac	363
ABCA7	38	(intron 33 54)	ccactgttggcacttgcctt G/A tctggcccttgtagcagg	364
ABCA7	39	(intron 34 245)	cagactttggaggagcgag G/A caggagagacttcttgagcc	365
ABCA7	40	(coding region 5057 (Gln 1686 Arg))	ggtagccgagacttgaag A/G ggttcttcttattctccccc	366
ABCA7	41	(intron 38 65)	ggcttcttcttcttctt G/A ggttcttcttattctccccc	367
ABCA7	42	(intron 40 154)	cttaccctccacacagga G/G caggcccttgagacacaccttg	368
ABCA7	43	(intron 40 277)	ctggccccggccccc G/C cccacgcttggcccgaggag	369
ABCA7	44	(coding region 5592 (Ala 1854 Ala))	gtgcccggagacccagatc T/C gcgactctcagatgggata	370
ABCA7	45	(intron 41 286)	ctcttgaacttgcctcttg T/C gggccttggcacttgcctt	371
ABCA7	46	(intron 41 389)	tggcgttccagtttgcag C/T gtttcttgccttcttccat	372
ABCA7	47	(intron 41 981)	cacactatggccttggccca G/T ac C/T cal C/g cc a/g gctcacca	373
ABCA7	48	(intron 41 994)	actatggccttggccca C/T ac C/T cat C/g cc a/g gctcacca	374
ABCA7	49	(intron 41 998)	tggccttggccca C/T ac C/T cat C/g cc a/g gctcacca	375
ABCA7	50	(intron 41 1001)	ccctggccca C/T ac C/T cat C/g cc a/g gctcacca	376
ABCA7	51	(intron 41 1051)	actatgttggccttggccca G/T accatggcccccgcacat	377
ABCA7	52	(intron 41 1131)	tgccttggccttggccca A/G tgccttggccttggccca	378
ABCA7	53	(coding region 5985 (Leu 1995 Leu))	ggagcgttcttgccttggccct G/A gccatcatgttggatggcg	379
ABCA7	54	(intron 44 201)	ggcgcagagacagagagcat G/C acccgagggccttgggtgga	380
ABCA7	55	(intron 44 233)	ctggcggatgtagagata C/T atcagatgtgtgttggat	381
ABCA7	56	(intron 44 313)	agttaggagagggctgtt A/G gtagcggggccataggaaa	382
ABCA7	57	(coding region 6133 (Ala 2045 Ser))	tggcggcgaggttcttggcg G/T cggagcttggagagagacat	383
ABCA7	58	(coding region 6159 (Gly 2053 Gly))	ctgcagagacacataggag C/T cccctggccttccagctgc	384
ABCA7	59	(intron 45 27)	acggcccccgggttggccct G/C gggagggcagcttggggcca	385
ABCA7	60	(3' flanking region 108)	cagcttgaatgtgtacatac G/A gccaatgtgtgtgttcatag	386
ABCA7	61	(3' flanking region 376)	cttacaggagccctgtgtcc C/T gtagcacacagccagagcccg	387
ABCA7	62	(3' flanking region 687)	cagcagagagacttggggag G/A g/a gggagagagttcacactgc	388
ABCA7	63	(3' flanking region 688)	agcagggagacttggggag g/a G/A gggagagagttcacactgc	389
ABCA7	64	(3' flanking region 1169)	cttcagactgacccacttca C/T ggggttgcagggcaggttga	390
ABCA7	65	(intron 9 388 422)	ctgtgacttaccacgtctgc (1) 22-26 aagagatgaggttcactct	391
ABCA7	66	(intron 12 175 184)	ggggacttggaggtctgtc (6) 8-10 actctgaggtctggggcc	392
ABCA7	67	(intron 30 81 87)	ccccctggagcttctccgg (6) 6-7 gggcctcagcttcccttccc	393
ABCA7	68	(intron 34 349 361)	agaagagaaagagagaaag (A) 12-14 cagaaatgtcttgggtga	394
ABCA8	1	(intron 1 204)	ctggatattatattagata A/G ataaacacatttagtagaa	395
ABCA8	2	(intron 1 266)	aacatagtgtgttttaaac A/G taactgattatagaaataag	396
ABCA8	3	(intron 1 733)	ttccatattatataaag T/A attcatgttttgcagctt	397
ABCA8	4	(intron 1 861)	agcttgggttttcactga C/T cttaagacttgaacttcttc	398
ABCA8	5	(intron 1 907)	ggggagacatcttcttggc C/T aatgttatttacttggcca	399
ABCA8	6	(intron 1 1262)	cagaacttggccttct G/A taggttgccttacttga	400
ABCA8	7	(intron 1 1537)	agcttcttaagatata G/C gctgaatttcttccactta	401
ABCA8	8	(intron 1 7622)	tgttataagacatataat T/C tagccacttctatcc C/T a	402
ABCA8	9	(intron 1 7639)	t/c tagcttcttctatcc C/T agaacaacaggtctataag	403
ABCA8	10	(intron 1 7720)	tccatcttataacacttgc C/T tggagacagaaagagaa	404
ABCA8	11	(intron 1 9397)	cataatataatataatgc G/A cacacacacataatata	405

遺伝子名	No.	存在位置	配列	配列番号
ABCA8	12	(intron 1 9519)	agtagtcatcttkaacaa /C alecttgagaaatgcagaaa	406
ABCA8	13	(intron 1 12973)	ttgataacagcagcagcga /C cacaataaataatgaagaaa	407
ABCA8	14	(intron 1 13100)	catggatattagctctgc /C tttttgtttgttgaggat	408
ABCA8	15	(intron 1 13128)	ttgttcagagatttctt /C ttttaagaacttattata	409
ABCA8	16	(intron 2 420)	caattagttttcttcaaaa /G gtagaagaatggaaattgta	410
ABCA8	17	(intron 2 505)	catataaaaattctta /T acttttgattatttataaaa	411
ABCA8	18	(intron 2 819)	gcaatgcttggaaactatct /T ttaaacacatttgcattca	412
ABCA8	19	(intron 3 915)	ttgttgatagatcagta /C agtgactagttaacaataat	413
ABCA8	20	(intron 3 1539)	aaaggaaatctgtgtgat /T gccctgtatcttctcatag	414
ABCA8	21	(intron 3 2341)	ttctttctttgtcaactc /T gtccaatttccactcaact	415
ABCA8	22	(intron 3 2882)	tattctatactgtactct /G ttaatacttataataaaa	416
ABCA8	23	(intron 3 3314)	attgaataatctatctct /G tatttaccatttcaaatia	417
ABCA8	24	(intron 4 89)	gaagttagatgcacaaat /G agaacacatcttgcataaa	418
ABCA8	25	(intron 4 3264)	ttccattgctctattatcc /T gtttatactcagttttaga	419
ABCA8	26	(intron 4 3403)	aaagaccacacaaattct /G alcagacaaaagcacagga	420
ABCA8	27	(intron 5 368)	gcttactgaatatataatt /C agaaaagcctatgcacagaa	421
ABCA8	28	(intron 5 479)	tgagaatgtagtactca /G aatctctgactcc g/a aggtc	422
ABCA8	29	(intron 5 494)	actca a/g aatctctgactcc /A aggtccagcaggtcaatga	423
ABCA8	30	(coding region 792 (Ala 264 Ala))	alggcttctggatctcagc /A tctgtgtgagtcacacag	424
ABCA8	31	(intron 6 200)	ccctccagtagcaggag /G a/caggiccg a/g ccaccatgcc	425
ABCA8	32	(intron 6 210)	agctggagtt g/a caagctccg /G ccaccatgctcgtataatt	426
ABCA8	33	(intron 6 1751)	gtgagttatttctgttgc /T tttccagctgtttgttttt	427
ABCA8	34	(intron 6 1808)	atttcaattatglttttcaaa /T aatatgttaaaaacaaagaa	428
ABCA8	35	(intron 6 2412)	tattctaaattcaagaat /T cctcccaaaacttttaccit	429
ABCA8	36	(intron 6 2506)	tgatgaataagatgaataaaa /G agttactttaga a/g tccattt	430
ABCA8	37	(intron 6 2519)	gaatga g/a agttactttaga /G tccattttagagtttcttt	431
ABCA8	38	(intron 7 28)	agtaaatataatcttctcc /G tccacctatagcttaaaaal	432
ABCA8	39	(coding region 991 (Gly 331 Ser))	taagaatcttcttccacc /G a/cctgctgtgttctctc	433
ABCA8	40	(intron 8 74)	tggaatcagagctataal /T atttacaacacagcaltg	434
ABCA8	41	(intron 9 1417)	acacatacttaataattt /C ctcgttcttctattttgttt	435
ABCA8	42	(intron 9 2504)	agagaaaattatgtgtttgc /A aatgaataaagcagaaata	436
ABCA8	43	(intron 10 2013)	tgccaaagatctttccaac /T tgcacagtggttccacaga	437
ABCA8	44	(intron 10 2376)	ctgaagaaaattgtcacttt /G aagttactttttttttt	438
ABCA8	45	(intron 11 -597)	aaaaaaaataaagagag /G gagaaagaaaataattgtta	439
ABCA8	46	(intron 11 -528)	tataaaagttagaataaaaat /T a a/g taigtitttaaaaatagat	440
ABCA8	47	(intron 11 -526)	taaaagttagaataaaaat g/a a/g tatgttttagaataatagat	441
ABCA8	48	(intron 11 -342)	c/caaagggttttagccat /G taataacttacttattactt	442
ABCA8	49	(coding region 1632 (Asn 544 Asn))	ggttcagtcacactataaa /T aataagctttcagaaatgsc	443
ABCA8	50	(intron 14 252)	ctatttgcataatagtaga /G ttgagtttcttaagagataa	444
ABCA8	51	(intron 15 130)	ttttgtttttagacagaaat /C tgcatactctcgtctcctg	445
ABCA8	52	(intron 16 534)	acataatcatttcaaat /G cacatttttatgtgacaca	446
ABCA8	53	(intron 16 588)	gaatacagaaagtgtta /T gcaatttctgatttactt	447
ABCA8	54	(intron 16 645)	atttaagaaaattttaga /T gttttaggttgaatgaagaa	448
ABCA8	55	(intron 17 431)	tctcaggtttttttttttt /T tttctttatattagaataatg	449
ABCA8	56	(intron 17 1390)	gcataaacctgtttttttaga /A ttgggtaccctcatatttca	450

遺伝子名	No.	存在位置	配列	配列番号
ABCA8	57	(intron 17 2452)	cagttatccatagtaac G/A cgaaga G/C tctaatacagag	451
ABCA8	58	(intron 17 2460)	actatagtaac G/A cgaaga G/C tctaatacagat G/C cttag	452
ABCA8	59	(intron 17 2475)	gaaga G/C tctaatacagat G/C cttagcagagccaactta	453
ABCA8	60	(intron 18 152)	gaagaacacagagagagag G/I agaatctgacatccaaagg	454
ABCA8	61	(intron 19 7477)	aaaactatitllgaagaca C/I ttgaacttaaaaaatctt	455
ABCA8	62	(intron 21 195)	lltllaaatlaataataa T/C G/C acacaacatitllcaag	456
ABCA8	63	(intron 21 197)	gtttaaagtaataataa T/C G/C aacaacatitllcaaga	457
ABCA8	64	(intron 21 287)	acttggtaggtggagga G/I gggagagagatagcaagg	458
ABCA8	65	(intron 21 403)	cttcacaaatgtcacat G/C ccttaaaccttaagataa	459
ABCA8	66	(intron 21 1207)	cccagcc G/A gactcagagc A/G ggaicagagcagcgtaac	460
ABCA8	67	(intron 24 682)	ctctatataagacaataa A/C caaggtgcacaaaggccaig	461
ABCA8	68	(intron 25 212)	ccgtaataataagagaa G/A aaggtaagagagtagtagga	462
ABCA8	69	(intron 26 67)	aaatattttagtctgtac A/G cactatgaactctttat	463
ABCA8	70	(intron 27 515)	gtgtcccaaacacatca G/I tttcatcttttgcattaca	464
ABCA8	71	(intron 27 661)	ccggaattatcacacta G/A aalggagagagaaagtaat	465
ABCA8	72	(intron 30 1967)	caaaaatagatacaagagg G/C tgaatigactttaattga	466
ABCA8	73	(intron 31 112)	ctctaaatgtccagcagg G/G acactggtagattacac	467
ABCA8	74	(intron 33 401)	ccttcacaggtgtgaga C/I gctgtgttaaatitattat	468
ABCA8	75	(intron 35 484)	taacacatactctc a/t tct A/G ttatlllctatagacaaa	469
ABCA8	76	(intron 36 288)	ttgcataatgtgtgtaa A/G cctagtcacaaactcaglla	470
ABCA8	77	(intron 36 375)	atatatttactctcttag C/G cctatataaanaactaac	471
ABCA8	78	(3' flanking region 674)	scggtagacataaagccc G/A gaagctctttagtgcctta	472
ABCA8	79	(intron 1 56 57)	tttgccttggtagagc T/T attcagaggttttctctt	473
ABCA8	80	(intron 1 186 1191)	taagtaataaataaagc A/G-11 gaaattctctctatcacag	474
ABCA8	81	(intron 1 9877 9885)	ctctcaaaaagtagtaac A/G-12 tcaactgagtagacaaaagt	475
ABCA8	82	(intron 1 12588)	gtactagagtagctctctt T/T gcaacagagagcccaagga	476
ABCA8	83	(intron 6 78)	lcaatcatctttttttt T/T gcaatgagctctctctct	477
ABCA8	84	(intron 9 265)	gtataggatititititit T/T agactctttagaagtagt	478
ABCA8	85	(intron 9 266)	atttttttagaagtagtca A/D tagtctctcaattcttc	479
ABCA8	86	(intron 11 -447)	ggatacttgggtttttt T/T ctacaaactcaagitttttg	480
ABCA8	87	(intron 15 8407)	gtggaataattttgactta T/D gcaattggtagaataaait	481
ABCA8	88	(intron 15 9458 9470)	tatctgagtagaataatgic T/T-15 ctgaatgccagcttgcagtt	482
ABCA8	89	(intron 16 54 56)	tgaataatgtagtcatcat CAY/D aattatataatcacacta	483
ABCA8	90	(intron 17 433)	tcaggtttttttttt t/a t T/D cttagttagaatttagac	484
ABCA8	91	(intron 24 1462)	actctctcaaaaaaaa A/D gagaanaaaaaatctgcac	485
ABCA8	92	(intron 33 155)	caatacttcaaaaaaaa A/D gacttttctctgtagatatt	486
ABCA8	93	(intron 34 184)	atactgaatgttttttt T/D cttctttctcatagaccic	487
ABCA8	94	(3' flanking region 1240)	atcttggaccacaaaaaa A/D ctttctctctcttggcag	488
ABCA8	1	(5' flanking - 196)	gctttgaccacatagtag T/C actcaaatattttatct	489
ABCA8	2	(5' flanking - 16)	tactcttaccgtgtagag T/C agaacatgagaatctact	490
ABCA8	3	(intron 1 + 7166)	cttctggagagaggtgtc A/C gaaatataccaatcccaag	491
ABCA8	4	(intron 1 + 80091)	gaaataatattcaggtctg A/C aataatatacagacttatag	492
ABCA8	5	(intron 1 + 103126)	gataatatacaaatctac T/C gtgtctcaagaagaagctat	493
ABCA8	6	(intron 1 + 103148)	gtctcaagaagaagctac C/T gataaatttagtctcttag	494
ABCA8	7	(intron 1 + 108428)	aataattatcatctc A/G taccatttcacacactca	495

遺伝子名	No.	存在位置	配列	配列番号
ABC81	8	intron 1 + 12042	catagttgaatgicccca A/G teattcagcagtcgcgctt	496
ABC81	9	intron 2 + 491	gtctcggcttcacggag G/A actagagttagctccacct	497
ABC81	10	intron 4 + 36	attaactatcaaatatctt C/T ggaatttcacatctctta	498
ABC81	11	intron 5 + 1596	ttagctctcttactcttca T/C agtggagaatcaaatctt	499
ABC81	12	intron 8 + 1789	aaacactcgaatatlaaac G/T cttcttggaccacacscica	500
ABC81	13	intron 14 + 24	agttgtcttcccttctcc T/C tttctagagtcgcaaaaata	501
ABC81	14	intron 14 + 81	tcaggaagttgagaacta G/T tataatcggagaagagggaa	502
ABC81	15	intron 15 + 38	caaacaccatgatttata A/G ctaagaacatttactact	503
ABC81	16	intron 17 + 73	gtttgggcttagggctac A/G gttagagttggagaacagaga	504
ABC81	17	intron 18 + 564	caacgttaagttacaatct C/A aaggaatctctctgttlla	505
ABC81	18	intron 18 + 2062	ttccclagggaaagttat C/T ctcgtgtcttcttggacca	506
ABC81	19	intron 18 + 2283	ccacatcagatttcccccag A/G cacttggagacatttazaa	507
ABC81	20	intron 20 + 557	aaacccclaccattacac G/A tataatgttttcttggccatt	508
ABC81	21	intron 21 + 24	cttcccttcttctactt G/A ttgtctttaaattggccatt	509
ABC81	22	intron 21 + 2725	gtgaccgttttttggcagc A/G ggttttagttcttccctca	510
ABC81	23	intron 21 + 4725	tttgtatttaagaatcca A/G aaggaatgaatatataatt	511
ABC81	24	intron 22 + 8507	tgcaacttaggaataaaca A/C atggaatgttgaataata	512
ABC81	25	intron 22 + 8537	tgtaaatatactttttttt T/A aaaaaaagacacatttat	513
ABC81	26	intron 22 + 8555	agacacattatcagcat T/C algatcagactattacattt	514
ABC81	27	intron 22 + 8952	cacttggcttacttggttt G/A caaatctactggccttacc	515
ABC81	28	intron 22 + 9520	caccacaataatcttttctt A/G cacttggcttggccttctt	516
ABC81	29	intron 22 + 9836	agacttctactttagacata C/T ggcagaagaaagagacatt	517
ABC81	30	intron 24 + 377	taaaacacatgttgtta C/A taattcttgcagccttgg	518
ABC81	31	intron 24 + 1493	ggggaggtctccagacaga A/A ctaggaacttggccttggat	519
ABC81	32	intron 24 + 1495	gggggtctccagacagaac A/T tggagacttggacttggat	520
ABC81	33	intron 25 + 342	tcagcccttgaatctcttgg C/T tgaagcatctcttggcctc	521
ABC81	34	intron 26 + 134	cttggataagcttggagc C/G taatatagtcttcccaatgg	522
ABC81	35	intron 26 + 1272	gtcttcaatttttggctga A/G cttaaaacagagactttaa	523
ABC81	36	intron 26 + 1394	tattagtggtgtgttgaag A/G ttgtctataataaattga	524
ABC81	37	intron 26 + (1987-1988)	aaggcttggagagatgaag AAGG aagcctatttgcctccagac	525
ABC81	38	intron 26 + (1987-1988)	aaggcttggagagatgaag gaggctatttgcctccagac	526
ABC81	39	intron 27 + 59	gcagctcttgcctcttag G/T ttgatttalaagggccttgg	527
ABC81	40	intron 27 + 80	ttgatttalaagggccttgg T/C tccagaagtgagaagaaat	528
ABC81	41	exon 3 + 3	aaacccctatttttagat C/T caagcagtcagtcagaat	529
ABC81	42	intron 3 + 45	caagccttctacttatacca T/C gccttctttaggcttctt	530
ABC81	43	intron 3 + 498	actcaataagttggtagag C/T agagacaattcaatcacag	531
ABC81	44	intron 3 + 515	gagagacacattcaatcaac A/G gacagaagctttagataga	532
ABC81	45	intron 6 + 1030	tagttttcagatagaat G/C aaaaatagatagaagttt	533
ABC81	46	intron 6 + 1437	gttaaccccttcaatcaaa G/A ttgttatttcttcttca	534
ABC81	47	intron 6 + 2449	tttacttgaacacactglla G/A cacttatttcttcttctt	535
ABC81	48	intron 7 + 451	cccttgcaccccttgcctt G/C taagtttggcttattatgt	536
ABC81	49	intron 7 + 530	agtagagacagcttggcaat C/G acacccagacagactaacg	537
ABC81	50	intron 7 - 152	aacagaatcaagaataag T/C ttgttaattttagagcct	538
ABC81	51	exon 8 + 40	aggataattttttagtctg C/T ctgggtaccatcatagccat	539
ABC81	52	intron 8 + 130	ctggttgaactccagatacca T/C aagaagattgttaaatctt	540

遺伝子名	No	存在位置	配列	配列番号
ABC88	7	intron 5 + 547	agttcatagcattctgcctc g/a gccccctagcctgcct	586
ABC88	8	exon 7 + 57	ggcaatgtcgcacatgcg a/ gcttgcctatgggcaacg	587
ABC88	9	intron 9 + 1231	tttcacagtcattggaca c/ cctgcctatgccttttgc	588
ABC88	10	intron 9 + 2164	cctctggaggtccttcag c/ gctcctatgtagagattct	589
ABC88	11	intron 9 + 2645	ttctgcctggctcctccc c/a ggtgcctttagcaagctct	590
ABC88	12	intron 9 + 2646	tctctgcctggctcctccc g/a gctcctttagcaagctcag	591
ABC88	13	intron 9 + 3229	caggcccaagaggagctc g/a taggtcagctggctcctt	592
ABC88	14	intron 12 + (113-114)	tctctcactaccacaagggg (c) ccttcttcttgggacaatc	593
ABC88	14	intron 12 + (113-114)	tctctcactaccacaagggg ccttcttcttgggacaatc	594
ABC88	15	intron 13 + 128	tgctctgggagaccctggc c/ gctctcacatgctcagct	595
ABC88	16	intron 13 + 305	atccaggtctagagagctt a/g tagtggaggtgcagctc	596
ABC88	17	intron 14 + 135	accagttgtgtaggagagac c/g agaacacagaccacaaggaa	597
ABC88	18	intron 14 + 159	accacagccaaaggagacg a/ gtcgttctgttgggacaggg	598
ABC88	19	intron 15 + 747	gttggagcttgggctcctt a/g aggggagacagaggaaatc	599
ABC88	20	3' flanking + 333	cctatccctggctcctccc c/a ggaacctacgtctcctc	600
ABC88	21	3' flanking + 1168	ccctcttctcagggctgcat g/a cagtgcatgtagggagc	601
ABC88	22	3' flanking + (1719-1721)	taaacccgagagaccgccc g/c/ tttctaacctggctcggcc	602
ABC89	1	intron 1 + 69	agggtctcagggcagggcag g/c gttggggggcgttgggac	603
ABC89	2	intron 1 + 8873	tggggccagcacttggggcc c/ ggaactacctcaaggcttc	604
ABC89	3	intron 1 + 8940	accagctcagcctggccagc g/a gacacagggcaccagctgg	605
ABC89	4	intron 1 + 11410	agatccagggatccagagg t/c tgggaatgagctcctggctc	606
ABC89	5	intron 1 + 12863	gggaagcagatgccacaaa c/a gctcgtgacttcacttcca	607
ABC89	6	intron 1 + 19731	gccaagtgctcagatcgagc c/a agggaggggcttgaagggg	608
ABC89	7	intron 1 + 29549	cagaaicagatgccgtaa t/c gttgttagagagcctggacaa	609
ABC89	8	intron 1 + 31793	ggccagggggggggggggg tac c/ ggcctagaccgttgggcaaa	610
ABC89	9	intron 1 + 37537	agaaicacaggggtggggg c/a cccgggaggggggcatcta	611
ABC89	10	intron 1 + 38293	taccagcctctcttttag g/a gaccatgtagccttctcaat	612
ABC89	11	intron 1 + 44661	ccgaggtggcttggctttag a/g gcaagatggcgtctctgac	613
ABC89	12	intron 1 + 49576	aaagtggccctgggcttgg c/ ccttgaagccttaagagacc	614
ABC89	13	intron 1 + 64659	ccacagaaagccgggtagc c/a cacttgcagctcaacacac	615
ABC89	14	exon 2 + 448	cctgttttggggcctcttc g/a tggagctatcatttcactc	616
ABC89	15	intron 7 + 3364	ggtaccaggggtggggtac a/g gtagacagaaagcgtgtc	617
ABC89	16	intron 11 + 113	gggcccaggagctctccca g/ actatagcctcttgggctg	618
ABC89	17	exon 12 + 370	cccagggcttggagcactaa a/g gacagctggccttggcctat	619
ABC89	1	5' flanking - 424	tcggctcggcgtctcggcc c/ ggtcggcggcgttgaagaaag	620
ABC89	2	exon 1 + 491	acaaagggggggttggggcc c/ g/ caagggcgggacgtccggag	621
ABC89	3	intron 1 + 37	ccacttccctggcggggc t/g cctcttctccacacgggggg	622
ABC89	4	intron 1 + 217	actcgttggagatttttca c/ ttttcttcttggagacac	623
ABC89	5	intron 1 + 405	ggctttatctttttttt t/a aaccaaaacacattatle	624
ABC89	6	exon 3 + 185	ggggccggggcagggcttc c/ gtaggcatcagatgagat	625
ABC89	7	intron 6 + 1269	caaatcacaacttggctt c/g cacagaaatgggttggagaaac	626
ABC89	8	intron 9 + 632	ccacacacacacacacac c/a gcaagggagggagggaggg	627
ABC89	9	intron 10 + 2373	tactcagagacacagaca c/ cctcaccatcagagctca	628
ABC89	10	intron 11 + 108	tccttctcgtttttttt t/g ttttttttttcttggaggg	629
ABC89	11	intron 11 + 2379	catggtttttagtatattc t/a gttttagtcatcattcatca	630

遺伝子名	No.	存在位置	配列	配列番号
ABC811	1	5' flanking - (2596-2595)	tggttttagagcttctct 11) gagacatttttctaagett	631
ABC811	1	5' flanking - (2596-2595)	tggttttagagcttctct gagacatttttctaagett	632
ABC811	2	5' flanking - 1746	agcigaaggaattagcac G/A acaactcagtacacact	633
ABC811	3	5' flanking - (326-314)	aggggaagtttaagga 11) 9-12 gcttggttaatttaagt	634
ABC811	4	5' flanking - 135	agaaggtttccaaagcac G/C cigtgttgggttaattct	635
ABC811	5	intron 1 + 51	aaataagatcacaataaa A/D tagcgttggaatcatgtt	636
ABC811	6	intron 1 + 58	aattcagtttttagtcac C/T caagcagtggaatcacat	637
ABC811	7	intron 1 + (1938-1951)	aaaacgttttaagacctt A 10-13 gaaagaagaacacgttag	638
ABC811	8	intron 1 + 4517	ggtttccaaatcatcat G/A aaaaanaaanttttgca	639
ABC811	9	intron 1 + 5651	aaaagaatagattagtaa T/C tagtatcttgccttaag	640
ABC811	10	intron 1 + (12200-12201)	aaagaaagtccttagcccc G/T Δ gtttatttggggcattac	641
ABC811	11	intron 1 + 13023	gttggcctacitltaalttaa G/A aagaagaagaataataat	642
ABC811	12	intron 2 + 739	ccgcattatcttgacctt G/T actgggaagaacagtagtg	643
ABC811	13	intron 2 + (921-922)	taattttagtcaaaaagt (CAATCTCTTCACTAATTTGAAA(G))	644
ABC811	13	intron 2 + (921-922)	taattttagtcaaaaagt (CAATCTCTTCACTAATTTGAAA(G))	645
ABC811	14	intron 3 + 644	agccacagtttctatttcc G/A tgggaatttaaaaaatggg	646
ABC811	15	intron 3 + 231	aaagaacctgatttagctt A/G tactgaatctctagaagag	647
ABC811	16	intron 3 + 2406	aaagggtgctttaaacc T/C tatgttttcttcaatagtt	648
ABC811	17	exon 4 + 10	tttctcaggtttacaaa T/C gagaagaaggttagtgcct	649
ABC811	18	intron 4 + 434	aaatttatagttatttca A/G tcccccacacatttatcta	650
ABC811	19	intron 4 + 518	gtatagcagtaactaaac G/T aaagtcagcttctgaataa	651
ABC811	20	exon 5 + 120	ggcaatagacagatgttt T/C atttactacacatttagtt	652
ABC811	21	intron 5 + 320	gggaagggacacatgaattt T/C acttgaatctatctccaa	653
ABC811	22	intron 5 + 16076	aaagaagtaaacagtaagcc T/C cctgattttagcacacatc	654
ABC811	23	intron 6 + 303	atttgcaggttctttagag C/C gggcagtttagtagcttga	655
ABC811	24	intron 7 + 1141	aaaggaatttcagacagca T/C ggaagaagaagcttccaa	656
ABC811	25	intron 8 + 2463	ccattgcttaattagaaga A/C ctatgcataggcttaactta	657
ABC811	26	intron 8 + 2677	tcaatgattttagacaga A/C tctaatatttattaaacc	658
ABC811	27	intron 8 + 2699	ctaattgttatttaacc A/T gccacatgtttaaataatct	659
ABC811	28	exon 9 + 24	gttccagttttagcacta T/C gaagcagaagccttagccaa	660
ABC811	29	intron 9 + 108	cactttagctttagcctcc A/G gagaagactttagtcaaga	661
ABC811	30	intron 10 + 2475	taattctcaacacacaga C/A ttatttatttagaacatg	662
ABC811	31	intron 10 + 2478	tcatccaaacacacagctt T/A attcattaaagaacatga	663
ABC811	32	intron 10 + 2711	ttttagaatttggaaagcca C/T taaatattttagcagtcaga	664
ABC811	33	intron 10 + 3539	agtgacttaatttagtctca C/G ttgtccacagaagaaagag	665
ABC811	34	intron 10 + 3623	tgcagaaggttcttcttca T/C gaccttcttagatttcagaa	666
ABC811	35	intron 10 + 3661	gaattcatttaataaataa A/T cacaataagacagcttagcat	667
ABC811	36	intron 10 + 5100	ggggcactttagcttggc A/G atagactatgccaatgaaa	668
ABC811	37	intron 10 + 5292	gctattttagtagaacatct G/A ggcataatcaggtagccttc	669
ABC811	38	intron 10 + 5312	gaataattttagtaaaaa A/Δ taaagttatttttaatac	670
ABC811	39	intron 12 + 116	tggttccagtaataaggaat G/A gaagttcttctctgaaag	671
ABC811	40	intron 12 + 326	gataatacaagcaattta G/C aacaatcaggaagacacaggt	672
ABC811	41	intron 12 + 335	caagcaatttaccacaatca A/G gaagcagaagtttctccaa	673
ABC811	42	intron 12 + 2572	ccctactttagcaatgttt C/T cttttactttagtttttaggg	674
ABC811	43	exon 13 + 23	tctaaatgacttcaacatag T/C callaaaccagaagaatga	675

遺伝子名	No	存在位置	配列	配列番号
ABC81	44	intron 13 + 70	atgcagatatatgaacaa C/1 aaaaagatagacatacat	676
ABC81	45	intron 13 + (1578-1579)	ttatggcctctatititc (C) tggcattggcagataga	677
ABC81	45	intron 13 + (1578-1579)	ttatggcctctatititc tggcattggcagataga	678
ABC81	46	intron 14 + 32	catatctctgggaac C/1 aaagctatagaagaana	679
ABC81	47	intron 14 + 80	cacatataacattctt C/1 tctatgattccaaatcat	680
ABC81	48	intron 14 + 439	tatigtcaaaaacattc A/G tigtatctccattctaa	681
ABC81	49	intron 14 + (1262-1263)	cagccttgcattatattt (T) cctgtgtgtctacagag	682
ABC81	49	intron 14 + (1262-1263)	cagccttgcattatattt cctgtgtgtctacagag	683
ABC81	50	intron 14 + 1283	gcgtgtgtctacagag A/G aaagacacagattgttc	684
ABC81	51	intron 14 + 1339	tgatagatttttggacc C/A tggcaattttatttgg	685
ABC81	52	intron 14 + 1359	atgaccaatttttttgg C/G tgaanaattttatttgg	686
ABC81	53	intron 14 + 1480	tatgatagaacaataccc G/A tctggagaaggatattct	687
ABC81	54	intron 15 + 370	cccttttaatactcaca G/A cctatttaagaatttcca	688
ABC81	55	intron 16 + (1550-1551)	aaagtttaagtgtttatca (T) 9-12 gctacttctgaagacttct	689
ABC81	56	intron 17 + 188	tttcttcccaattcagg C/G ttttggtaagcttctc	690
ABC81	57	intron 17 + 194	ttcccaattcaggctttt C/G gtagcttctcattcttct	691
ABC81	58	intron 17 + (197-198)	caattcaggcttttgg (T) agcttctcattcttctgg	692
ABC81	58	intron 17 + (197-198)	caattcaggcttttgg agcttctcattcttctgg	693
ABC81	59	intron 17 + (289-296)	ggagcttcttttaaaaaa G/A A/4 tctgtgttgaattctct	694
ABC81	60	intron 17 + 1070	tcagacttgggttttctat C/1 tttcttctgagaacagtt	695
ABC81	61	intron 17 + 1651	tgttaataatctatgta C/G atgctcagagattttctg	696
ABC81	62	intron 17 + 2226	ccttaactctctatca C/A gcaacttctctcaccact	697
ABC81	63	intron 17 + 2979	ctctctctctctcag C/Δ ctaattctcagttgact	698
ABC81	64	intron 17 + 3248	aatcccaatctcactta C/G ccatctcactcactt	699
ABC81	65	intron 17 + 3289	atcccaatctcacttag C/1 caictcactcactt	700
ABC81	66	intron 18 + 97	aataagattttctagat A/G tatctacagattttcag	701
ABC81	67	intron 18 + 98	ataagattttctagat C/1 atctagcagttttcag	702
ABC81	68	intron 18 + 897	ctctgaagtttgaatata C/1 cttattgtgttgaatca	703
ABC81	69	intron 18 + 2681	atataagatcagctcag A/G tcaaatatagacaccata	704
ABC81	70	intron 18 + 3780	ggaccatctctgggcaat C/G gtctcagaatgtctgta	705
ABC81	71	intron 18 + 5741	ctacccgataataaac C/1 agacaaagttttctt	706
ABC81	72	intron 18 + (5882-5883)	tggatttctctcagttcag (C) tttttatcaagccacga	707
ABC81	72	intron 18 + (5882-5883)	tggatttctctcagttcag tttttatcaagccacga	708
ABC81	73	intron 19 + 10022	tggtaagttaaaaaaaa A/Δ agattcaactataatgct	709
ABC81	74	intron 21 + 322	caagatcaatctctcccc C/Δ aggggttgggtaacagggc	710
ABC81	75	intron 22 + 257	ctatcaatttctctcga C/1 aetgattcttccattcc	711
ABC81	76	intron 22 + 552	taataatacttctctctg C/G ggggtaataagagagagla	712
ABC81	77	intron 22 + 569	tggggataatggggat C/A gtagataaacacttctca	713
ABC81	78	3' flanking + 243	aaacacacagaatgacata C/A aactaaagggcaggaatc	714
ABCC1	1	5' flanking - 1661	catccacttggggagccc A/G ggcataaaaaatcacag	715
ABCC1	2	intron 2 + 635	gattgcttctcactcactt C/G ggttggggcagcttgggg	716
ABCC1	3	intron 2 + 4769	ggcagagagagctcaggg C/Δ ttctgtgttcaaalgggttc	717
ABCC1	4	intron 2 + 10059	tatggagattttctctctt C/1 tcttgggtttctctctga	718
ABCC1	5	intron 2 + (11965-11964)	taaaacaaatcaaatcaac (T) 18-20 aaacagccagcttggc	719
ABCC1	6	intron 4 + 4302	catctgataatcagacct C/G gggagggcagggcagagla	720

通配子名	No	存在位置	配列	配列番号
ABCC1	7	intron 4 + 4394	gcttactataaatacaaa A/C attagcaggcatagctggc	721
ABCC1	8	intron 4 + 4524	ccatgcctcagccctggg T/C accaaggtagaactctgc	722
ABCC1	9	intron 6 + 9045	agctcctlaaataccctgc G/A ccccaagaatcagctggc	723
ABCC1	10	intron 7 + (3059-3071)	agctttttagtaccctt (A)11-13 gccatttttccgtagacc	724
ABCC1	11	intron 8 + (885-889)	ttctatgacagaaagaa GAA/Δ agcaactcccaattaaaca	725
ABCC1	12	intron 11 + 193	taaatctcagatgaatt C/A tcttggatgcatggcttt	726
ABCC1	13	intron 11 + 784	tgatgattgctcagaaat C/G aagcaatgttgatctac	727
ABCC1	14	intron 12 + 122	agcttgcctggcatggg C/G tcaacttggagaccltca	728
ABCC1	15	intron 12 + (3138-3148)	acctatcttatgaaag (A)10-12 tcaataaaaacatttac	729
ABCC1	16	intron 12 + 3227	tggtatgttgatgaagg C/T tatcccaaggctcccccag	730
ABCC1	17	intron 13 + 2050	tgctattacaacttctt T/C ctggatcaggttggcaatt	731
ABCC1	18	intron 13 + (2061-2062)	ctattacaacttctt (C) ttggcagggtggcaatta	732
ABCC1	19	intron 13 + (2061-2062)	ctattacaacttctt ttggcagggtggcaatta	733
ABCC1	20	intron 13 + 1176	gccacttggggggggccaa G/A cagcttccaggccctgtca	734
ABCC1	21	intron 14 + 179	aaagaagaataacatttg A/T ctcttgcagagaaactgc	735
ABCC1	22	intron 16 + 219	ctagacagagggttccctg C/T gattatagttacacaccc	736
ABCC1	23	intron 16 + 310	ggaagtctcttctcagtg C/T ggatgagtcaggacatcg	737
ABCC1	24	intron 16 + 890	ctctcagagaataatcl C/T tagagggcctgcttgaata	738
ABCC1	25	intron 17 + 1171	aaaccaggtcagaagag G/A tgggaaataacatctcc	739
ABCC1	26	intron 17 + 1332	cacctttttagtctgtgc A/G actgcacatttcttcttgg	740
ABCC1	27	intron 18 + 53	gattcagaatgattcttcc G/A aaaaacatcttcttggat	741
ABCC1	28	intron 19 + (3373-3379)	ctagcttagatctcttca C/Δ tggcacttccagctggcgg	742
ABCC1	29	intron 20 + 2730	gcctggctctctctctc C/T ccttgcctcagtagca	743
ABCC1	30	intron 20 + 2789	cttggccctcagtagtctc G/C caccctcccttcttctcc	744
ABCC1	31	intron 20 + 2919	gagcaaatggccaccca C/T cctggacctctgctgttca	745
ABCC1	32	intron 20 + 3024	cttaccataacttggggac C/T cccctcttccaccctacc	746
ABCC1	33	intron 20 + 9733	gtggcctggcctcagtagca A/C caggagaatgaagcttag	747
ABCC1	34	intron 20 + (9895-9896)	gagcaacagagagagtagg C/C cttaggcttataagaggttg	748
ABCC1	35	intron 20 + 9952	gcctgtccagctgtagac A/Δ gtagtggggacaggtctca	749
ABCC1	36	intron 20 + 1120	ggatctcttcttctctg C/A gtagtggcttcttctt	750
ABCC1	37	intron 20 + 1147	tcactagttatgtgaacc G/A ggaagagatatgactcttg	751
ABCC1	38	intron 20 + (11629-11631)	tatttgaatacattctt C/T/Δ tcaatgcttgggaatcagg	752
ABCC1	39	intron 20 + 11854	gagctcagatacccttgc C/T ccaacacagacagctctt	753
ABCC1	40	intron 21 + 3860	tggagagtagatggctgggg G/A tatgtgcatattatcat	754
ABCC1	41	intron 22 + 878	ttaaagatgctctatttgg C/A caaggttataatattctcca	755
ABCC1	42	intron 22 + (4445-4446)	gtgggcttggggctggggct (G500C) ggggtgctcagtgctaaag	756
ABCC1	43	intron 23 + 62	gtgggcttggggctggggct ggggtgctcagtgctaaag	757
ABCC1	44	intron 24 + 3171	gtttagcttllgttaatta T/C agaaatgtagctttagagtc	758
ABCC1	45	intron 24 + (3349-3358)	aacctagagcttaccat C/T tcaacacagctcagact	759
ABCC1	46	intron 24 + 3369	ctcttgaatattggctcagc (T)19-22 ccttgcatattaccaatag	760
ABCC1	47	intron 24 + 3584	tttttttttttttttttttt T/C ccttgcatattaccaatag	761
ABCC1	48	exon 25 + 60	ccaagatttttatttttca A/G caacaagaagaagaatttla	762
ABCC1	49	intron 27 + 4539	gagtcagctaccctctccc C/A gtctattccatttcaaga	763
ABCC1	50	intron 27 + 4539	tccttttactcactcact G/A tagagaacaatacatattia	764

遺伝子名	No	存在位置	配列	配列番号
ABCC1	50	Intron 30 + (1708-1714)	gaccacacacatctctccgrr 1116-7 ctctgggtcaagctctggggc	766
ABCC1	51	exon 32 + 652	tggaaaatactttctcc C/T ctggcagctgtccaggcc	767
ABCC1	52	3' flanking + 158	ctgctgctctccagcac G/A aaaaagaccatcttggaa	768
ABCC1	53	3' flanking + 1187-1199	ccatttgaataatcaaga 1111-13 agtactgttccggagaa	769
ABCC1	54	3' flanking + 2227	catagaalaggtagataca G/A ccagccscatggggc	770
ABCC2	1	exon 177	catataagaagagattt C/T gttccacacccagctcaga	771
ABCC2	2	Intron 1413	gataatcttagactgca A/G claatgataagactagaag	772
ABCC2	3	Intron 21182	atcaagtgcttgaattt 1/G gcataaataagactctt	773
ABCC2	4	Intron 21020	agtcggcagatagaacct G/C acccctcacacacccicg	774
ABCC2	5	Intron 213639	gtcatacccccacccaaal C/A gcccataaggtacaaagaa	775
ABCC2	6	Intron 213830	aaactggcagagagatttc A/G ctggagctgcagcagact	776
ABCC2	7	Intron 213989	aglaagaaccatttttc C/T gggactgtgttcttclac	777
ABCC2	8	Intron 214078	aggttccagatgtctcc 1/G agcatctcttgaatagaa	778
ABCC2	9	Intron 214171	cttattcttggctcagttgg C/T ttctaccaccctcttasc	779
ABCC2	10	Intron 214257	gggtattggaaagtcttcc G/A gctgctgagagctgcagat	780
ABCC2	11	Intron 214436	ggactagggagaataaga C/G ctctctgaaataaataac	781
ABCC2	12	Intron 215227	taccataatttattgtctt A/G tatgacatgaatttcattgg	782
ABCC2	13	Intron 215373	gttaagataagtagactca A/G gteletctatagaataa	783
ABCC2	14	Intron 215538	ttatgaggttaagcacag C/T tcaatgttttaaaagcttt	784
ABCC2	15	Intron 31772	ggataagcagaattttt A/T aaaaattatgcttaac	785
ABCC2	16	Intron 31145	acatctctctctctcagc C/T tgggttagtcagttattct	786
ABCC2	17	Intron 71658	ggactttaccagcttagtt C/T cctggtttctatctaaa	787
ABCC2	18	exon 1040	tggcagagaagagtagacac C/A ttgagaaaagagtagactg	788
ABCC2	19	Intron 111672	aaatttttaagtcttaagc 1/A ggaagccctgtctctagcc	789
ABCC2	20	Intron 21148	cccttcaccccccacac A/G ctcttctctcttcttaccal	790
ABCC2	21	Intron 31180	catagatttctggcccca G/C ttatctaatataaataga	791
ABCC2	22	Intron 311497	gtgcaggttccctctatagc 1/G atagcagcttctctttaga	792
ABCC2	23	Intron 51169	atgagctgaagaagaagtt 1/G tcaagcccttccctctgaa	793
ABCC2	24	Intron 51949	ttccaggtgacacatttgaat A/G cctaatttgggaaatgttaa	794
ABCC2	25	Intron 51984	tatttaactagtcacatccc A/G ttatganaagaagagagc	795
ABCC2	26	Intron 1614059	catcttgatgacagttatt C/T aaatttaagcttccatttatt	796
ABCC2	27	Intron 19110899	atataagagattatataaga G/A taaagtattctcagctglat	797
ABCC2	28	exon 2151	caagcaatagaattgttttc G/A atattcttcaatccttcc	798
ABCC2	29	Intron 23156	tatctgaagatcttctcga C/T agggaggaattatattgctc	799
ABCC2	30	Intron 231432	tggcagatagaacacagagag G/A aggaattattctgcagagaa	800
ABCC2	31	Intron 231734	tggcgaactactatctatag G/A cactggcagctcaatgaat	801
ABCC2	32	Intron 231801	atggcgaacacacacacac 1/G gatttttttagtatcttag	802
ABCC2	33	Intron 261154	ctggcttccatcttcttccca 1/G ggaaglatcttctctctc	803
ABCC2	34	Intron 271124	gggtccctaaagtcttctt C/G ctctaactaaagagcttaa	804
ABCC2	35	exon 28152	cagattggccagagaagcc A/G agatccagttttaaactaac	805
ABCC2	36	exon 28184	aacaactacagatctctgta C/T ccacttgactgactctgct	806
ABCC2	37	exon 281129	agagagatcactctctgacat C/T ggtatgcatggagaagtagg	807
ABCC2	38	Intron 291154	ttctctagatggacacacac A/G ttctcagaacttgaataatg	808
ABCC2	39	Intron 301191	gttttagagtagccttagca 1/G agaatttttccacagctc	809
ABCC2	40	Intron 311170	gccaaaatttcatatcagc A/G aatgaataacacaaabggtta	810

遺伝子名	No	存在位置	配列	配列番号
ABCC2	41	3' flanking + 371	ggaatttttataaact C/T gttctcctaacaatttalc	811
ABCC3	1	5' flanking - 1064	tccttctgagcccaacag C/T ggtctgagttgctcttgg	812
ABCC3	2	5' flanking - 1027-820	ctggggttcccttgcctt C/T -8 aacctgaacaggtgaac	813
ABCC3	3	intron 1 + 1226	tatttataataatcctt C/T gtagtgaacacacacag	814
ABCC3	4	intron 1 + 1389-1399	aaacttgggcaataaagt C/T -10-12 ctgtaaaaggcatatgg	815
ABCC3	5	intron 1 + 2070	agcacttctcttgatct C/T gtaactatacacctctct	816
ABCC3	6	intron 1 + 4477	gccttgcctccacagacag C/A aaaggcttgaacacagg	817
ABCC3	7	intron 1 + 6189	agtaccatagaatttgcga C/T gaggggcctcttccacgtg	818
ABCC3	8	intron 2 + 268	ttgtattttatagaaag C/A gtttttccatlltggcagg	819
ABCC3	9	intron 2 + 376	tgtccacccagcattctg C/C tttaataaggccctctcc	820
ABCC3	10	intron 2 + 446	ctacacttgccttgggg C/T catggaaatctaacactga	821
ABCC3	11	intron 2 + 2323	ggagcttgagtgagggagct C/G atcgataggagtgagcag	822
ABCC3	12	intron 2 + 85	ctcatctgacttaccctga C/A accacttccacagctgacag	823
ABCC3	13	intron 19 + 1581	ttctgttacccttcaac C/T cctcatatttatttalcag	824
ABCC3	14	exon 22 + 180	aaacttctcttgaagctgg C/T gttatgctacttttagaat	825
ABCC3	15	intron 30 + 1979	ccctgtctgttcaatct C/G tcttaccctcaccctccact	826
ABCC3	16	intron 30 + 2340	atgacacacacagcttga A/C aaatagtaagattggagg	827
ABCC3	17	3' flanking + 1555-558	ttttcttggagcaacacaa ACA/A gttcttcttgcagcag	828
ABCC3	18	3' flanking + 1455	aaacctatattataact C/A tagtgcctttaggaagcca	829
ABCC3	19	3' flanking + 1650-1659	aattccacttanaagct C/A -11 tcttgttataaatacaca	830
ABCC4	1	5' flanking - 644	attcatctgagctact C/T aatttaccctgcttcttga	831
ABCC4	2	exon 1 + 67	ggagcagacccggggccac C/T gcccctatcacagcagcc	832
ABCC4	3	intron 1 + 1864-865	ctttgaccagcttcttccc C/A gtttccatatttacttctc	833
ABCC4	4	intron 1 + 21255	ggatggaaaagtagagaca A/G acccttgcatttaagacag	834
ABCC4	5	intron 1 + 21503	ctgttttaccacttggag C/C cagcaatcaccccttcta	835
ABCC4	6	intron 1 + 21900	tgaatctcaaacatacaca C/G taagaatataagagcttgg	836
ABCC4	7	intron 1 + 22005	aagggggagctacttccag C/T gtagattttagtttggctt	837
ABCC4	8	intron 1 + 22256-22264	tttgggtgttatttggctt C/T -9 cctggaagagtgatggc	838
ABCC4	9	intron 1 + 27784	ccagggaacttgatggcac C/G ctgacttctactagtaggct	839
ABCC4	10	intron 1 + 27821	gctaaagactcaaacctt C/T ggaagaggccagaaagaa	840
ABCC4	11	intron 1 + 27837	cttgaaggagggggccagga A/G aagaagagagccatggccta	841
ABCC4	12	intron 1 + 27880	gggtgttatttggagccca C/T accatccagccgacacag	842
ABCC4	13	intron 1 + 40310	accagcagaggagagtaaa A/T ttgtcacacttggagatatt	843
ABCC4	14	intron 1 + 40372	ttcttcaaatccattct C/A actgatttcttcttcccttcca	844
ABCC4	15	intron 1 + 40413	gaagtttaccgaaaaacaa A/G caagaacttccagtaaaa	845
ABCC4	16	intron 1 + 40558	tgtagctataggagacata C/A gclcatagaacatgaagact	846
ABCC4	17	intron 1 + 50060	gcttggggaagactcctt C/T ccttgccttccgttagagct	847
ABCC4	18	intron 2 + 181	gggtctctccctctagctg C/A aagttgttgggttggagag	848
ABCC4	19	intron 2 + 254	aggaggtgttctggcctt C/T ccttgccttccgttagagct	849
ABCC4	20	intron 2 + 290	ttacgaacttttcttccat C/C gtaggttcttggagataaaga	850
ABCC4	21	intron 2 + 543	gggttgcacttggagctgg C/A gtagatccccagagcttga	851
ABCC4	22	intron 3 + 557	gtatcttcttcttggctga C/A agtggatctcgttggtagag	852
ABCC4	23	intron 3 + 718	acattcatgaaaaacaa C/A acaaccagaaagcaataac	853
ABCC4	24	intron 3 + 801	gggggtggatgttctgtt C/C tacaagaagggttggctttaa	854
ABCC4	25	intron 3 + 1022		855

遺伝子名	No.	存在位置	配列	配列番号
ABCC4	26	intron 3 + 141	tcctggggtgctccagat A/G agtttccacatggcccccga	856
ABCC4	27	intron 3 + 140	tagttttccatggcccc G/A atcagtttcagttgggaaga	857
ABCC4	28	intron 3 + (1833-1834)	gggttcgagccacattgggg G/C tgggttcctaaaccacaga	858
ABCC4	28	intron 3 + (1833-1834)	gggttcgagccacattgggg tgggttcctaaaccacaga	859
ABCC4	29	intron 3 + 1870	cagatggtacagacacaa G/A tggatttgggtgaagcttt	860
ABCC4	30	intron 3 + 1927	gaagtgaaggctgaagc G/A tgaatttctcagacttg	861
ABCC4	31	intron 3 + 1970	ggcagcccccacatgggtc A/T agcagcagtgtaacttllac	862
ABCC4	32	intron 3 + 2039	gatcgaaggagctttaata T/C aggtacagtgggtggagagc	863
ABCC4	33	intron 3 + (2067-2068)	tgggtgaagagctgcttt C/Ttt tggcgggtgggtttatgggc	864
ABCC4	33	intron 3 + (2067-2068)	tgggtgaagagctgcttt tggcgggtgggtttatgggc	865
ABCC4	34	intron 3 + 3563	catlgaactgaagctgggc G/A gatttcaagttccctgcttt	866
ABCC4	35	intron 3 + 3696	tgcttggcagaagatgaagc C/G ccagatgaagtcactagtag	867
ABCC4	36	intron 3 + 4093	aagtaatccttggatttttt T/C ttcttttttctcttagcag	868
ABCC4	37	intron 3 + 4097	aatcttggatttttttt T/A ctcttctcttagcagtag	869
ABCC4	38	intron 3 + 9724	aaaacacagatttactcacc A/G aagacccatttgcctgact	870
ABCC4	39	intron 3 + 9988	gaagcaagaagacacacac G/A tctggcagagagccagggtg	871
ABCC4	40	intron 3 + 10952	gttaaaatgcatctccctac A/G tctgttcagaaggtagcc	872
ABCC4	41	intron 3 + 1125	gctcaattctctgctgttt A/G atttttgcacacacac	873
ABCC4	42	intron 3 + 11244	ccaagaccctggaaactcc G/A aagctgtgctttttcccca	874
ABCC4	43	intron 3 + 11916	gcttggcagcaaaaaaa A/A tttagctctcagtagctg	875
ABCC4	44	intron 3 + 12047	actatctaccacaggggt G/G cagagcaagaacatattgaa	876
ABCC4	45	exon 4 + 205	tgagttacagtaggagcagc T/C gccatagttttatccagag	877
ABCC4	46	intron 4 + (412-414)	ttatgaaaattttttgctt G/T/A cattaaaaccttacttaca	878
ABCC4	47	intron 4 - (9757-9756)	tgacatgctgatttttttt Cctctgacacaaactcttc	879
ABCC4	48	intron 4 - 6373	atctttgtctagatagta C/G agttttctgttaactcaaa	880
ABCC4	49	intron 4 - 6267	acttccacattcacatatt T/C gttcttaattggcagtcggat	881
ABCC4	50	intron 4 - 6096	agactcttacttcttaggg T/C gtaaaaatttcaagccttt	882
ABCC4	51	intron 4 - 6057	ttactatctaatattgatt C/T ctcccaagagttattatt	883
ABCC4	52	intron 4 - 5295	agttctgagcttagagtag A/G tcttactaaatggtagctt	884
ABCC4	53	intron 4 - 803	agcttaccctgttccagcc C/T gcttccatagcttccagc	885
ABCC4	54	intron 4 - 736	attcagagcctccacatcc C/T ctcttccgacttctc	886
ABCC4	55	intron 4 - 728	ggctccacatctctcttc C/T gtacttctgcttagctagg	887
ABCC4	56	intron 4 - 824	ccaccagcttctctcagtt A/G gaactgtccctacttctc	888
ABCC4	57	intron 4 - 470	ttgacttactatttttca C/T ttccattcaacacatigaa	889
ABCC4	58	intron 4 - 411	ggtagagagactaaagcccc G/A tctgtttaaataagttctac	890
ABCC4	59	intron 4 - 323	gttcttctaaagcttctc C/T gtttcttctaaatttggctc	891
ABCC4	60	intron 4 - 246	gtctttgttacttggaggg A/G tctcaaatcttataatga	892
ABCC4	61	intron 4 - 199	agaatttttcttcttacc C/T ctctgcttctgcttctaca	893
ABCC4	62	intron 5 + 73	cttttatttcttggagg C/T agggcttccacttctgttaca	894
ABCC4	63	intron 5 + 403	aaagaaacagcttcttctc G/A caggctgttctcaagattct	895
ABCC4	64	intron 5 + 937	ccagaatggcttacccttg G/C tgggttcttcttcttctct	896
ABCC4	65	intron 6 + 150	ggctcagcagaaggagctc C/T gttcttactgctgaagcaca	897
ABCC4	66	intron 6 + (380-381)	tgttllagagctgltttcac A/T gtttatataatgtgttatt	898
ABCC4	66	intron 6 + (380-381)	tgttllagagctgltttcac gtttatataatgtgttatt	899
ABCC4	66	intron 6 + (380-381)	tgttllagagctgltttcac gtttatataatgtgttatt	900

遺伝子名	No	存在位置	配列	配列番号
ABCC4	67	Intron 7 + 884	ttttgttctgtccacaga A/T agctcaaacctcctggcttc	901
ABCC4	68	Intron 8 + 82	tattagacatcattgttc C/G agtataatgacatttaactc	902
ABCC4	69	Intron 8 + 100	tcagtgatagacatttaa C/T tctcctaaacaaaacgtg	903
ABCC4	70	Intron 8 + 5212	tcaggaaatttctgtctcaat A/T tcagctataggagaataatcc	904
ABCC4	71	Intron 8 + 5244	gaacatttaatttccctca T/G ctacatagatttctcgtggaga	905
ABCC4	72	Intron 8 + 8569	tcacctctcagtgactag A/G aaagtctcagctagccctc	906
ABCC4	73	Intron 8 + 9106	ccagtctcaataggtttac T/C gtgtcatalgttttttatt	907
ABCC4	74	Intron 8 + 9412	tttttgaagtcagcaatag G/A agacatctctgcctgta	908
ABCC4	75	Intron 9 + 116	tagcttcttatttactgaa A/G ctagtctacaagaattctca	909
ABCC4	76	Intron 9 + 1384	cacggaaggaagctgcaccc T/C agggctggagatgatgtc	910
ABCC4	77	Intron 9 + 1459	agatttggagagcagaggcg A/G aggtctctcctggagagct	911
ABCC4	78	Intron 9 + 1632	agcagactctcggcagct C/A cactgctctcggctccctc	912
ABCC4	79	Intron 9 + 3630	gtaatttttctatttgaag C/A taatctgactcttattcc	913
ABCC4	80	Intron 9 + 3830	ggatctccacctctcagaa C/T accagatcatttgaagaa	914
ABCC4	81	Intron 9 + 3940	ggacatttcccaagagctct C/T gtgcagaagaatagccact	915
ABCC4	82	Intron 10 + 1504	ggcagaagctgcttgctag C/A acttattctgtctcagtg	916
ABCC4	83	Intron 11 + 1817	ttttagggagallcgaagaa C/G aaggcaaatlttgcattgt	917
ABCC4	84	Intron 11 + 3342	actggaatttctcgtgttg T/C aggtacagagattgtatgtg	918
ABCC4	85	Intron 11 + 3377	catgtgtaatacaaacctgc T/C ggacagaataagctctcagc	919
ABCC4	86	Intron 11 + (3610-3675)	tcctggcaccctccccc (A)16-17 gtcttagagaaaaatagg	920
ABCC4	87	Intron 11 + 3737	ataagttcatcactataaa A/C tatattttagaataaataat	921
ABCC4	88	Intron 11 + 6953	agagtacacaaagaataa C/A cacttgaatctctataagag	922
ABCC4	89	Intron 13 + 442	ctatacagatttgaagtaa C/C gtcttggaccacacataag	923
ABCC4	90	Intron 13 + 459	tgaactcttgggaccaca T/C agagcttctcttggagaagct	924
ABCC4	91	Intron 13 + 633	taaacatttaaacaccacag G/A catatagccttggcttgcct	925
ABCC4	92	Intron 13 + 645	accacagcagctgtagcct G/T gcttgccttgaacttagtt	926
ABCC4	93	Intron 13 + 3306	aagtcttcacagattaga A/C aatggatttgaacaaatgc	927
ABCC4	94	Intron 14 + 252	taattgaacttttttttt A/G cctcttccatgacttaatic	928
ABCC4	95	Intron 15 + 124	tgaattctgttggcttcaggg C/T tctattccatgatatgta	929
ABCC4	96	Intron 15 + 1552	tttggacttctcctgttgc C/T ccacagcttcttgcacagag	930
ABCC4	97	Intron 16 + 157	cctactggttctcatatcc G/A ttacaaagaccctggagaataa	931
ABCC4	98	Intron 17 + 329	cccaaatgtgttcatatt T/C aaaaaatgtatttattca	932
ABCC4	99	exon 18 + 56	atggagaggaataatlaacc C/A agaacctagatcttaactg	933
ABCC4	100	Intron 19 + 7202	aatlaaaaaatatttttt T/A cacatacaatgggtatag	934
ABCC4	101	Intron 19 + 7445	ttttagcataattttaatc T/C actagaatgttctgattcat	935
ABCC4	102	Intron 19 + 9018	tacgtgtagctctgaagaa A/G aaacctacatgtgtcttt	936
ABCC4	103	Intron 19 + 11388	agageltcagagattttagg A/G gttagagagaataatagcat	937
ABCC4	104	Intron 19 + 11646	catatttttttttttttt T/A cctcctgttgggtgcagaat	938
ABCC4	105	Intron 19 + 13517	ggagaatttcatatttttt A/T aaaaatctataactagctc	939
ABCC4	106	Intron 19 + 21033	tggaggtcccttggcctagc G/A ctgaacttcaagttttcag	940
ABCC4	107	Intron 19 + 21095	agacttttggaaagagcaga A/T ctgaaggttaagacttagtaa	941
ABCC4	108	Intron 19 + 21634	gtactatttctgagacaca C/T gggcccatggcacttaggct	942
ABCC4	109	Intron 19 + 21715	tgtttcttaccctctaca C/T ascttgcctctcagctctc	943
ABCC4	110	Intron 19 + 23090	agcacacagactttagagctt C/A agcttctaaagtttcatla	944
ABCC4	111	Intron 19 + 24297	cgaatctatgaagtgaag A/G ccttttttagatagcagcac	945

遺伝子名	No.	存在位置	配列	配列番号
ABCC4	112	intron 9 + 25947	gagctcaatlaaataagc c/a aaacatagaacattttaa	946
ABCC4	113	intron 9 + 30193	acgaatttgcagaagcttc c/a aaagtgaataatctctga	947
ABCC4	114	intron 9 + 36938	aagccagcaatcctctgg c/g taatctctgtggactacttt	948
ABCC4	115	intron 9 + 37322	gttccatgaaggctaaccc c/t ccttacccttggttaaccgc	949
ABCC4	116	intron 9 + (38361-38362)	gggggttacccttccctagct (t) cgggaagggtttcttgaagaaa	950
ABCC4	116	intron 9 + (38361-38362)	cggggttacccttccctagct cgggaagggtttcttgaagaaa	951
ABCC4	117	intron 9 + 38746	taagacatgcttgatata c/g gtaataaagaataagcaaa	952
ABCC4	118	intron 9 + 42343	tataaggacataatcagcag c/t aacgatgtagtggtccgaa	953
ABCC4	119	intron 9 + 44733	accagcctggagaaaaaaa a/d lacagaggttacttatgt	954
ABCC4	120	intron 20 + (405-410)	aaggcaataacttaggcg (t) 13-15 ggaagaacagctgtgtt	955
ABCC4	121	intron 20 + (637-648)	ctaagcttaagctgtctt (a) 12-13 ccaacaatcctacagaaaa	956
ABCC4	122	intron 20 + 842	caagctggggcactttttt t/d tcccaagttttatttggaa	957
ABCC4	123	intron 20 + 843	aagctggggcactttttt t/c ccaagttttatttggaa	958
ABCC4	124	intron 20 + 1347	ggactctgatttttttt t/d ctttccaacaattttttaa	959
ABCC4	125	intron 20 + (14533-14567)	tccctacacccctcactc (a) 13-15 tcagcagcttaacgagctt	960
ABCC4	126	intron 20 + 15487	ggtttttccagtgtagtag c/t acatgaagaagcagtagc	961
ABCC4	127	intron 20 + 16161	ggctttagctcagaagcga t/c atgaccttgtagctgcga	962
ABCC4	128	intron 20 + 30891	agctcccccactgtctatc c/t tttcagaagaacagcgttgc	963
ABCC4	129	intron 20 + 31180	cttgcagctgctacalac g/a taatttctatgtttatcat	964
ABCC4	130	intron 20 + 31283	gtgttaagcttaaaaaaaa a/d cctgttagacattttgact	965
ABCC4	131	intron 21 + 4204	ttagccctgcctcaaaccc a/t gttggagataaacagctgc	966
ABCC4	132	intron 22 + 1026	gtgccttactcctcaataaa a/c tcttctgactcaactgag	967
ABCC4	133	intron 23 + 377	ggcttggcagcaggttag a/g aaattctcagcagagagat	968
ABCC4	134	intron 25 + 4122	ccctttgatttaaatgca c/g t gggagaagaccaccctca	969
ABCC4	135	intron 25 + 6418	ttagcagtagtaagctgc c/a agaaataaagtagaggtat	970
ABCC4	136	intron 25 + (8765-8775)	tcatcctgtgttttttctc (t) 5-11 aatcctgccctcgaactc	971
ABCC4	137	intron 26 + 67	taagttaattctcttacti g/c ttatgtcttttttaattgg	972
ABCC4	138	intron 26 + (101-109)	taattggaagaagagttgt (t) 8-9 caccatagaagcattgtt	973
ABCC4	139	intron 28 + 391	tagatagaacttttttt t/d aaatctctatgttagagtag	974
ABCC4	140	intron 29 + 2569	atcctcttttttctaagc c/t accatctctccacatttaa	975
ABCC4	141	intron 29 + 7820	gaaaaaacctctctctgc c/t ttggagcttcagcatattct	976
ABCC4	142	intron 30 + 6269	tagatgtcttttggcagtg a/g aaataggtgttattctt	977
ABCC4	143	intron 30 + 6320	gttataaggtttaattag c/t tctacttgtttaattacatt	978
ABCC4	144	intron 30 + 6474	ctttagctatgttttca a/g tccacagatcttcaactt	979
ABCC4	145	intron 30 + 6519	ttcccatagaattatttt c/t ctgcattttaacacacctt	980
ABCC4	146	intron 30 + 6574	aatgttttggctcttaact c/t acactgttcaaacctagac	981
ABCC4	147	intron 30 + 6680	agctgtgtcttctgtatag a/g cgtgtttaggtttttctctg	982
ABCC4	148	intron 30 - 704	acgtttttagaataacctgt a/c tcttcttctgttgcagtag	983
ABCC4	149	intron 30 - 228	atctatgaatcagctgact a/c gaactaaatagatctacag	984
ABCC4	150	intron 30 - (14-5)	acaatttttttagtctacc (t) 9-10 ctaggtaacttcaaaaa	985
ABCC4	151	exon 31 + 146	agctccttcagagagcattt c/t ccaatagtttttggactatg	986
ABCC4	152	3' flanking + 173	atttttaaggagtagagaca a/g agttctacagctttttgtt	987
ABCC4	153	3' flanking + (430-440)	tgacccttacttcccctc (a) 10-11 tggatcatgtttaagat	988
ABCC4	154	3' flanking + 556	aaggtgttttagatacga a/c gaacaaatgtgacctcca	989
ABCC4	155	3' flanking + 1144	ctctccctgaatttgcata t/c gtaataagacatgacacgt	990

遺伝子名	No	存在位置	配列	配列番号
ABCC4	156	3' flanking + 1426	tttagtgactgaatgaca A/I cagtgatcataatgagttt	991
ABCC5	1	intron 1 + 528	ttctccacacagaccgg C/C gtgcctttgtgtttatcaca	992
ABCC5	2	intron 1 + 1834	tgaattcagtgaccttc C/I gtccaacgtcaccggc	993
ABCC5	3	intron 1 + 3055	agaagcttttaaaaaaa A/A ccaactttctatgtatatac	994
ABCC5	4	intron 2 - 20280	gaagcactcactactaagta I/C ttgttgaatttcagacaca	995
ABCC5	5	intron 2 - 20260	tttttgaatttcagacacc A/I tctagaatcgtctgacct	996
ABCC5	6	intron 2 - 19204	tgaataaagcattgcgaca C/I ctaccacatttcttcggac	997
ABCC5	7	intron 2 - 19043	ttagtgcattatagctggc C/A ttacttacttaacatgaag	998
ABCC5	8	intron 2 - 18824	ttgaacacttcaagatgc A/G tccacagcactgaacgaat	999
ABCC5	9	intron 2 - 18807	tgaatgcacagactgaacc C/A atggctctgtgtcagataaa	1000
ABCC5	10	intron 2 - (18735-18734)	atagaagcttaaacitcaa W/ cactactctacataatga	1001
ABCC5	10	intron 2 - (18735-18734)	atagaagcttaaacitcaa cactactctacataatga	1002
ABCC5	11	intron 2 - 15903	tactaaagcttgcctataga C/A gtaaaagcagactgacat	1003
ABCC5	12	intron 2 - 15901	ccaaagcctctcatalgaggg C/I agaaagcagactgacat	1004
ABCC5	13	intron 2 - 15847	tgaatgaagcctcaaaagcc C/A tcttcccagctccattta	1005
ABCC5	14	intron 2 - 15505	agaaacccacacagacatga C/I agcttaccctgacctgaggg	1006
ABCC5	15	intron 2 - 13571	ccatttgcctccacatacc C/A cttattttaggggtgccc	1007
ABCC5	16	intron 2 - 13402	taccctgcgtttctggccc C/I ccaggaaggatggatgt	1008
ABCC5	17	intron 2 - 13325	ccagagcctctcctgacag C/C gaaaagccttggttgccc	1009
ABCC5	18	intron 2 - 7293	tttgttagataaaattgca C/I tgaatgcctgttctaaaca	1010
ABCC5	19	intron 5 + 374	ccggctgtagtgcagcagac C/I ggaacataccagtgcttg	1011
ABCC5	20	intron 5 + (2212-2213)	cgctcttgcagtgctctct C/A lgtgaatgtaacitcct	1012
ABCC5	21	intron 5 + 3283	accagaagagcttggctt C/I tgaatcagctagctacc	1013
ABCC5	22	intron 5 + 3459	ttggctttctttgtgtgg C/I ttgttttttttttttttga	1014
ABCC5	23	intron 7 + 443	cactttttaaaagacata C/I gattacataacatttggccc	1015
ABCC5	24	intron 7 + 458	cagtagattacataacatt I/G gcccacccctgacagcaggg	1016
ABCC5	25	intron 9 + 176	caaaacaaaacaacaaa C/A acaaaaaaaatgccacat	1017
ABCC5	26	intron 9 + 214	cataagagaatgactgtg C/I tctctcttcttactgacctg	1018
ABCC5	27	intron 10 + 703	tgaggcttggaatttcttga I/C gtggcactgcatagattag	1019
ABCC5	28	intron 10 + 3580	catagagcttgagactgtgaa A/G accataggttactgacatgt	1020
ABCC5	29	intron 10 + 3655	atctttaaataactcttla C/A ggaagaaatgatggaat	1021
ABCC5	30	intron 10 + 3854	gaatttgaatcatgacac I/C tggggaagataagatcaggg	1022
ABCC5	31	intron 10 + 5040	ctttgaacataagagttt C/I tggcagaagaatttctct	1023
ABCC5	32	intron 10 + 5316	cagttaaatgctatagctc C/I cctttagcttgcctgagggg	1024
ABCC5	33	intron 12 + 234	tgcattttctccagctgga C/A ccatlgtcttctatcccttc	1025
ABCC5	34	intron 12 + 300	tgcacagatgtccctgtt A/G ttgaanaatgacagataag	1026
ABCC5	35	intron 12 + 318	gtattaaaatgtcagat A/G agaatgagcagacacacctta	1027
ABCC5	36	intron 12 + 1545	gtagcatccctaaacacaga C/I aaagtctactatcagttccc	1028
ABCC5	37	intron 13 + 20	ggcaagaattttgtgcttc I/C gtatgcttcttcttctggc	1029
ABCC5	38	intron 14 + 278	ttctatccagataatttttaa A/G actacaagatgagctgtgca	1030
ABCC5	39	intron 16 + 1653	tgaatgagacttttttttt I/A aaattattatgataatc	1031
ABCC5	40	intron 16 + 1664	gcctgagacttttttttt A/I aaattattatgataatc	1032
ABCC5	41	intron 17 + 20	ggtaatggcctttttttgaaa I/G tttagattttgtcatcaag	1033
ABCC5	42	intron 18 + 232	ggacacttcaggctctctg C/I tctatccgttgttgattag	1034
ABCC5	43	intron 19 + 249	ggaccagttagaagagagcc C/A tccctgggcttgcaccttc	1035

遺伝子名	No.	存在位置	配列	配列番号
ABCC5	44	intron 20 + 846	ttaccagaagaaaaagcc c/a gteggg tgggagagacagcca	1036
ABCC5	45	intron 20 + 1154	tcctgagcagaaaaaaa a/d tggagcatccaggttcta	1037
ABCC5	46	intron 22 + (1424-1425)	ggggaatgcagcgaatat (a/t) caactctgttttaacagg	1038
ABCC5	46	intron 22 + (1424-1425)	ggggaatgcagcgaatat caactctgttttaacagg	1039
ABCC5	47	intron 24 + 132	gcccacagaatctccagca a/g tctcacaaccg tgc tggaa	1040
ABCC5	48	intron 24 - 874	gtctggagagtttagaatt a/g ggtcagtggttgacaaag	1041
ABCC5	49	intron 24 - 530	taataaanaattaccac a/a cagttatatacacacattt	1042
ABCC5	50	intron 24 - 102	acagggtggcagctacct c/c tctgtactata tggttatcc	1043
ABCC5	51	exon 25 + 120	taccagaaaactctctct c/t gtcctcagaagaatctct	1044
ABCC5	52	intron 26 + 263	ctgggctcagggctctct c/t gtcacttggagacagttatt	1045
ABCC5	53	intron 26 - 3257	cgagggtgaattgtctgt g/c gtcacactttggagata	1046
ABCC5	54	intron 27 + 873	gttttctctctctctat c/a gaattctctctctllgaga	1047
ABCC5	55	intron 29 + (2733-2734)	gtgtcaaaagagagacacg t/gtccaaagcagcacc	1048
ABCC5	55	intron 29 + (2733-2734)	gtgtcaaaagagagacacg t/gtccaaagcagcacc	1049
ABCC5	56	intron 29 + 2959	gtgtcaaaagagagacacg cttatgtctctctctctggcc	1050
ABCC5	57	intron 29 + 4020	acatgatttccacagctac a/g tagagttccatcatagaat	1051
ABCC5	58	exon 30 + 684	atataaanaalaggggggga c/a gtcacagcagggctagtga	1052
ABCC5	59	exon 30 + 947	cccctcgcctctctccac c/a gtcctcaggggtggctgg	1053
ABCC5	60	exon 30 + (1145-1150)	agctataccacagagatcc c/t actgctcaggttctatagg	1054
ABCC5	61	3' flanking + 4	tcacgcagtcgtccacag t/c 6-8 cctcacaagtctcaacttt	1055
ABCC5	62	3' flanking + 2008	attatttggatttllgataa a/c cttctctgtatcaacaat	1056
ABCC5	63	3' flanking + 2052	ccgcagagcttgacacagcc c/a gttctcaagggagctcc	1057
ABCC7	1	5' flanking - 834	ccgcagtaggacagcagc a/g ccagcaggttagaccctgg	1058
ABCC7	2	5' flanking - 729	gctaaacactccaagct t/g ccttaaaaagccac tggg	1059
ABCC7	3	exon 1 + 125	cctcttgcagattttttt t/d cttctcagtcagtgctcta	1060
ABCC7	4	intron 1 + 6200	tagcagagaccacagcc c/c agagaccatgcagagctgc	1061
ABCC7	5	intron 1 + 7538	ctatgtgagcgttaagag c/a tagagtgcccaagaagaa	1062
ABCC7	6	intron 1 + 13519	agttcttctttttagatgg c/a ctacagaggtgcaactct	1063
ABCC7	7	intron 1 + 14110	gaacttaaatcttagtca t/c acaattgtctacatact	1064
ABCC7	8	intron 1 + 14293	allacacagattttttt t/d aailltggggaagtgatt	1065
ABCC7	9	intron 1 + 14316	gcccagcagattctgact c/d tataaccagagcttatacg	1066
ABCC7	10	intron 1 + 14433	taaccagagcttatagag c/g attatgtcccaagaagaa	1067
ABCC7	11	intron 1 + 14824	cagaatacaaatatagct c/a gaanaataaggatttctg	1068
ABCC7	12	intron 1 + 23401	acatttgcagttgacaa c/c ttcttctttagctttaa	1069
ABCC7	13	intron 3 + 879	aatatttggaaatccta c/g ggtatcttgcataagatt	1070
ABCC7	14	intron 3 + 922	gaaaatttcagttatata c/a cccataaanaatacattta	1071
ABCC7	15	intron 3 + 933	actatcttaacaagaaga c/c tacacttagggccagaatgt	1072
ABCC7	16	intron 3 + 13704	caagataaglacac tggg c/t cagaattcttctatgct	1073
ABCC7	17	intron 3 + 13758	ttttccaaataaaaaaa a/d tgggtaatacttgaatg	1074
ABCC7	18	intron 4 + 240	tataaagaalagatt a/g aacagattagggaacaa	1075
ABCC7	19	intron 4 + 376	ctctgttagttttttt t/d cttctatcatgttatact	1076
ABCC7	20	intron 4 + 586	ttatgtcagaagaaggt a/g taataatagtttgaatga	1077
ABCC7	21	intron 4 + 1089	tgtccagaagaagacaaa t/c tggcagagcatattaggt	1078
ABCC7	22	intron 4 + 1615	tttcaatcgaacatttac c/a taagtgaagacttttaga	1079
ABCC7	23	intron 4 + 1946	aaagttaggttagtttat c/t tgtcttcttcttcaatgtt	1080
ABCC7			aatacaacaacttagct t/c tgcataacttttcaagaat	

遺伝子名	No.	存在位置	配列	配列番号
ABCC7	24	intron 6 + 783	taataagtttggatcaaa A/G tagcacttggttgaatccc	1081
ABCC7	25	intron 6 + (1104-1131)	gattgatgattgaatgatt (G) 6-7 tacagatcaaaaagctag	1082
ABCC7	26	intron 7 + (731-732)	gtacaaatgacacattttt (T) ctacagtgagcttcatttt	1083
ABCC7	26	intron 7 + (731-732)	gtacaaatgacacattttt ctacagtgagcttcatttt	1084
ABCC7	27	intron 7 + 1434	gaatttggtttgaacctg T/C ataactgagatgaatggt	1085
ABCC7	28	intron 8 + 752	catctctcttcagctccc A/G ttcttcattatataccta	1086
ABCC7	29	intron 8 + 1109	tagcccaagcttcagat G/A cgtggacttaattcttcctt	1087
ABCC7	30	intron 8 + 1312	atgaacatctattttt T/Δ ctccctcattatggatta	1088
ABCC7	31	intron 9 + (6521-6522)	gtgtgtgtgtgtgtgtgt (C) tttttacagggatttggg	1089
ABCC7	31	intron 9 + (6521-6522)	gtgtgtgtgtgtgtgtgt tttttacagggatttggg	1090
ABCC7	32	intron 10 + 2119	gaacatttatagtttttt T/G ggaacaagaatctagcga	1091
ABCC7	33	intron 11 + 3867	ttttcttcaagaattaga A/Δ gaggagagaattggllta	1092
ABCC7	34	intron 11 + 11844	taatacaaatcatcaaaa A/Δ gcttcagaaacacattt	1093
ABCC7	35	intron 11 + 12144	atattaaacagattacata T/C acttaacattcatatatt	1094
ABCC7	36	intron 11 + 20975	gttggatagtaaatccag G/A gtaaatcacatagatctaa	1095
ABCC7	37	intron 11 + 27057	atgaagaagaatttttt G/A gaggagagaagaagggtg	1096
ABCC7	38	intron 11 + 27131	gaggagacttttttttt T/Δ aagggcagagllactacct	1097
ABCC7	39	intron 13 + 152	gtattactcaatctgact T/A gctctctggcagagattc	1098
ABCC7	40	intron 13 + 287	tttcagataatgtgcttg T/C gataataatctttta	1099
ABCC7	41	intron 15 + (85-86)	atcatatataagcacac A/T/Δ aaatagtataatacacat	1100
ABCC7	42	intron 15 + 106	taataatgatatatacaca T/A gataatgatatagtagtc	1101
ABCC7	43	intron 15 + 3341	ggaagtataaattgttaaa A/C actggagcccaacttaca	1102
ABCC7	44	intron 15 + 5556	tcctatgactaaatgaat A/T atttgggcagcttttga	1103
ABCC7	45	intron 15 + 5919	tggtagttctatgggaac C/A gtgaggaataattttatat	1104
ABCC7	46	intron 17 + 2479	caaaaggataggaagtcag A/C ggaagaaggagccctatgt	1105
ABCC7	47	intron 18 - 81	aagatgcaaaaataaaaaa A/Δ gaaataaatctacgacac	1106
ABCC7	48	intron 19 + 751	catataaanaatacaatc A/G taltatlcanaagaalggca	1107
ABCC7	49	intron 19 + 820	tgacatttgatagatgalla T/C tctaatttagctttttcag	1108
ABCC7	50	intron 21 + 1532	ttacttttaacttttttt T/Δ agtttgaacagctcttita	1109
ABCC7	51	intron 21 + 1607	atgcttttggagattgggtct C/T ataagtatagaatgttt	1110
ABCC7	52	intron 21 + 11260	atgtagcaatcatgacta T/C atgcttttttactttcttat	1111
ABCC7	53	intron 22 + (130-131)	aaataaatatgaacacac A/T/Δ gttttattatagagttcat	1112
ABCC7	54	intron 23 + 1837	ctgtctaaagttttaaag A/Δ aaaaaaagaagaaggaa	1113
ABCC7	55	intron 24 + (7100-7112)	cttttaaacacttttagaca (T) 2-14 agtttaacatgttcaaac	1114
ABCC7	56	intron 25 + 237	acttttcccccttgtaaca C/T atgaagaacttttlaaatat	1115
ABCC7	57	exon 27 + 115	gggtgaagcttttccccac C/T ggaactcaagcagagtcag	1116
ABCC7	58	exon 27 + 334	gaagaatgaatttttttt T/Δ aaaaagaacatttggtaa	1117
ABCC7	1	5' flanking - 1099	aaaggagctgaagggtctt T/C cttttgtttccccctgacg	1118
ABCC8	2	5' flanking - (424-422)	ccccccaccaccaccacac CAC/Δ aagctacatctctccccc	1119
ABCC8	3	intron 1 + 1212	agcttggcacaatagtag A/G cccccccaccctttctaca	1120
ABCC8	4	intron 2 + 1003	aggagagctatgaatccccag C/A ctgcatgtttggctcgat	1121
ABCC8	5	intron 2 + 1253	catctactaagaagaatc C/T agtaaccacagaagaataaa	1122
ABCC8	6	intron 2 + 1382	ccagacigcaatccctacag T/C atgcttgcctctctgtatgt	1123
ABCC8	7	intron 2 + 2371	tttcaagctgtctggaat T/A tagggagcaggtggagggg	1124
ABCC8	8	intron 3 + 1957	ccctacccttagcccccggg C/T ccccatatgagtagaattgg	1125

送付子名	No.	存在位置	配列番号
ABCC8	9	intron 3 + 2088~2089	agaagacctttcatacca (UCA) gggcgtggcctgaccagatgtc
ABCC8	9	intron 3 + 2088~2089	agaagacctttcatacca gggcgtggcctgaccagatgtc
ABCC8	10	intron 3 + 2204	taagacacaagtattacacc G/A tgaatgaattttcttttc
ABCC8	11	intron 3 + 2286	ttatctcccttttaagaagc A/G ctccacagaaccagaatc
ABCC8	12	intron 3 + 2312	caagacagaaaattctaga C/G agggaaaagtgaaggagag
ABCC8	13	intron 3 + 2356	ctgtgaacttcacagggacaga A/G ggaataatggattttggagaa
ABCC8	14	intron 3 + 2359	tgaacttcagacagacagaag A/C aatggattttggagaaatgg
ABCC8	15	intron 3 + 2370	gacagagaaataatggattt G/A ggaagaaatggccagccctcca
ABCC8	16	intron 3 + 2382	tggattttggagaaatggc A/G ggcctcaagggccctgatgt
ABCC8	17	intron 3 + 4910	gggacaccccttcagctgt G/A aattccacagctcttagaga
ABCC8	18	intron 3 + 4969	cattttcagctcttaggc A/G tgaracacagaaagcccgatgc
ABCC8	19	intron 3 + 5003	ccgaatctctggccctcat C/G ctaatgtctctctggcagga
ABCC8	20	intron 3 + 5019	ccatctaatctctctctgc A/C gggaccacaagatggatggca
ABCC8	21	intron 4 + 14	ggtagggtagcagagccac C/T tggccagggtagggtagga
ABCC8	22	intron 4 + 187	agacatgcctatcggccac G/A tggctctaccctcagggctc
ABCC8	23	intron 4 + 204	cagctgtctctaccacag G/C tcccagagagagagaggggt
ABCC8	24	intron 4 + 254	gttgcgtgaggttggcgaat G/A actttccgtagaagggagag
ABCC8	25	intron 4 + 357	tgtatcatatcgtcacct G/C gtaaatgaaatgaaagatgt
ABCC8	26	intron 5 + 92	ggcattaggtcaaaatcttg G/A tggacaaaagggggaactg
ABCC8	27	intron 6 + 4205	ttctgaagatgacatggg G/A catgaagatcatatggcttga
ABCC8	28	intron 6 + 6519	aattccacaggaattttaa A/C agaacgggcttctctaaac
ABCC8	29	intron 6 + 5575	ctgaacccgtaccagcag G/C gggcgaattttccatcccc
ABCC8	30	intron 6 + 6587	gttccatctcagatcttgc C/T gggacacacagagacccct
ABCC8	31	intron 6 + 6747	ttccactggccttttctgt C/T agtaattctacattacag
ABCC8	32	intron 9 + 191	aaagagcttgcctcccggt A/G ggaacggagcggcgcatggc
ABCC8	33	intron 10 + 1963	ccagagatctcaacttctt G/G tgtccagctagacatgggtg
ABCC8	34	intron 10 + 2724	cttggacatgattttctat A/G taacacagatcaaaagatgt
ABCC8	35	intron 10 + 2938	ggccgcccacagctctcac G/C tgtccagctacttagggag
ABCC8	36	intron 10 + 3094	tccgagatgtattttttt T/A ccttcgttagtcacagctg
ABCC8	37	intron 10 + 3368	ttcttgcctatagggcacc A/G tcaagcttctggcgaggcaa
ABCC8	38	intron 10 + 8897	ggatatgattaaagcttca C/T gggcagagaatctgcctatc
ABCC8	39	intron 11 + 308	tgtglatgtgaagtgatg G/A gaatactcagacaagaact
ABCC8	40	intron 11 + 1171	ggcctctcatcttcttcca G/A tcttggccttttccatgtg
ABCC8	41	exon 12 + 7	ggcctcttccacagcttct G/A tggccacagctagcttcttc
ABCC8	42	intron 12 + 356	accagaatggggcctatccc G/T tccccagctggctggcccat
ABCC8	43	intron 12 + 334	tgggttcaagaagtgaatgg G/A gataactcagacaattat
ABCC8	44	intron 12 + 1370	gggagagagcttgcacagc G/G atgaagcgaagccttggtgg
ABCC8	45	intron 15 + 412	ggagtggaagcccaaggatg G/T gtttcttgggaccacaaga
ABCC8	46	intron 15 + 688	acttccccggccctactcac A/G tctccaccttctctctctg
ABCC8	47	intron 16 + 4464	actcatctcagatgcatc G/A aagagaggttaggtactgg
ABCC8	48	intron 16 + 4574	ttagagatcttaagtgttt T/C tggcttacttatttcgcaa
ABCC8	49	intron 16 + 5011	agctaaagcaaaacagctt G/T tgaacttggcaagcatctcca
ABCC8	50	intron 16 + 7608	tgtctctattttcttttgc G/G cttaatacttctacttgc
ABCC8	51	intron 16 + 7730	ccagctcttagtggcttga G/A ggaagagcatcggttggag
ABCC8	52	intron 16 + 8369	ttagcaacttgaattgggccc T/C ggaagcttacttctgtctctg

遺伝子名	No.	存在位置	配列	配列番号
ABCC8	53	intron 16 + 9708	tgcaattgcccctacttat /G cagagcccaatgatgggic	1171
ABCC8	54	intron 17 + 651	tatagattaaagggcttg A/G gtccctcaaaccttccctc	1172
ABCC8	55	intron 17 + 692	ccctaccctcccaaac A/G cttagatacccttagagtg	1173
ABCC8	56	intron 17 + 1541	ctcagatctcttgagga C/T atggttactccatagag	1174
ABCC8	57	intron 18 + 580	actaagcagatlltaccac C/T tgcactcccatcccttg	1175
ABCC8	58	intron 18 + 658	gaacagccctcagagtc C/T tccgacccctactcccg	1176
ABCC8	59	intron 18 + 660	acagccctcagagtcct /G cccgacccctactccccc	1177
ABCC8	60	intron 19 + 93	gccttcatgatcacca /G accagcacttactcccc	1178
ABCC8	61	intron 19 + 123	ttcacttcccaagtccta /G ctgactccagctcttcat	1179
ABCC8	62	intron 19 + 219	catagggagggagagagaa C/T gtaggagagagagagagccc	1180
ABCC8	63	intron 19 + 845	tagtatttaacttcccacaa C/T actgtgtagagtcgaact	1181
ABCC8	64	intron 20 + 338	tcccttccacagcttagac A/G aacagatcttctctgact	1182
ABCC8	65	exon 21 + 10	tttggaacagggcatcac C/T tgtctgggtgctaacctcag	1183
ABCC8	66	intron 21 + 192	caaggatagacagatgacc C/Δ attgcaacttcagatgag	1184
ABCC8	67	intron 23 + 17	gaaggctgatatccaggg A/G tggcgaagcagcccccctg	1185
ABCC8	68	intron 23 + 67	gttctctagaccctgaact C/T ataaagcttctctgtcct	1186
ABCC8	69	intron 26 + 268	gtgagctctgacatccaa C/T taagatttttttctctcc	1187
ABCC8	70	intron 26 + 308	cgataagtggtgtaattg C/T ccatccacccatgagttc	1188
ABCC8	71	intron 26 + 348	cagctccctgcccctccctc A/G ctctctctctctcagccac	1189
ABCC8	72	intron 26 + 807	gacagcgtctgagtcagggc G/A agcggcagcttgagaagcc	1190
ABCC8	73	intron 26 + 834	cagctgagaagggagcaat G/C gttagatggcttgaagaaac	1191
ABCC8	74	intron 28 + (118-121)	cttccaaaaaataaacaa AAA/Δ cagaatgaagaaataga	1192
ABCC8	75	intron 28 + 1348	tgaggataacagagagaggg G/A ttagagctttgagttggt	1193
ABCC8	76	intron 29 + 1253	ctcttagagatcttgctaa G/T taagagagagagagagaaag	1194
ABCC8	77	intron 29 + 1589	cagatccagcttctctgtaa A/G cagcttcaatcagggcaca	1195
ABCC8	78	intron 29 + 2322	ggccttcaracttccatasc G/A cgcacatgcccctgacaca	1196
ABCC8	79	intron 29 + 2348	atgcccctgagcacacat /C ttcaacacacacttactcta	1197
ABCC8	80	intron 29 + 2418	agacacttaccctccaca C/T gtctccacccctggggggtg	1198
ABCC8	81	intron 29 + 2494	tcagtcccttcagacatg C/A cctctctccagcagagaca	1199
ABCC8	82	intron 29 + 2735	ggggcagaagaagatgata C/T ggcagccagagllgacaga	1200
ABCC8	83	intron 30 + 386	gcttctgggcttccagcct C/T gcagccttctgtgtctg	1201
ABCC8	84	intron 33 + 93	ggcttccagtcactctg /G ccttccagggccagagccic	1202
ABCC8	85	intron 33 + 358	aggaaccttggggagagacag C/T agagcacacttctgtatgag	1203
ABCC8	86	intron 38 + 54	cccaggaacagagactggcct G/C ttgaggccctcagtgaca	1204
ABCC8	87	intron 38 + 456	aggacattctgggcacatgc C/Δ tcatctctctctccaaacc	1205
ABCC8	88	intron 38 + 529	tggcccccacccggggctt A/G ttcccccacatccgacccg	1206
ABCC9	1	intron 3 + 38	tggttcttctttaaazag C/A taattgttttcccccacaa	1207
ABCC9	2	intron 3 + 305	gcggccttctggcttgcag /A acttctatlttaagaaacag	1208
ABCC9	3	intron 3 + 320	tgcagaagtgtatttaag A/G atcagagcttctgtgagagag	1209
ABCC9	4	intron 3 + 631	ttcttgaatcagagct G/C tctaaataatcttaatttt	1210
ABCC9	5	intron 3 + 8644	tggagcacctcaacatttc A/G agttatttacttctcaactc	1211
ABCC9	6	intron 4 + 757	agatatcatgaaactgaa A/C tcttagtaaaactatcttt	1212
ABCC9	7	intron 4 + 1022	tacttgaagattttcttgc A/C acagagatagtatttttca	1213
ABCC9	8	intron 5 - 1217	caatgtagatgtgtttct A/G ttgcacatcttcaaatat	1214
ABCC9	9	intron 6 + (100-106)	tatagattgttcaaataggc (1) g-g cagagaatgaagctttct	1215

遺伝子名	No.	存在位置	配列	配列番号
ABCC9	10	intron 5 + 1347	tcagctatctactactaaa A/Δ caaaatttgaagtaagt	1216
ABCC9	11	intron 6 + 1618	cttttatttgctgtacc C/A ttttactaaggltgataata	1217
ABCC9	12	intron 6 + 1835	cttlaataaaagcaacig C/T acaccigtctataaataa	1218
ABCC9	13	intron 7 + 407	ccataaaattttcttttc Y/G tttttccaaaaaataaaa	1219
ABCC9	14	intron 7 + 423	ttttcttttttccaaaaa C/T taaatgtttgtattattt	1220
ABCC9	15	intron 8 + 743	ttctgataagagcttaag A/T gctagatctatttgaaaaa	1221
ABCC9	16	intron 8 + 850	tttttaacttatgttttgc Y/G tttaattttttaaagaaa	1222
ABCC9	17	intron 9 + 585	caaatgtctgttttttag A/T aatcttggcaataataaaa	1223
ABCC9	18	intron 9 + 1394	attttcttcttgaagt C/G agtaagagcgtactacag	1224
ABCC9	19	intron 12 + 1167	atttaagacttttaaat C/A agataatttgcgtgtctt	1225
ABCC9	20	intron 12 + 1195	tgctgtgtgtctatactt A/G ctgagaaaactagaatttat	1226
ABCC9	21	intron 12 + 2123	ataagctctctccagttt C/A attgacttagagcaatttc	1227
ABCC9	22	intron 12 + (2653-2656)	caaaacagaataaagaag AAC/Δ tattatctaaaataaaaa	1228
ABCC9	23	intron 13 + (3043-3044)	aacatactctctctctct C/T ttttcaaaaataattaglat	1229
ABCC9	23	intron 13 + (3043-3044)	aacatactctctctctct C/T aagtcataataattaglat	1230
ABCC9	23	intron 13 + (3043-3044)	aacatactctctctctct aagtcataataattaglat	1231
ABCC9	24	intron 14 + 85	ttctgaaagtgctccaaa Y/A tggcctttaaattgtttt	1232
ABCC9	25	intron 14 + 275	agtgcatagtattttt C/G ggtattctatgttttcaaa	1233
ABCC9	26	intron 14 + 453	ctcatttcaacttggctat Y/C tggactctccagcagatg	1234
ABCC9	27	intron 14 + 3709	atcccttagtgatgacct C/A agcttgcctccatcttctt	1235
ABCC9	28	intron 14 + 3813	ctatttatatatagctga C/T ttccaagtctcagacata	1236
ABCC9	29	intron 14 + 4000	ttcttttacttaagttagc A/Δ ccaatcagaagtgacatt	1237
ABCC9	30	intron 16 + 1466	atccacagatataatctac A/C ttgtgactgtctacacca	1238
ABCC9	31	intron 16 + 5357	atttggaaagaataata Y/G aactctccacactgaattt	1239
ABCC9	32	intron 17 + 1368	aatctgtgtttttttt Y/Δ ctitttcaattttcagtagg	1240
ABCC9	33	intron 20 + 98	aagtaactcaagaagaag C/A tttaacttggaaatcgtaa	1241
ABCC9	34	intron 22 + 28	ctcatagtcagaagagtc A/C gaacccaatcagaagagtt	1242
ABCC9	35	intron 22 + 194	tgaactataaatttcaat C/Δ ccaattttgagtaggttcca	1243
ABCC9	36	intron 22 + 1370	ccagagcaaaaagaaga C/T gtaacttaagagattggagc	1244
ABCC9	37	intron 22 + 1487	agcaagccagaagaagtc C/G attaatgttatttagaat	1245
ABCC9	38	intron 23 + (455-462)	atagccaagaagaataaaa AATAGAA/Δ tccatttggtaatttccag	1246
ABCC9	39	intron 24 + (460-465)	aactcttcttctctctctc TTTAAA/TTTTAA gcaagccttgaagaagagtg	1247
ABCC9	40	intron 24 + 595	gcatacaaaaataagaaga A/G acaatctgtcttcaataga	1248
ABCC9	41	intron 28 - 976	aaataattcaaatltggag C/A tgaagcatatttccgtcat	1249
ABCC9	42	intron 29 + 2692	cttgaagcttttttttt Y/Δ aagtaataaanaatttctaa	1250
ABCC9	43	intron 29 + 5464	agcaaacctgtctttttt C/A tgtcacaaattcaacagag	1251
ABCC9	44	intron 29 - 1830	aacttgcagaagaagaaga A/T tcatattcttataaattt	1252
ABCC9	45	intron 31 + 102	tgcatttcttcttccat C/A taccagaagaacttctcat	1253
ABCC9	46	intron 33 + 877	aacataagactatagtaaat A/G tagtttttttgggttcaga	1254
ABCC9	47	intron 36 + 1281	aatttacctttttttt Y/Δ gcagaagaataatttgcaga	1255
ABCC9	48	3' flanking + 197	aattgagctcatcatgct Y/G ttcaaatatatacatgcaa	1256
ABCC9	1	15' flanking region -1772)	agtcacagcttaggcacaa C/A gcaacctcttgcctaacctg	1257
ABCC9	2	15' untranslated region -59)	acattcttccagccactg C/T ctcaacttcttccaccagca	1258
ABCC9	3	intron 1 906)	gggacacatggcatcatcc C/T ccaagggcttctgtgtctc	1259
ABCC9	4	intron 1 2924)	gagacctggccccccaat C/T gtaaccttggctctcggcc	1260

遺伝子名	No.	存在位置	配列	配列番号
ABCD1	5	(intron 1 3056)	aagcctctctctctctca C/T ccccccagctggagctgac	1261
ABCD1	6	(intron 2 2972)	agaatttcccttcttcc G/A tcaagcttggctctgctga	1262
ABCD1	7	(intron 2 3258)	ggagacagaccctggagcc G/A ctctgctcattggctgcat	1263
ABCD1	8	(intron 2 4612)	ggctcttcacagagcttcc C/T acccatttggccacacccca	1264
ABCD1	9	(intron 5 2748)	aatggcctggagctggcct C/T gggcatttggagctctcaa	1265
ABCD1	10	(intron 5 212)	atctgttggagctgttctca C/T gggcagcagatgagcgtgt	1266
ABCD1	11	(intron 5 2835)	ggcctcaagcctgttggcc C/Δ tgcagctggagaaagagatg	1267
ABCD3	1	(5' flanking region -2834)	acatccttcttcttcttcc G/G gatttgaacttcttgaagca	1268
ABCD3	2	(5' flanking region -2118)	tacaaatcaccttcttcttca G/A ccttgaaccttcttgaag	1269
ABCD3	3	(5' untranslated region -40)	gtagccgcgccgcgcgcgc C/T gccgcgtcccccgcgcct	1270
ABCD3	4	(intron 1 -6763)	atacttggcatttgaata T/C cgttttggagttgtagctg	1271
ABCD3	5	(intron 2 731)	ctttgacacttactagatt C/T cttagcatttggcttagaa	1272
ABCD3	6	(intron 2 3551)	accagtgctcttcttctt A/G taittaaaaaaattattgg	1273
ABCD3	7	(intron 2 5936)	cagacacacttcttctt A/G gtttttagatgaacttctt	1274
ABCD3	8	(intron 2 6083)	tgttcttcttcttctt A/G tctttttagatcttctt	1275
ABCD3	9	(intron 3 614)	tcttcttcttcttctt A/T tttcttcttcttcttctt	1276
ABCD3	10	(intron 3 651)	gtgaatcttgggtcttctt C/T atcagcttcttcttctt	1277
ABCD3	11	(intron 4 395)	aagcatttcaagaatcac G/A ttgacatcttcttcttgaag	1278
ABCD3	12	(exon 7 555)	gacacacaaatgaacttacc A/G gaccagcttcttaccacaa	1279
ABCD3	13	(intron 7 124)	aaatatttgaacttctt A/G gaatttgaagttgtagtaa	1280
ABCD3	14	(intron 7 838)	ggtcacatttgaacttctt A/C acggttttgaagacaaagaa	1281
ABCD3	15	(intron 8 1150)	aatcttgaacttcttctt A/C catatttcttcttcttctt	1282
ABCD3	16	(intron 9 1493)	tcatcttcttcttctt A/G ggttggagagagagagagaa	1283
ABCD3	17	(intron 13 1534)	tcttgggttggagcttctt A/G tggaaaccttcttcttctt	1284
ABCD3	18	(intron 16 4310)	gaagatgaatggcttcttctt C/T ttgcccagcttcttctt	1285
ABCD3	19	(intron 20 273)	ttctaaagttcagagaaac T/A cgttgcctcttcttctt	1286
ABCD3	20	(intron 20 1664)	ctcaaaaaaaacaaaaa A/C aaaaacacatgattcttctt	1287
ABCD3	21	(intron 20 5693)	cttaaggttcttcttctt C/T tgaacaaatgatttcttctt	1288
ABCD3	22	(intron 21 7171)	atcataaacagagaaataat A/G tctttaaagcttcttctt	1289
ABCD3	23	(intron 22 1220)	ctagaatacagagaaataat A/G aatagcagccttcttctt	1290
ABCD3	24	(intron 22 1358)	agtagcaaaaatcatctac C/A cttagtctcttcttcttctt	1291
ABCD3	25	(intron 4 4448 4461)	taacttcttcttcttcttctt C/T aactgttcttcttcttctt	1292
ABCD3	26	(intron 5 268)	gttttcttcttcttcttctt T/Δ acccttcttcttcttctt	1293
ABCD3	27	(intron 5 891 902)	ttgttgaagccttcttcttctt C/Δ ttttcttcttcttcttctt	1294
ABCD3	28	(intron 7 1226 1227)	gggaatgggggggtcttctt tctaaacttcttcttcttctt	1295
ABCD3	29	(intron 8 1129)	caaatcttcttcttcttcttctt tctaaacttcttcttcttctt	1296
ABCD3	30	(intron 13 1595 1596)	gaacataataaagcacac tttatcttcttcttcttcttctt	1297
ABCD3	31	(intron 13 1595 1596)	gaacataataaagcacac tttatcttcttcttcttcttctt	1298
ABCD3	32	(intron 15 7337 7351)	ttatcttcttcttcttcttctt tttatcttcttcttcttctt	1299
ABCD3	33	(intron 18 12)	gttcttcttcttcttcttctt C/Δ tttatcttcttcttcttctt	1300
ABCD3	34	(intron 20 1652 1670)	gcaagctcttcttcttcttctt A/T tttatcttcttcttcttctt	1301
ABCD3	35	(3' untranslated region 2072 2079)	ttatcttcttcttcttcttctt C/Δ tttatcttcttcttcttctt	1302
ABCD3	36	(3' untranslated region 2080 2091)	ttatcttcttcttcttcttctt C/Δ tttatcttcttcttcttctt	1303
ABCD3	37	(3' untranslated region 2072 2079)	ttatcttcttcttcttcttctt C/Δ tttatcttcttcttcttctt	1304
ABCD3	38	(3' untranslated region 2080 2091)	ttatcttcttcttcttcttctt C/Δ tttatcttcttcttcttctt	1305

遺伝子名	No.	存在位置	配列	配列番号
ABCD3	37	3' untranslated region 3349-3368	actatattctcttcagatt w 10-19 ctacagatactctatacaacc	1306
ABCD4	1	(intron 1 276)	tcgattcttttttgaag C/A aagaaccttcaggtgcacaaa	1307
ABCD4	2	(intron 1 329)	cttcagctctttacaccc C/C ggggcaatcaaggctcc	1308
ABCD4	3	(intron 3 171)	ttaacagttatcttctt A/G ttgctccacgtgggactgat	1309
ABCD4	3	(intron 3 449)	cttaccctcatatcagtag C/A gggctaccacgtctcactc	1310
ABCD4	5	(intron 5 273)	gacaggctactcagtag C/T aacagagttcagcctcaggg	1311
ABCD4	6	(intron 7 240)	taactctagttccctcaggt C/A gggcttgaatgttcaaatg	1312
ABCD4	7	(intron 7 267)	gaatctacataataatga T/C gctctatctcttctctctg	1313
ABCD4	8	(coding region 910 (Ala 304 Thr))	tcataagagaccctgagcc C/A cagagcttcagacccctggc	1314
ABCD4	9	(coding region 981 (Leu 327 Leu))	atcagctctcaccagct C/A atcagctctcaccagct	1315
ABCD4	10	(coding region 1102 (Glu 367 Lys))	gcagatctcgggcagagc C/A agtgggcttcagacagctg	1316
ABCD4	11	(intron 13 191)	tggattgggcccactacta C/C agcactctctgaggtcaggt	1317
ABCD4	12	(intron 13 262)	agcctatgtctaacaccca A/G gctggattctggggccct	1318
ABCD4	13	(intron 17 848)	ctctctctctctggccat C/G ctctctctctggggccct	1319
ABCD4	14	(intron 17 946)	ggcctggaggagagagagaa C/T ccaaggcttcagccttccca	1320
ABCD4	15	(intron 18 41)	ggcctggaggagagagagaa C/T ccaaggcttcagccttccca	1321
ABCD4	16	(3' untranslated region 2001)	ggcctggaggagagagagaa C/T ccaaggcttcagccttccca	1322
ABCD4	1	(5' flanking region -386)	gcataatctatggctagag C/A tatgtatataatgatcatt	1323
ABCD4	2	(intron 1 189)	caccataatggtagctg C/T cggatttgggagatcgagct	1324
ABCD4	3	(intron 1 291)	acttgggctctgtagtag A/C tcttccactcgtttctctg	1325
ABCD4	4	(intron 1 318)	acttgggctctgtagtag A/C tcttccactcgtttctctg	1326
ABCD4	5	(intron 1 468)	ggcttctgtagtagtag A/C tcttccactcgtttctctg	1327
ABCD4	6	(intron 2 434)	ctgggacaggtttgttcc C/A gttgctctctttagat	1328
ABCD4	7	(intron 3 1839)	ttaaaatgatttcttct C/G ctgaagccttttaggagttg	1329
ABCD4	8	(intron 3 3076)	tttgcactctctctct C/T ggtctctctctctctctg	1330
ABCD4	9	(intron 3 3352)	gttcttctgtagtagtag C/A gttacacagtttctcagta	1331
ABCD4	10	(intron 3 8030)	acagtagagtagtagtag C/T gtagacacagcagcagctc	1332
ABCD4	11	(intron 3 8092)	ggctgc a/g tgcagcagct C/T gggcaggttagagagcaga	1333
ABCD4	13	(intron 3 8285)	ctggacatgtgactctctg C/T accacccctcacagcaca	1334
ABCD4	14	(intron 3 8860)	caggttagatagtagtag C/A gttacacaggttctcagta	1335
ABCD4	15	(intron 4 2319)	ggggtagacagtagtagtag C/A gttacacaggttctcagta	1336
ABCD4	16	(intron 4 2557)	ggggtagacagtagtagtag C/A gttacacaggttctcagta	1337
ABCD4	17	(intron 5 139)	tgaccacggcagccttagag T/A gggcctggcctcagcct	1338
ABCD4	18	(intron 5 177)	gcttccctctccctctcag C/C gggcctggcctcagcct	1339
ABCD4	19	(intron 6 13)	cagttactatagtagtag T/C caggggttagtag a/a gaatct	1340
ABCD4	20	(intron 6 27)	gctgtt T/C caggggttagtag T/C caggggttagtag a/a gaatct	1341
ABCD4	21	(intron 6 1191)	gctgtt T/C caggggttagtag T/C caggggttagtag a/a gaatct	1342
ABCD4	22	(intron 6 1449)	gctgtt T/C caggggttagtag T/C caggggttagtag a/a gaatct	1343
ABCD4	23	(intron 6 2282)	gctgtt T/C caggggttagtag T/C caggggttagtag a/a gaatct	1344
ABCD4	24	(intron 6 3853)	gctgtt T/C caggggttagtag T/C caggggttagtag a/a gaatct	1345
ABCD4	25	(intron 6 3871)	gctgtt T/C caggggttagtag T/C caggggttagtag a/a gaatct	1346
ABCD4	26	(intron 6 4175)	gctgtt T/C caggggttagtag T/C caggggttagtag a/a gaatct	1347
ABCD4	27	(intron 7 4)	gctgtt T/C caggggttagtag T/C caggggttagtag a/a gaatct	1348
ABCD4	28	(intron 7 576)	gctgtt T/C caggggttagtag T/C caggggttagtag a/a gaatct	1349
ABCD4	28	(intron 7 576)	gctgtt T/C caggggttagtag T/C caggggttagtag a/a gaatct	1350

通称子名	No.	存在位置	配列	配列番号
ABCG1	29	(intron 7 1426)	aattctctctcaacttaa A/G gaattattttatagaaaat	1351
ABCG1	30	(intron 7 2342)	agaccctcaataggcccc G/A agggaccctccataactaa	1352
ABCG1	31	(intron 7 2399)	gagggttcaacagagat A/G tgcig c/g tgtctccagcig	1353
ABCG1	32	(intron 7 2406)	tgacagagat a/g tgcig C/G tgtctccagctactgttt	1354
ABCG1	33	(intron 7 2911)	ctctctctgcccactgtt C/G tcccaaacaccctgtttc	1355
ABCG1	34	(intron 7 4383)	tataataattctactagga A/C aacataattatagagaaac	1356
ABCG1	35	(intron 7 4752)	gctttcagaccctatccca C/T aagggtcatttattagg	1357
ABCG1	36	(intron 7 5076)	ccaggtctctgagattttag G/A ccaaaagagagctagcaag	1358
ABCG1	37	(intron 7 5532)	gggttaaatattccggggag C/T gcaagtcagattatcgtta	1359
ABCG1	38	(intron 7 5681)	gctaaagtcatagagagca T/C catgaataaatctttcagg	1360
ABCG1	39	(intron 7 9243)	gcttgaagccctcagcagta G/A gaagggtccagcagtgagac	1361
ABCG1	40	(intron 7 11371)	gggtctctctgagccctt T/G tctctccagccctctgtct	1362
ABCG1	41	(intron 7 12420)	gggtttcaaatctcaaac T/C ctgagctctgtgttccccc	1363
ABCG1	42	(intron 7 12985)	ctattgagctctgagca T/C tgttctgagatttgcataa	1364
ABCG1	43	(intron 7 20041)	acatggccgttctctt T/C cctc g/a gaatgcccagaaat	1365
ABCG1	44	(intron 7 20046)	ggcaggtctcttct T/C cctc G/A gaatgcccagaaat	1366
ABCG1	45	(intron 7 21058)	acagagattagaatttacc G/A taattttaactattctaa	1367
ABCG1	46	(intron 7 26183)	ttcttgaatgagca tga C/T gggggcagaggtttgatgag	1368
ABCG1	47	(intron 7 27453)	atcatgtgttggggaaa G/C ctggaccctcacttgatca	1369
ABCG1	48	(intron 7 29810)	attgttctctggtttt T/C tatgttacttttccctttaa	1370
ABCG1	49	(intron 10 2116)	aaatgggtcttgatctctc G/A taaggatcagagaccttcc	1371
ABCG1	50	(intron 13 1196)	taaaagaaaatgagat G/A gaa a/c ccaaaagagagaaat	1372
ABCG1	51	(intron 13 1200)	aagaaaatgagat g/a gaa A/C ccaaaagagagaaatgag	1373
ABCG1	52	(intron 13 2041)	aaacagagcttttccacc G/A gacgttcagagagcgtctcc	1374
ABCG1	53	(intron 13 2490)	gtgtgaagtaagctaac A/T cacgggagagccttccatcc	1375
ABCG1	54	(intron 13 2822)	cagcagctctctctctaac T/C cacagcagaccagcctcttg	1376
ABCG1	55	(intron 13 2850)	agccagccttggccctcc G/A gacgttgagagaccagaca	1377
ABCG1	56	(intron 13 2919)	gcttcagagatctctaac C/T gggaccccaagagcagaagcc	1378
ABCG1	57	(intron 13 3506)	ggcagcctgggttccgaaa T/C ctctctggagacccctccg	1379
ABCG1	58	(intron 13 3538)	ccctccggagagagccccc G/A ggggtcagagcagaa a/g agtgc	1380
ABCG1	59	(intron 13 3554)	ctag g/a ggggtcagagcagaa A/G gtagccttggcagcttttgc	1381
ABCG1	60	(intron 13 3721)	ccagctcataggcagagagc C/T ggaagaaagagcagccacag	1382
ABCG1	61	(intron 13 3921)	gaagcagcagctctgagcc A/G gcttggaaagagccttccg	1383
ABCG1	62	(intron 13 3979)	accaccagccttttccaga C/T agccttcagagagcttctc	1384
ABCG1	63	(intron 13 4291)	gagccttgagatagagctcc G/A ctctctatgcttcccaaggg	1385
ABCG1	64	(intron 13 4958)	tattactgagacactcttc C/T gtaggggacacttggcctagg	1386
ABCG1	65	(intron 16 672)	atcagtaacgggtcactaac G/A gatactctgagctggagcag	1387
ABCG1	66	(intron 16 891)	tggccactcttgaaggtgt G/A ggtgacagagagggccttgcg	1388
ABCG1	67	(intron 16 1616)	cttggagagaaacagagata A/C agcttaagacgtg c/t tctcac	1389
ABCG1	68	(intron 18 1630)	agata a/c agcttaagacgtg C/T tgtcagagatcagggctcc	1390
ABCG1	69	(intron 18 1674)	gcttccaaagggcagctcc C/T gttgtcttctgagc c/t gaaga	1391
ABCG1	70	(intron 18 1689)	atccg g/t gttgttcttctgagc C/T gaggacgcttttccagacc	1392
ABCG1	71	(intron 19 446)	tggcagagatcaaacagc G/A gctgtcttccagactttaa	1393
ABCG1	72	(intron 22 243)	accggaagacatagagcag A/C ccaagcttcttggagcttgc	1394
ABCG1	73	3' flanking region 1257)	atggggccacagaccccttgc T/C cagaagcagctttgtgtctgc	1395

遗传子名	No	存在位置	配列 番号
ABCG1	74	3' flanking region 1438	GGGGGAAGAGCTGGGAAC A/G TGAAGGCTGTGAAGCTCAAA
ABCG1	75	3' flanking region 1518	TGAAGGTGAAGTGAAGTAG C/C TGAAGATCTCAATGAAG
ABCG1	76	(intron 3 3754 3755)	CTCACCCTGACCTCCCTG C/C CCTCTGATCTCCCTCATC
ABCG1	77	(intron 3 3754 3755)	CTCACCCTGACCTCCCTG C/C CCTCTGATCTCCCTCATC
ABCG1	77	(intron 3 7848 7854)	CAGTTTCAAAATCTGGGG A/G 6-7 TCCATAAGCTGCTACTT
ABCG1	78	(intron 4 190 191)	TGTGAAGCTCCCTGACC C/C TGGTGAATCTCAGGTCTT
ABCG1	78	(intron 4 190 191)	TGTGAAGCTCCCTGACC TGGTGAATCTCAGGTCTT
ABCG1	79	(intron 4 198 206)	AGTCCCTTGGCTGGTGA TCTTCAAGG/Δ TTTACTAGAAATGCCGAA
ABCG1	80	5' untranslated region (-713) (-741)	CGAGCTCAAGCTCCCTCC C/C 8-10 CCCCAGGCTAGCTGTCT
ABCG1	81	(intron 6 376 387)	TCTTGGCTTAGCTCAAGAG A/G 10-12 TAGCCAGTCTTCTGCAAG
ABCG1	82	(intron 7 19944 19945)	CTGA TAGAGAGGGAGAGGGG (CACCAGGCACGACACTCTGATGAGAGGGAGGGG)
ABCG1	82	(intron 7 19944 19945)	CACAGGACGACACTCTGA
ABCG1	82	(intron 7 19944 19945)	CTGATGAGAGGGAGAGGGG
ABCG1	83	(intron 7 25136 25137)	CATAACTTGGCTGGACATA C/C CCTGTGAAGAGCTAGAGCT
ABCG1	83	(intron 7 25136 25137)	CATAACTTGGCTGGACATA CCTGTGAAGAGCTAGAGCT
ABCG2	1	(intron 1 152)	TCATTGAAGTGGGTATGC C/A GTTTAAACTGACAGTCAA
ABCG2	2	(intron 1 614)	AGCTAGTAAATAAATAC C/A CCAAGTAGTAGAAGAGAGA
ABCG2	3	(intron 1 1002)	CCTGAAGTAGTATACATG T/A CCAACATATCTCTTGAT
ABCG2	4	(intron 1 10123)	ACAATGATCCTTTGGGTGC C/A TATCCCAATCTCTGATA
ABCG2	5	(intron 1 10768)	ATAGGATAATTAGAACAG C/A GTCTAAGAACTCTGACAGA
ABCG2	6	(intron 1 10791)	CTGAAGACTCTCAGAAA T/C G/A AATAGTCTCTGCTTT
ABCG2	7	(intron 1 10792)	TEAAGAACTCTGACAGAA T/C G/A AATAGTCTCTGCTTTA
ABCG2	8	(intron 1 14183)	TCATTAGGTTTCTGACGG T/G GTCTAGGACACAGAGAGAA
ABCG2	9	(intron 1 14934)	AAGATCTTAAATATTC A/G TCTTAGTACAGTAGAGTAT
ABCG2	10	(intron 1 14955)	TCTTAGTACAGTATCT C/T AATCTAAGCAATAGTAT
ABCG2	11	(intron 1 17251)	CTGTGGAGACAGACATC A/C ATCATAGCAGAGAGAGAGT
ABCG2	12	(intron 1 17347)	ATTCAACCTGTTTACAA C/A TTGTAAGTCTCATTTAAG
ABCG2	13	(intron 1 17626)	GAAGTGAATAACAATTC T/G ACATAAAGTCTGAGGCTATA
ABCG2	14	(intron 1 18369)	CTATTCTTCTCTCTCA C/T AAGATAAAGTCTCTCTCA
ABCG2	15	coding region 34 (Val 12 Met)	ATGTCAAGTTTATCTCCA G/A TGTCAAGGAAGAACCAAT
ABCG2	16	(intron 2 36)	TGTAAAGACACTTTTA A/C TTTACTACAGTGAACCTCA
ABCG2	17	(intron 2 4230)	CAACCTAAATGGAGGCC C/T GGCCTGTGATTGAGAAG
ABCG2	18	(intron 2 4518)	GTGTGACACTTTATAGT A/C GGGACACTGACTCTGATGA
ABCG2	19	(intron 2 6278)	ATGTATGACAGTCTCA T/C ATCTTAAGATGACCTTA
ABCG2	20	(intron 3 10)	GGCAATCTGTGAGTATA C/G GAGAGTAAAGTAAGGTTT
ABCG2	21	coding region 421 (Gln 141 Lys)	TAAGGTGGAGAGAAACTTA C/A AGTCTCTGCACTCTCTGG
ABCG2	22	(intron 6 3203)	TCTATTCTGTTTATAAA A/G GCATGAATTTAAGTTTCT
ABCG2	23	(intron 6 3287)	GTCAAGCTGAACAGAACAA A/G CAATCAAGGCAAGAAAG
ABCG2	24	(intron 9 5974)	TATCTAATAATGGTGT A/T TAAGTTTATCTCTAATG
ABCG2	25	(intron 10 1908)	GGCTTATGTGAGCTTAT G/T TTAGTCTGGAAGAGCTGA
ABCG2	26	(intron 10 2094)	CCTTGAAGGCTTGAAGTAT C/A GATTATTCAGACTTCTA
ABCG2	27	(intron 11 20)	TGTAGTAGTCTTTTCT A/G GGAACGGGCTGTCCAGAG
ABCG2	28	(intron 11 1447)	TGTTCTCAAGAGAGCCCT C/T GTCAAGAGAGAGAGAGC
ABCG2	29	(intron 12 49)	ATGCTTTAGTCTTGGTAT C/T GGTGAAGTCAAGTTGCACTT
ABCG2	30	(intron 12 1566)	TATCAATTCATAGGACGA C/T ACAACTTGAAGACCTGAGGG

遺伝子名	No.	存在位置	配列	配列番号
ABCG2	31	(intron 13 40)	gcctgaagaagatgttt c/ tttccttattcttcctgc	1440
ABCG2	32	(intron 13 1823)	ttactcaagagccctgact c/ ttagtatttgcctttttag	1441
ABCG2	33	(intron 14 497)	ctaataaanaaacaagaa t/c gaaagatgtcactgtaaat	1442
ABCG2	34	(intron 14 815)	taactctttgaaactctt c/ g aaatttaaaacttttacct	1443
ABCG2	35	(intron 15 110)	ccaggagacatgaattttc c/ t gaccctacgtttttcctcc	1444
ABCG2	36	(intron 15 566)	gcgcgatactatgtgtgt t/ a gtttttaatttaacttgaaa	1445
ABCG2	37	(intron 15 639)	aaacaataacatigaalaa c/ a ttaaaaaaacccgtttt	1446
ABCG2	38	(intron 15 1197)	ttagtagctggattacaag c/ t gccaccacacacctggct	1447
ABCG2	39	5' flanking region (-998) (-995)	gttggatggctacacacac tca/△ aagccctgagccgtttc	1448
ABCG2	40	(intron 13 405)	ctgctatttttttttt t/△ aacatttttaatttatgtt	1449
ABCG2	41	(intron 13 692 702)	tcaatatttttcttctatc ttg-ll aatgtttacttaattcctaat	1450
ABCG2	42	(intron 15 645 650)	aaactttgaatac/Attagg (A) 7-8 cccctgtttcacaatgtt	1451
ABCG4	1	(intron 1 84)	ggcctgggtgtccatcttc c/ a gaaagcttgcacacgtggg	1452
ABCG4	2	(intron 2 77)	aaacataagaagatatttcta a/ g aagcatttgcacccatctt	1453
ABCG4	3	coding region 679 (Leu 227 Leu)	tggtgtccctcacaagatgc c/ t tggcagagggggccctacc	1454
ABCG4	4	(intron 7 95)	ggcctctttaggggtagagat c/ t tcaacttcccttgccttccc	1455
ABCG4	5	(intron 7 158)	cttgccttgggaagtagat c/ a tgaatctaaacttagcttc	1456
ABCG4	6	(intron 8 106)	cccacagggcatttgaacca a/ g tgggtacttagaagaacacta	1457
ABCG4	7	(intron 11 120)	accgataaagtaa t/c ggtcat a/ g tggccagggagaaaggagac	1458
ABCG4	8	(intron 11 173)	gggggacagcttgaataaaa a/ g tgttgaagcagagatggacac	1459
ABCG4	9	3' untranslated region 2758)	gagtagacagacacatacag a/ c gaaagccctctgacccct	1460
ABCG5	1	(intron 3 40)	cccctggccctcccccctcc c/ a cggggactttaggtacacgt	1461
ABCG5	2	(intron 4 841)	gcttgggggcatcttgaag c/ t gccatcccaacacacacac	1462
ABCG5	3	(intron 4 1145)	ggcacaatccagccacac c/ a tctaaat c/ a ctataagtaa	1463
ABCG5	4	(intron 4 1154)	cagccccacg a/ a tctaaat c/ a ctataagtaa	1464
ABCG5	5	(intron 4 1590)	acagataagagagagaggt t/ c ggaatcttaccctggctgt	1465
ABCG5	6	(intron 4 1806)	tcttttttccagataat t/ c tatatctaatatttatatc	1466
ABCG5	7	(intron 4 1878)	atttcagatatcttcttct c/ t tgggtggttcaagctacat	1467
ABCG5	8	(intron 4 2052)	gggtcttggacaacaaat c/ t attccataagtagtacttc	1468
ABCG5	9	(intron 4 2108)	tcccctgggggttcttcac a/ t tagaggtaatcagtagacag	1469
ABCG5	10	(intron 4 2230)	agcttcttgattagaatc c/ a gtaagaatttttttagtc	1470
ABCG5	11	(intron 4 2318)	ggagttcacagctttagta c/ c agcagaagaatttgaagaa	1471
ABCG5	12	(intron 4 2367)	ttaatgtgcttgggggta c/ t aatttgggtcccttataag	1472
ABCG5	13	(intron 4 2464)	gattatagctttagtg a/ g actcacactagagattgacc	1473
ABCG5	14	(intron 4 2586)	aagcattttatataataaa c/ a ttcaaacacccaacactta	1474
ABCG5	15	(intron 6 1318)	cagagacatcaaatgtcat c/ t gctacctttagatcacaca	1475
ABCG5	16	(intron 9 164)	caactatttagttaccaca t/ c gttatataaatgagctcac	1476
ABCG5	17	(intron 9 365)	gtacgttagcttctcttgc a/ g acgttaatttagacaccca	1477
ABCG5	18	(intron 10 64)	tcatgagactagtgactc c/ a tgcagagagagcttccaggt	1478
ABCG5	19	(intron 10 246)	tcaacagcctgcttactgc c/ a gttatgttgcacattgtct	1479
ABCG5	20	(intron 10 2442)	tgtcttaagtaatttattgt t/ g tctatagagctgaagag	1480
ABCG5	21	(intron 11 4150)	aagcccttgaatagcttct c/ t ctggctatttttccagctc	1481
ABCG5	22	(intron 11 4823)	caacagaagaattttata c/ t cttttgattgacagaata	1482
ABCG5	23	(intron 11 4737)	attttcaatgaattgtgg t/ g tgggtcttcttcttctttt	1483
ABCG5	24	(intron 11 4791)	ggttagttctaacattttctac c/ a ttgtaaccttcaactttctg	1484

遺伝子名	No.	存在位置	配列	配列番号
ABCG5	25	(3' untranslated region 2578)	gaagattaaataaataac C/T gaagaaatggcgaacagt	1485
ABCG5	26	(3' flanking region 1560)	catagcactcagcaaaac G/C tggctaaagcagagcttc	1486
ABCG5	27	(intron 4 1078 1080)	gggacagctccctggagac AGG/A agaacctccatagcagagt	1487
ABCG5	28	(intron 10 2321 2327)	agcgggttggtagccctt TAAAT/T agttaggtatgtttggct	1488
ABCG5	29	(intron 11 422 433)	ggaaataagactatcagac A/T 10-12 ccctgacagataaagacig	1489
ABCG5	30	(intron 11 3988 4004)	ctttttttgtgtgtcttc T/T 15-17 ctctctgtttcttactctg	1490
ABCG5	31	(3' untranslated region 2719 2731)	tacctaaacttaagtat A/T 11-13 cctacgaaaaaataaata	1491
ABCG8	1	(5' untranslated region -19)	agagagctggagccagagg G/T caccagaccctggggcccat	1492
ABCG8	2	(intron 1 898)	cttttgactgaattcggat A/G tggcagatttgaagcaga	1493
ABCG8	3	(intron 1 1548)	cctcacactgaagagcca G/T gtgaatttgaagaaattcta	1494
ABCG8	4	(intron 1 1611)	tgttacggggggccattc C/T agcccaagcccaaccctgic	1495
ABCG8	5	(intron 1 3245)	tggaacaaatgaagcaatgg T/C acatgacagcggagagggc	1496
ABCG8	6	(intron 1 3430)	gggttgggtgggaatgaa A/C tctggatttctactcaggg	1497
ABCG8	7	(intron 1 3509)	ttacaaatcagcttaaaa T/A cttcatgtatcacaccacca	1498
ABCG8	8	(intron 1 3980)	gaataaacccttgctcaga G/T gcttggagctcagctccic	1499
ABCG8	9	(intron 1 4123)	aagggttcttggctctccc G/A taagtgtttgttgggtgcat	1500
ABCG8	10	(intron 1 5354)	cagcttctaaggagccctt A/C atctctctgtct t/c ccacag	1501
ABCG8	11	(intron 1 5368)	ggcct a/c atctctctgtct t/c ccacagcctccagatag	1502
ABCG8	12	(coding region 161 (cys 54 Yyr))	ggagtcagagcccttcacac G/A ccagtagagggcagccctgg	1503
ABCG8	13	(intron 2 86)	gaataaaagggtgggcca C/A cttgagggcctctctccc c/g c	1504
ABCG8	14	(intron 2 105)	a c/a ctccagggcctctccc C/G caagacagagctcagcca	1505
ABCG8	15	(intron 4 43)	ggcccaagctcagaagc C/T acagtgctcctccctccic	1506
ABCG8	16	(intron 6 1035)	cagagagcagggccccc C/T gcccttgctacacattct	1507
ABCG8	17	(intron 6 1085)	cacagaagctcacctccc C/A cctgtcagctgagcagcc	1508
ABCG8	18	(intron 6 1184)	gcacttgcacacggcctt C/T ggggaataattaaagtaac	1509
ABCG8	19	(coding region 1199 (Thr 400 Lys))	tgggctgctcagcacttta C/A agcgtatccgtaattat	1510
ABCG8	20	(intron 8 137)	gaataaacagacalcagca G/A ggcgttgggttataccct	1511
ABCG8	21	(intron 9 412)	ttcttttcttcttctta T/C tttttaggttactcagagag	1512
ABCG8	22	(intron 10 343)	agaagacagaggttcagaga C/A gctacgtgctctccaggg	1513
ABCG8	23	(intron 10 614)	cttttaaacatttaataa T/C ggcataaaggctcagctt	1514
ABCG8	24	(coding region 1695 (Ala 565 Ala))	gctctcttctcagcaatgc C/T cttccacactctctcct	1515
ABCG8	25	(intron 11 82)	tgttttctctggaataga C/T acttaccattagatccaac	1516
ABCG8	26	(intron 1 2882 2893)	ttctttagaatagataaga T/T 11-13 gacagagctcagcgtctgg	1517
ABCG8	27	(intron 1 3554)	ttttctttctctcttttt T/T 13-15 cgtlataatttggctctt	1518
ABCG8	28	(intron 1 5045)	tcagagcagaggtttttt T/T 13-15 atagactctctccgtcca	1519
ABCG8	29	(intron 9 237 302)	tgtcttactgtctctatt A/T 10-12 tagagacttggcctaafg	1520
ABCG8	30	(intron 9 417 418)	tttcttctctctta t/c ttttt tt aggttactcagagagcaaa	1521
ABCG8	31	(intron 10 28 34)	tttcttctctctta t/c ttttt aegttactcagagagcaaa	1522
ABCG8	32	(3' untranslated region 2118)	ggcaggttgaagcagatg C/T 7-9 accacagaggttaggggttaa	1523
ABCG8	33	(5' flanking region -158)	tcctggagcagtgaggaca A/T tgacctacagatctcagc	1524
ABCE1	1	(intron 9 237)	aactagattctcggcact C/T cagcacttggcttcccaac	1525
ABCE1	2	(intron 9 237)	cgaatataatgaatc C/T gtagctttatagaagcaga	1526
ABCE1	3	(intron 9 4203)	ttgttaggaagctatata T/G taattgacataagaatgt	1527
ABCE1	4	(intron 10 1811)	ccaagaacttcagcttct C/T ttcacttaataatagaaac	1528
ABCE1	5	(intron 17 2301)	atatccagaacagataagta T/C gtccagaacaggttgtacag	1529

道伝子名	No.	存在位置	配列番号
ABCEI	6	13' untranslated region 1810	1530
ABCEI	7	(intron 1 5349 5363)	1531
ABCEI	8	(intron 1 5845 5854)	1532
ABCEI	9	(intron 5 836 851)	1533
ABCEI	10	(intron 8 1153 1169)	1534
ABCEI	11	(intron 9 1023 1024)	1535
ABCEI	11	(intron 9 1023 1024)	1536
ABCEI	12	(intron 9 2338 2346)	1537
ABCEI	13	(intron 9 3213 3221)	1538
ABCEI	14	(intron 10 284 299)	1539
ABCEI	15	(intron 10 840 853)	1540
ABCEI	16	(intron 16 163 172)	1541
ABCEI	17	(intron 16 1372 1382)	1542
ABCFI	1	5' untranslated region -60	1543
ABCFI	2	(intron 1 101)	1544
ABCFI	3	(intron 20 69)	1545
ABCFI	4	(intron 23 35)	1546
ABCFI	5	(intron 7 342 354)	1547
ABCFI	6	(intron 7 356 369)	1548
ABCFI	7	3' untranslated region 2425	1549
ABCFI	8	3' flanking region 1067 1068	1550
ABCFI	1	5' untranslated region -127	1551
OAT1	2	5' untranslated region -20	1552
OAT1	3	(intron 3 160)	1554
OAT1	4	(intron 4 211)	1555
OAT1	5	(intron 5 33)	1556
OAT1	6	(intron 6 168)	1557
OAT1	7	(intron 1 58 71)	1558
OAT1	8	(intron 3 1306 1310)	1559
OAT2	1	(intron 4 842)	1560
OAT2	2	(intron 5 183)	1561
OAT2	3	(intron 5 184)	1562
OAT2	4	(coding region 1269 (Ser423Ser))	1563
OAT2	5	3' untranslated region 1792	1564
OAT2	6	3' flanking region 1386	1565
OAT3	1	5' flanking region -463	1566
OAT3	2	5' untranslated region -16	1567
OAT3	3	(coding region 153 (Pro51Pro))	1568
OAT3	4	(intron 2 177)	1569
OAT3	5	(intron 2 6201)	1570
OAT3	6	(intron 3 79)	1571
OAT3	7	(coding region 723 (Thr241Thr))	1572
OAT3	8	(intron 5 524)	1573
OAT3	9	(intron 7 386)	1574

遺伝子名	No	存在位置	配列	配列番号
QAT3	10	(intron 9 81)	atgttcctgctctaccga c/a agagagccatcccttataagac	1575
QAT3	11	(5' flanking region -661) (-660)	tacatttgcctccaggggg (b) aagcgactatcagagaga	1576
QAT3	11	(5' flanking region -661) (-660)	tacatttgcctccaggggg aagcgactatcagagaga	1577
QAT3	12	(intron 8 212)	tctacttgcctccagggga aa/Δ gtagtgggtatcttgatag	1578
QATPI	1	(5' flanking region -916)	acagagtagatcttcaalaa c/a tatgtgttatacttctgaga	1579
QATPI	2	(5' flanking region -843)	tagtgcagcagatagctt c/a atgtgtatgtttgggaatt	1580
QATPI	3	(5' flanking region -526)	aaatgtgtccttgatatta t/c acatctctacatatattcc	1581
QATPI	4	(5' flanking region -172)	aaacacacactcaagat c/a tctattattttaaataagcta	1582
QATPI	5	(intron 1 206)	ttgattcagcagatagtc c/g taatagcctttagagacatt	1583
QATPI	6	(intron 1 454)	caacatacaaalatttct c/a taagaataatggcattttg	1584
QATPI	7	(intron 1 999)	gttttagcaggttagatatt a/g atgtagatgtaaacacaaa	1585
QATPI	8	(intron 1 1223)	ttgcagaagctagtagaac c/a ascittataatcacagat	1586
QATPI	9	(intron 1 1326)	aacttagttagcaaccatg t/c gtttaggg g/a aaagcaatg	1587
QATPI	10	(intron 1 1336)	gaacccatg t/c gtttttaggg c/a aaagcaatgaggtcatgat	1588
QATPI	11	(intron 1 1498)	atagtttgcctttaaaga c/a acttgaagaagttttagt	1589
QATPI	12	(intron 1 5041)	ttatgtctccagggaggttag c/a tcttataatcacaaggaga	1590
QATPI	13	(intron 1 9532)	aaagcttggagagacttcc a/g atgcataatcagactaga	1591
QATPI	14	(intron 2 961)	aaaagtattatagaatat a/g agtgcactcttcttagtt	1592
QATPI	15	(intron 2 1110)	gttactagttgtacatcc t/c ttatagcttagcctctatca	1593
QATPI	16	(intron 2 1419)	aaagcttaagaaggatcag t/c gcaatagccttagtgagaag	1594
QATPI	17	(intron 2 3339)	taagtttgcataaactta t/c tcttataattgttttttca	1595
QATPI	18	(intron 3 66)	caggaaatgaagtgcatt t/c cctcttagagagcaatcatt	1596
QATPI	19	(intron 3 205)	tcagttttgcatattacac a/g atgggaatttgggaactttt	1597
QATPI	20	(intron 3 6377)	aatgaatagacatttagta c/a tggatttttagtgataaat	1598
QATPI	21	(intron 3 7238)	tgaatgtacattttttaa c/a ttgtgttcttctatcatal	1599
QATPI	22	(intron 4 1016)	ttttatcttgattcatgtt t/c ggggaattgcagtagtcca	1600
QATPI	23	(intron 5 110)	tccacaaatgatagtagagt a/g tcttggcacagtggccttc	1601
QATPI	24	(intron 6 496)	agttcttgaattataacca a/g ttttatagttgggtgggaacc	1602
QATPI	25	(intron 7 1934)	aaagtgaagaagaattaaa c/c tgaagacttgaacttgaatg	1603
QATPI	26	(intron 7 2140)	tgaatgtaccacaaatgaac a/g gcatcttgagagatgggaacc	1604
QATPI	27	(intron 7 2365)	tgaatcttcttatacaact c/a gatitctccagactttac	1605
QATPI	28	(intron 8 88)	gcaactcttaagttagagt c/c ttttagatatatttttagct	1606
QATPI	29	(intron 9 534)	tcatattttatattttaa c/a ttaactgggttttctacgaaa	1607
QATPI	30	(intron 9 1286)	tattctctagataaata c/c tgaagagatggctatagctt	1608
QATPI	31	(intron 11 215)	ttactcttatcttcgcta c/a ttttcttcttatttcttag	1609
QATPI	32	(intron 11 663)	ttcttcttctttggagctc t/a aaagttagagttcagttatc	1610
QATPI	33	(intron 11 999)	atcatctacataagagatt a/g gaattatacactttagat	1611
QATPI	34	(intron 11 16727)	ttcttttatttacaactt a/g ttactttttagagttatga	1612
QATPI	35	(intron 12 48)	ctatcagaacataatttta t/g tattatttttttattacatt	1613
QATPI	36	(intron 12 686)	tatgttttgaataacttgc c/a gtacaaataagaagaattga	1614
QATPI	37	(intron 12 708)	tacaaataagaagaattga a/g tatcttcaataagaatcaggt	1615
QATPI	38	(intron 13 418)	tcttggcttccaaatcat a/g tatcttctctcttctt c/a at	1616
QATPI	39	(intron 13 436)	at a/a tatttcttctctctt c/a attttctgaacaatcttc	1617
QATPI	40	(3' untranslated region 2130)	gtcttgaagaaccttaaaa c/a ctttaacttaaaaataaa	1618
QATPI	41	(3' flanking region 57)	agtgactaaagattttctt c/a aaacaagtgcttgaalcaaa	1619

遺伝子名	No	存在位置	配列	配列番号
OATP1	42	3' flanking region 572	aatcactatggtatttatt C/A tgcataaaatggagtga	1620
OATP1	43	3' flanking region 788	atttctaataatcagaig C/T atcataaaagaagaagc	1621
OATP1	44	3' flanking region 1356	aggtaacacataaaagg C/A scaagacataatagatt	1622
OATP1	45	5' untranslated region (-189) (-188)	atttctaataatcagaig (A) agatccaggatttttga	1623
OATP1	45	5' untranslated region (-189) (-188)	atttctaataatcagaig agcttccaggatttttga	1624
OATP1	46	Intron 4 725 726	tgatcttaataagaaggaa AA/Δ caggcaagtcagctaat	1625
OATP1	47	Intron 4 1082 1083	atteeatcaggaaacaaaa CA/Δ attcaaaaatttgaaaaat	1626
OATP1	48	Intron 4 2301	aalgtaatctttttttt I/Δ aagcagagtgatcaagaa	1627
OATP1	49	Intron 9 241 46	attgaatgcatatgggtg TG/GC/Δ caigatttcttggat	1628
OATP2	1	5' flanking region -2574	gaataagcaacccciatg A/G tcacitcgcagaaagaa	1629
OATP2	2	5' flanking region -1723	tccttcagacttcaaggcc A/G tgatatttcacagactgt	1630
OATP2	3	5' flanking region -1180	tccttatttaacagataa Y/G ctitgtctcgcagccaga	1631
OATP2	4	5' flanking region -811	taigcatatgtgataca C/A gtaaaagtgtatatagt	1632
OATP2	5	Intron 1 7188	aatcattgaanatttaaga A/G aaaaatgttcagaaaaa	1633
OATP2	6	Intron 1 7331	gtaaaatgaggaacaaagtc Y/C ccaccttttttctgaata	1634
OATP2	7	Intron 1 7391	agaagaatggaatagat Y/G ttcttgagaaaglaaggaa	1635
OATP2	8	Intron 1 7886	ttgttaagaagaataat C/A aagcttaaaactaaaggaa	1636
OATP2	9	Intron 1 7958	ttcttataataattttt V/A A/T aaaaagatttcttaatat	1637
OATP2	10	Intron 1 7959	tccttataataattttt V/A A/T aaaaagatttcttaatat	1638
OATP2	11	Intron 1 8036	ggaanaatggagtaaat A/T atcaagagcagcttattac	1639
OATP2	12	Intron 1 9164	acattataatcataaaa C/T agtcagttgaagtaaaagt	1640
OATP2	13	Intron 2 193	taallaagattttcttggc C/A aaatttttgaatgcttaag	1641
OATP2	14	Intron 2 1020	ttgaatcaattttagccaa C/A tggcagtcataaggaagaag	1642
OATP2	15	Intron 2 1465	aaggaatcaatcataag C/T ttatttggcctaagtgaca	1643
OATP2	16	Intron 2 14931	gttaataaagaaacaaa A/T taccagaattttaaanaat	1644
OATP2	17	Intron 2 15417	ttcctaaataagtaagccta A/T tattctatatttactacta	1645
OATP2	18	Intron 2 20823	ttatagaagatacaaac A/C aatttcctactaggaataa	1646
OATP2	19	Intron 2 20852	ctaggaaataaagcttca C/C taaggagtgagcattagct	1647
OATP2	20	Intron 2 21360	ttcaaaagctgatttctca Y/C tagtgccttttttgaalaa	1648
OATP2	21	Intron 2 21467	tataacacatactcttc C/A gaagatggtgataagccaa	1649
OATP2	22	Intron 2 21621	tatcaactcttaagaa A/G ctacatatttcactaagaa	1650
OATP2	23	Intron 2 22760	ttccctccctgttgggt C/G tctctttaaacttctcttg	1651
OATP2	24	Intron 2 23193	ccctatcgcataacata C/T aaacttaagcaatata a/g a	1652
OATP2	25	Intron 2 23218	a C/T aaacttaagcaatata A/G aactcaacatatttact	1653
OATP2	26	Intron 2 23330	gaccttctcttctctct C/A tactctctcaactacatag	1654
OATP2	27	Intron 2 23673	ctggagacgtagctcaaac Y/C gaggatgaaaaagacattt	1655
OATP2	28	Intron 3 89	ggtaacactgggttaaat Y/G tctctcagaggaatttgg	1656
OATP2	29	Intron 3 224	ttcctaaatattcataagc A/G caaagaatgataatgaa	1657
OATP2	30	Intron 4 971	tccttataagcagcttac C/A ttittgaagaatgccacta	1658
OATP2	31	Intron 4 568	ttcatgtcaaatgttggc A/G acgtatttctaggcaacag	1659
OATP2	32	Intron 4 590	aggaacagatagaagaag A/G aagaatagaagaacacaa	1660
OATP2	33	Intron 4 753	aaaatagacattttccaag T/A taccagtttccggataga	1661
OATP2	34	Intron 4 781	ttccggtaaaaatcccaa C/G tataatttacttgagaaag	1662
OATP2	35	Intron 4 1196	aaggaacacattatagata C/T catctcttaaatatccat	1663
OATP2	36	Intron 4 1229	tatgcataatagtgacac Y/C ttitgcacctggatttctac	1664

遺伝子名	No	存在位置	配列	配列番号
OATP2	37	Intron 4 1623	catctagtgtaaatgataa c/c attttattttctacatt	1665
OATP2	38	coding region 388 (Asn130Asp)	attctaaagaactaatatc A/C attctacgaataatcaaca	1666
OATP2	39	coding region 452 (Asn151Ser)	taatacaatttttaactca A/G tagagatcaccatgaatag	1667
OATP2	40	Intron 5 165	ttatatacactgttccccc A/T ttacacacacagtttaaac	1668
OATP2	41	Intron 5 189	acaacacaggtttaactac G/A c g/a ttctactttctatgcaaa	1669
OATP2	42	Intron 5 191	aacacaggtttaactac g/a c G/A ttctactttctatgcaaat	1670
OATP2	43	Intron 5 507	ataaactgtttctatg C/T aaaaagcaact a/g ttatatac	1671
OATP2	44	Intron 5 520	ttcatg c/t aaaaagcaact A/G ttatatacatttaagacattt	1672
OATP2	45	Intron 5 856	agctatgataaacctaaag A/G ataaacacacacacacacacac	1673
OATP2	46	Intron 5 1157	acagataattttactattt Y/C gtcgttttctgtatataag	1674
OATP2	47	Intron 5 1226	cccttaattgtaataatctc A/C c a/c tgcacacagttgagccag	1675
OATP2	48	Intron 5 1228	ttcattgtaataatctc a/c c A/C tgcacacagttgagccaggt	1676
OATP2	49	Intron 5 1304	actgtttctgaggttaagaa G/T aagttctcaaaatctgaig	1677
OATP2	50	Intron 5 1348	ttataaagagagttccctt G/A caaaagctcttgcctgccc	1678
OATP2	51	Intron 5 1407	ttgctcttcttctatctc G/A ccatgattgtgagccccc	1679
OATP2	52	coding region 521 (Val174Ile)	gtcatatgtgataatag Y/C attcaggttaataatgcttc	1680
OATP2	53	coding region 571 (Leu191Leu)	ggagactctccatagtaacc A/C tggagctttcttcatattg	1681
OATP2	54	coding region 597 (Phe199Phe)	ctttctcatatgaattt C/T gctaaagagacattcttc	1682
OATP2	55	Intron 7 33	agacaagttacatgataa C/T gcttttaagcacatgac	1683
OATP2	56	Intron 7 267	caaaaataccaaatgaana A/G gtcctctcccaactgact	1684
OATP2	57	Intron 7 1260	gtatctcatatttctctc A/G ttacacttggtaaaacttt	1685
OATP2	58	Intron 7 2273	ttctacactctatcagc C/T gattatgaccccttgaact	1686
OATP2	59	Intron 8 207	gtgagagaaatttgccttgc Y/C actttttagcagagaaac	1687
OATP2	60	Intron 8 546	tccggaagagtttccctc A/C gtaattagaataattt a/c t	1688
OATP2	61	Intron 8 565	a t/c gtaattagaataattt A/C ttgtgtaattatctatc	1689
OATP2	62	Intron 8 668	taagtaattgaattagat G/T catcawcatttgcagagcc	1690
OATP2	63	Intron 8 739	tggagactattgagatca A/G taacacacagagatgacttg	1691
OATP2	64	Intron 9 112	attttgataatcagataa G/G tataatttctgtattctt	1692
OATP2	65	Intron 9 266	ttagaggtatgtatctgala A/G ttgagatcttataattttagt	1693
OATP2	66	Intron 9 305	tgttagagatcggagacac G/G ctttgglaattataatcatt	1694
OATP2	67	Intron 11 10224	tacactgttccataaaaa Y/C tctctatattatctttagt	1695
OATP2	68	Intron 11 10359	attatagattcaagtag G/C ttcccttaaacctttagccia	1696
OATP2	69	Intron 11 10916	cttatagaaaataatcca C/G aaaaatttttaccittttat	1697
OATP2	70	Intron 11 10997	aatatattgtttgaacag Y/C ggaacttcaactaaatataa	1698
OATP2	71	Intron 11 11018	ggaacttcaactaaatataa G/A caatgtatttgcagcacgt	1699
OATP2	72	Intron 12 442	aaacttcaaaaacttttaac C/T ga c/t t c/a acagcagactttaa	1700
OATP2	73	Intron 12 445	atttccaaacttttaac c/t ga C/T t c/a acagcagactttaa	1701
OATP2	74	Intron 12 447	tccaaacttttaac c/t ga c/t t c/a acagcagactttaa	1702
OATP2	75	Intron 12 907	aatgaaaagaagctggcaga Y/C tgaacatactactgaatagag	1703
OATP2	76	Intron 13 65	tatatatatatatata C/T acacacatacatatata	1704
OATP2	77	Intron 13 870	aatcttgatctctatttc G/A atgtatccaatctgagcac	1705
OATP2	78	Intron 13 1935	taaaaaaaaagaagctgccc Y/C ttacagcaattgagccag	1706
OATP2	79	Intron 13 2261	aagcaatctccaattttt C/C aacttttatttaacaaat	1707
OATP2	80	Intron 14 248	tcaagataataaccactt G/A tcaaaaatcagagataatag	1708
OATP2	81	Intron 14 2463	atttcttactaataatgaaa C/G cttcttcaagacataatttt	1709

遺伝子名	No.	存在位置	配列	配列番号
OATP2	82	(intron 14 2857)	tcaatgattatcaggac A/ cctggcaagatgctcicag	1710
OATP2	83	(intron 14 11458)	atctccaggctctcgtcgt C/ tcccaagtcacigacc	1711
OATP2	84	(3' untranslated region 2243)	ataataacaacactagg 1/C agaaaaatagagatcica	1712
OATP2	85	(3' untranslated region 2404)	tcttaataaacaataagat A/G tcatcaggtagaggttaa	1713
OATP2	86	(3' untranslated region 2515)	cagagttgaactataac 1/C aagcctgaagctacttg	1714
OATP2	87	(3' untranslated region 2539)	gcctgaagctactacttgat A/G taltcaataataatcgt	1715
OATP2	88	(intron 1 457 458)	taattggcaacataaaaa A/ cagggtcicaagtcacat	1716
OATP2	88	(intron 1 457 458)	taattggcaacataaaaa cagggtcicaagtcacat	1717
OATP2	89	(intron 1 753 7538)	gacacattacacacaga G/ aaggaaatgacatcagga	1718
OATP2	89	(intron 1 753 7538)	gacacattacacacaga aaggaaatgacatcagga	1719
OATP2	90	(intron 1 10032 10035)	tgatgattatattatctt A/T/Δ gttaaatctcicacaca	1720
OATP2	91	(intron 1 10068 10061)	ttaaatctctccacaaa T/A/Δ tttttatataatgtat	1721
OATP2	92	(intron 2 413 423)	acttattaaaattcttt A/ 11-13 caaaaacaggaattaaaa	1722
OATP2	93	(intron 3 1595 1603)	ttgccaagtaattcaagtc 118-10 gtatttaaacacatttca	1723
OATP2	94	(intron 4 10 23)	ttcaggaagtaagtgat A/ 12-14 cctctgaccatcagta	1724
OATP2	95	(intron 5 1567 1572)	atgaataaaattacttgta C/T/Δ/Δ aatataaaaaaataagtag	1725
OATP2	96	(intron 5 1577 1585)	attactgtacttgataat A/ 9-10 taagtagaataatgaagat	1726
OATP2	97	(intron 8 1939 1941)	ttctcaactctctcactc C/T/Δ atttcaacagatgaacag	1727
OATP2	98	(intron 10 3077 3078)	aaattcttactactttt C/T/Δ ttccctctctcgtcttc	1728
OATP2	98	(intron 10 3077 3078)	aaattcttactactttt ttccctctctcgtcttc	1729
OATP2	99	(intron 11 11011)	aacaag t/c gaactctacaa A/Δ tataat g/a caatgatttcca	1730
OATP2	100	(intron 12 1160 1169)	agcatagatgtagatg A/ 9-11 gcatttttacatttgtaa	1731
OATP2	101	(intron 12 1310 1312)	tccatttaataataat G/Δ ctactcaaaaggagaagct	1732
OATP2	102	(intron 13 8 34)	tacagacactaggttag A/ 24-27 tatatatatatata	1733
OATP2	103	(intron 13 35 64)	aaaaaaaaaataaaaa A/ 10-21 c/ acacacacacataat	1734
OATP2	104	(intron 13 1379 1387)	aaattattaccacatac A/ 8-10 caaagtaagttatgaacac	1735
OATP2	105	(intron 13 1916 1928)	aatctcttaataaagat A/ 11-13 gctctc 1/C ttacagcaatg	1736
OATP2	106	(intron 14 588 596)	caatttacttactcttt A/ 8-10 ctaatttcaattcatat	1737
OATP8	1	(5' flanking region -1413)	aataggagcttaataact G/C aaacttacttctctat	1738
OATP8	2	(intron 1 38962)	atgaattagttaaaaa G/A caacttacttactcttc	1739
OATP8	3	(intron 2 253)	acagacttccacaacagaa 1/C taacttcccaaatgtctca	1740
OATP8	4	(intron 2 329)	agcatagttgcaattaa G/G ttittaggaacatttctc	1741
OATP8	5	(intron 2 2568)	ccattctgactctcttc G/A taacttatttccatcact	1742
OATP8	6	(intron 2 2679)	ccttattctctcttcca 1/C gtittatctaaataattia	1743
OATP8	7	(intron 2 2753)	cagaaacttccacaagcc G/A ctaataatttgaactccct	1744
OATP8	8	(intron 2 3132)	tgttttaattagagagt 1/C accctcacagtttaattaca	1745
OATP8	9	(intron 2 3193)	aatgcttggcatalltcc A/G ttcalltgaggca 1/C tcaagt	1746
OATP8	10	(intron 2 3207)	atttgc a/g ttacttgggca 1/C tggcttactatagataaa	1747
OATP8	11	(coding region 334 (Ser112A1))	gaactggaagtatttggca 1/C cttaccacatttcttctc	1748
OATP8	12	(intron 3 76)	agaattttatttact G/A taagtgagcagttactttt	1749
OATP8	13	(intron 3 2443)	tcaatttctgctcttca C/ agttataggtattcttaaa	1750
OATP8	14	(intron 4 67)	taatcagctctaaagtt G/G taatattctttaaacaatt	1751
OATP8	15	(intron 4 91)	taattttaaacaattgat 1/A taagaacaatagagaac	1752
OATP8	16	(intron 4 197)	ggttgaactgacactctc G/A ctatataagcatttctcc	1753
OATP8	17	(intron 4 813)	tttaacagaataaaaaaa 1/A atttttgaacacaaaagaa	1754

遺伝子名	No	存在位置	配列	配列番号
OATP8	18	(intron 4 9/4)	ataagaccataaataaac C/G tgaatttttaaaatgaat	1755
OATP8	19	(intron 4 10/3)	taataatgaatgataataa C/T gaataatgataatattgt	1756
OATP8	20	(intron 5 15/1)	catlaaataacagataaaa A/G agaaatttgcctctattia	1757
OATP8	21	(intron 6 7/50)	atcaacttgcctttagatt T/G cctcttctgcctctctcc	1758
OATP8	22	(intron 6 7/80)	gcccctctccatctgacc C/T tctctttcttccagcaaca	1759
OATP8	23	(intron 6 12/48)	ctaagccctgaattctaca C/T ticcctttattttaaatttg	1760
OATP8	24	(intron 6 15/00)	tctgtctgtttagataat A/G aaacacacacaggtttgtg	1761
OATP8	25	(intron 6 20/8)	ataacataatgaataaaa A/G tataagagcagaaaattag	1762
OATP8	26	(intron 6 20/87)	actctctcccaataacac T/G aaacacacacgtctcccccag	1763
OATP8	27	(intron 6 12/305)	tcaatctagagagactgaa T/G cattatcattatttccccaga	1764
OATP8	28	(intron 7 3/63)	taacaaatataccaccat C/G atactatctctgtaataag	1765
OATP8	29	(intron 7 4/11)	ccctttatttttggaaacct G/A gtagatgataaaga C/A gla	1766
OATP8	30	(intron 7 4/28)	cct g/a gtagatgataaaga C/A gtagatgatacagtaata	1767
OATP8	31	(intron 7 6/34)	aaaataataataacataat A/G taatttaccataatattca	1768
OATP8	32	(intron 7 7/91)	tgattttttagagataaga T/G gtagatgataaagaaccttt	1769
OATP8	33	(intron 7 20/00)	agtagaataattctctca G/A gtagatgataaagtcacttgaa	1770
OATP8	34	(intron 7 20/43)	gttatgatacattttta A/G tggatcaacatgttagtag	1771
OATP8	35	(intron 7 21/1)	atttattttagcaaggct G/A c g/a actct C/T cttagaagcct	1772
OATP8	36	(intron 7 21/3)	ttattttagcaaggct g/a c g/a actct C/T cttagaagcctcag	1773
OATP8	37	(intron 7 21/9)	tgaaagaagct g/a c g/a actct C/T cttagaagcctcacaatca	1774
OATP8	38	(intron 7 22/19)	atttgaattttagcttla T/G ataactataatttacaact	1775
OATP8	39	(intron 7 22/61)	cagataataataattttt A/T ttattgaataattttttt	1776
OATP8	40	(intron 8 1/50)	acaaaatttccatctgt A/G ata t/a calctgttctgcat	1777
OATP8	41	(intron 8 1/54)	aatttccatctgt a/g ata t/a calctgttctgcat	1778
OATP8	42	(intron 8 1/303)	tttttttagagataagct C/T gctctgttccagcgttggg	1779
OATP8	43	(intron 8 1/372)	agcttccctctccagctt C/G ccaccttctcttaagaaa	1780
OATP8	44	(coding region 1272 (Leu424Leu))	tctctgttctcaacttct A/G tatcttcccttaacttctcga	1781
OATP8	45	(intron 10 6/3)	tcaagattttagttaataa A/T tacttataaacttctctat	1782
OATP8	46	(intron 10 9/11)	cttgcacaatactctaccac C/T gattatttaacagcagtaga	1783
OATP8	47	(intron 10 9/2)	tcttagtttctttagaata G/A gctacacttttagtaactt	1784
OATP8	48	(intron 10 11/01)	tcttggctctgtgttctcc A/T g t/c agtagaagccttgaagaag	1785
OATP8	49	(intron 10 11/03)	ccgtgtctgtgtgttct a/t g t/c agtagaagccttgaagaag	1786
OATP8	50	(intron 10 20/27)	ccattttcagtagtctca A/G g/a tttgtcccttccaact	1787
OATP8	51	(intron 10 20/28)	ccattttcagtagtctca/g G/A tttgtcccttccaact	1788
OATP8	52	(intron 10 23/2)	tgatttggcaatcttatt G/T ttaatatttcaaaaactatt	1789
OATP8	53	(intron 11 10/38)	caacagagagcaatgaata T/G gaaatctttaaataaaca	1790
OATP8	54	(intron 12 5/1)	ataaataatagtttaata C/T taagagctgaatgcaattaa	1791
OATP8	55	(intron 12 18/02)	taaaataatagtttaata T/G tcaatgataaactcactca	1792
OATP8	56	(intron 12 26/12)	atagcataataactctt C/A ttcctctgtatataagagag	1793
OATP8	57	(coding region 1833 (Glu616Glu))	acacacgttggagcaag G/A gtttggagataataatc	1794
OATP8	58	(5' flanking region -1590 (-1587))	tacataacataactat C/A/T/Δ gttatgtctgtcttata	1795
OATP8	59	(5' untranslated region -28 (-1))	agcattcagcaataataa A/T/Δ/CTG/Δ tggtttaataatggaccaac	1796
OATP8	60	(5' untranslated region -7 (-4))	tatcatttggatctatag T/T/Δ/Δ atatggaccaatcaaca	1797
OATP8	61	(intron 4 213 214)	ttc g/a cttaataagagcttt (T) gtccaaccaacagagag	1798
OATP8	61	(intron 4 213 214)	ttc g/a cttaataagagcttt gtccaaccaacagagag	1799

遺伝子名	No.	存在位置	配列	配列番号
OATP8	62	intron 4 505	taatacttcttcttaaaa g/a atcaaatgttataagcatt	1800
OATP8	63	intron 4 816	aaagaagtgagagaaaaa A/Δ taattcaagttttcttct	1801
OATP8	64	intron 4 804 812	acatcatgttaacagaat (A)9-11 t/a atttgttaacgacaaaaa	1802
OATP8	65	intron 4 855	agaatttaacaaatag G/Δ aaactattattcaacacact	1803
OATP8	66	intron 7 619 628	ttttatataaataat (A)4-5 catat a/g taatttacttaag	1804
OATP8	67	intron 7 1773 1779	attttatataataacag (U)7-8 aaggttagta t/c gtaataag	1805
OATP8	68	intron 8 1270 1290	tagtgcacaccttcttc (U)19-23 agataggatct c/t gctctat	1806
OATP8	69	intron 10 665	actcaagaagcttttttt /Δ ccatatgacacataacctgt	1807
OATP8	70	intron 11 247 250	aaaactttaagcacacac tga/Δ taacagttcttgaattga	1808
OATP8	71	intron 12 1622 1630	aaataaattgttgacalcia (U)8-10 atttttaagggcgcgt	1809
OATP8	72	3' untranslated region 2464 2465	ccatagcttttaaaaaa A/Δ taaaacatttgaatatt	1810
TAP1	1	5' flanking - 673	agctaaagctaaagacacc G/C ctttttcaccagctcgcg	1811
TAP1	2	5' flanking - 646	ccatcagcttcgctctcig t/g tcccttcacggacacttag	1812
TAP1	3	5' flanking - 563	ttgcaagcttcgctctctac A/G ggcacccctcctgcctccc	1813
TAP1	4	5' flanking - 236	gctttgcgcagcgcctaac G/T tctgttagggcagatctgccc	1814
TAP1	5	intron 3 + 408	aggaacacagagccagac G/T cttaaagctgaacacgcaca	1815
TAP1	6	exon 4 + 153	ccctcaccatgctcctcig A/G tcaacctcctcctgctttc	1816
TAP1	7	intron 4 + 289	gtaattcttaacatcaag G/T gcatagcgtgctctcttc	1817
TAP1	8	intron 4 + 291	attttttagactcaagg C/G catagcgtgctctcttctc	1818
TAP1	9	intron 5 + 1139	ttcctcaagttatgacig C/T gttcttctgtgctctctca	1819
TAP1	10	intron 7 + 375	gtcttcctctgctcttcc C/T cctcttctatctctctcc	1820
TAP1	11	3' flanking + 71	agcacacttttcaagtcag G/A gctcctcttttctatcc	1821
TAP1	12	3' flanking + 129	aaagcaccacttttccct t/c aagctttttaaactctatga	1822
TAP1	13	3' flanking + 459	catlcaggagagccagagc G/A gtagcgttcgacagttctg	1823
TAP2	1	intron 3 + 8	tccttttgcaggttagtg G/A tgggcagctgggtccatttg	1824
TAP2	2	intron 4 + 104	cttcacagtttccagac C/T tgggagcttttctctctg	1825
TAP2	3	intron 10 + 219	ggcagcgttgcctctcc A/G tgggcagccctgcaggtcc	1826
TAP2	4	intron 11 + (317-319)	atggctccagcttgaaatcc t/c gteggatgcacagttctg	1827
TAP2	5	exon 12 + 19	agctgcagagcttgaaatcc t/c gteggatgcacagttctg	1828
TAP2	6	exon 12 + (356-357)	aggggggggggggggggg G/T tcttgcggttgcagggaaa	1829
UC1N1	1	intron 1+6602	aggggggggggggggggg G/T gaggatagggcctcttccc	1830
UC1N1	2	intron 1+6790	gacaaagggggaacacac C/T atgtaggcagtttctga	1831
UC1N1	3	intron 1+14019	caactctccactggcctcc G/A ccatgctactgttaaccaca	1832
UC1N1	4	intron 1+14136	ccggtttcciaagaaaagcc t/c ttctaaaggaccccttta	1833
UC1N1	5	intron 1+14266	agctttccaaagagacact G/T cggcaca taactccccaaa	1834
UC1N1	6	intron 1+14412	ctgggcaaacacccac C/T gtagcagtgctctctctg	1835
UC1N1	7	intron 1+15776	acalaggacactctcttc G/A gactcagttatcagaacaa	1836
UC1N1	8	intron 1+15817	ctgctcttcggaataagc A/G gactcagttatcagaacaa	1837
UC1N1	9	intron 1+15889	agagccagtttggagccccc G/A tctggcagacagcagccccc	1838
UC1N1	10	intron 1+16063	acctctctctgacagat A/G aggttgatataaataatg	1839
UC1N1	11	intron 2+1105	atattccacagggctctg C/A gtagcgtctctctctctt	1840
UC1N1	12	intron 3+1022	cttcctcaggttgcagaa t/c ggaataatccaactact	1841
UC1N1	13	intron 3+1217	ttccctctctcagagggaa G/A gaggcggcagagatttctt	1842
UC1N1	14	intron 3+1596	agccagagaacgtctctcc G/A tgggaatgggaacaaggtgg	1843
UC1N1	15	intron 3+1720	ggagcctccacacccctccct G/A tatgagcgggttaaggcaagg	1844

遺伝子名	No.	存在位置	配列	配列番号
UC1N1	16	Intron3+2104	la gaaacgttctgtgttgg g/a ttcacagctcgaagttta	1845
UC1N1	17	Intron3+8323	celltcccttttctaagtg g/c tgaatgttgaacttaact	1846
UC1N1	18	Intron4+925	tttttgaactcacaattta g/a actagacctcatgttgccc	1847
UC1N1	19	Intron4+1055	ccctgtctgaagagatasc g/a cagtcagtgaggctcacic	1848
UC1N1	20	Intron5+ (1197-1202)	caacacacacacacaca ACANCA/Δ ttgaagtgcttaacattc	1849
UC1N1	21	Intron5+ (2071-2083)	gttcgtcatttctctatgc (U)11-13 caaaataaataactaaagca	1850
UC1N1	22	Intron5+2781	taataattctagaataaag g/a acatcatatttggagagga	1851
UC1N1	23	Intron6+ (882-917)	tctctctatgatggcagc AC115-18 gatactcagaacttgta	1852
UC1N1	24	Intron6+924	acacacacacacacacat A/C gtcagactgttagatttag	1853
UC1N1	25	Intron7+511	attatagatgaatagaag g/c acatatttcllaataaag	1854
UC1N1	26	exon8+124	ggtcagaaatggcggtag g/a ggtcacatccacggctcca	1855
UC1N1	27	Intron8+3514	acacacacacacacacat g/a tatgaattctcagaagaagt	1856
UC1N1	28	Intron8+3902	aaacacagatagagatctgtt g/c tctctcgtgttgaagtaagc	1857
UC1N1	29	Intron8+ (4064-4083)	gtgaacataactatgttg (U)18-26 agctctatagacctataga	1858
UC1N1	30	3' flanking+115	aaacaaa gattatatacag g/a attctatccagaacacct	1859
UC1N2	1	5' flanking - 225	cgagcttagagagagaggtt c/g ggaactggacctcaagacct	1860
UC1N2	2	5' flanking - 124	gc tggcagaggggggctc g/t coaggtcccccagggcagggcc	1861
UC1N2	3	5' flanking - 13	gggcgcgcctctctctccag c/g gggcgcgcctttccgaccca	1862
UC1N2	4	Intron 1 + 232	gggtgtcgtcttgcctccc g/a tcttgaaggccacttgaag	1863
UC1N2	5	Intron 1 + 314	atggcctgttcttccagga c/g ttactctatgttgggttggg	1864
UC1N2	6	Intron 1 + 5055	catgggtaccatagacacat g/a tctgacgtgtgatacagctca	1865
UC1N2	7	Intron 1 + 6437	gaacttggcttccacaca g/c aggcggcagccttgcata	1866
UC1N2	8	Intron 2 + (173-174)	tagtaagaagacacacaaa t/c Δ aicgacccglaatttgc	1867
UC1N2	9	Intron 2 + 608	agcaggttatttgtataatt c/a taagacttttaccacagga	1868
UC1N2	10	Intron 2 + 4370	taatttatatatacaggt g/a cccctataatagaactca	1869
UC1N2	11	Intron 5 + 969	caccagaaagggctctgtg c/g gcaaggtcagcagaggtg	1870
UC1N2	12	exon 10 + (1028-1044)	ttagctctgggttgggtc (U)16-18 aaacagaatcaccttggca	1871
UC1N1	1	Intron 1 + 7715	tagcttcactcacatagg c/t tctgtgtcttttctctctct	1872
UC1N1	2	Intron 2 + 97	ggtagagaaatgacacatt c/a gaattaacgtcagagagctc	1873
UC1N1	3	Intron 2 + 737	gttaggttgtctgaacact c/g tttaaagatgttggagagg	1874
UC1N1	4	Intron 2 + 1768	ctgaagctggagagggtctg g/c gggcactgtccggcttagct	1875
UC1N1	5	Intron 3 + 1244	gcaga tggataagggagaga c/t gggagaaagcagcgtcaggg	1876
UC1N1	6	Intron 4 + 885	agcgtccagtggttaggaag g/a cttcacaggtggcaattcca	1877
UC1N1	7	Intron 4 + 1028	gtatctctgtctctctccc g/g cttcttcttattttatagtc	1878
UC1N1	8	Intron 4 + 1040	cttctccacttctctatt g/g tatagtactatttattatt	1879
UC1N1	9	Intron 4 + 1485	agcctgcccttcccctgctt c/t gtccttggaaacagggatc	1880
UC1N1	10	Intron 4 + 1997	tgaaggatttaccagccccc c/a tgggagagggcagcttgcact	1881
UC1N1	11	exon 5 + 9	tggtgtcagaggtgtgtgtc c/t ggaagctccctcagtgactgt	1882
UC1N1	12	exon 5 + 20	gggtatctcggaggttccct c/g ggtgtgtttatcacaaaa	1883
UC1N1	13	Intron 6 + 379	gaggaagttcatttctctat g/g tctaaacaccttagagacc	1884
UC1N1	14	Intron 6 + 2125	tattggccaaatcttctct c/a acaatgaataatctactga	1885
UC1N1	15	Intron 6 + (2935-2953)	tttctccattctcggagggcc (U)18-20 ctttagcttcttactcagc	1886
UC1N1	16	Intron 7 + (6-7)	tttttctcactctggaggt (U)G(M)G tggtaagtgtctgtcttca	1887
UC1N1	16	Intron 7 + (6-7)	tttttctcactctggaggt tggtaagtgtctgtcttca	1888
UC1N1	17	Intron 7 + (1780-1781)	gttttcttcttctcttttttt tt catggagaaagacagagaa	1889

遺伝子名	No.	存在位置	配列	配列番号
UC11	17	Intron 7 + 1720-1781	gtttcttttccctttttt catggagaagacagagaa	1890
UC11	18	Intron 8 + 3247	ccagccaacattccatt C/T tcttccacatggccaaag	1891
UC11	19	Intron 8 + 10521	cccttaacaaagaccca C/A tggcagatccctatctga	1892
UC11	20	Intron 10 + 393	tcaatcttttagaactt G/C ttcaaaatcttllgaca	1893
UC11	21	3' flanking + 1755	tgaatgaattttcaatg T/C gttataaaatgtctctt	1894
UC11	22	3' flanking + 1799	cttttagaatctcttgg C/Acaaacitctgagaagcc	1895
UC12	1	Intron 2 + 1329	tggcagcaagaggaagag G/A ataaagtggagacacagc	1896
UC12	2	Intron 2 + 1867	ctctgcaagtagtact C/A atattcttccccaaagcc	1897
UC12	3	Intron 9 + (340-343)	cagcagcccttaactctt C/C/T/A gctgattccaccttctg	1898
UC12	4	Intron 9 + 396	atcataatctatctt A/G ttctatgaaatgatcaag	1899
UC12	5	Intron 9 + 386	catctttttatcttgcaga A/C algaaccaagtcttgcatt	1900
UC12	6	Intron 9 + 86	atgaaaaatcttaaaaa A/A gtttaacaaaataaaggg	1901
UC12	7	Intron 10 + 1725	tggaaagagccttgaatc C/A agcagaggtcacacatcgc	1902
UC12	8	Intron 10 + 195	caagataatllagaataa C/T tctatcacaatgatataca	1903
UC12	9	exon 11 + 328	gtttctggaggtttttt T/A ccatctttgtattttttaa	1904
UC12	10	exon 11 + 427	agccaacaaaatagaaaa A/T gtdtgaataacagtaagtt	1905
UC12	11	exon 11 + 455	aaacagtaagttggagag C/A agcatctattttcttaaaaa	1906
UC12	12	3' flanking + 34	aaatgatatcagaattt T/A agatagccttttcaglaaca	1907
NTCP	1	exon 1 + 307	tatgcatcagccctcac C/A gcttttgcctggcaaggt	1908
NTCP	2	Intron 1 + 607	ccagaccacatccagata C/C gccaccccatctcagccac	1909
NTCP	3	Intron 1 + 702	gcagaaatcagacagcctc C/A cttctggaaacacagcac	1910
NTCP	4	Intron 1 + (3950-3966)	cacatcccttaacacattgc T/A 14-17 gagaatagacatgtataga	1911
NTCP	5	Intron 1 + 9597	aaggcatattatcagct C/G tgaatgataattttttt	1912
NTCP	6	Intron 2 + 4808	ccataggaagcaactacc C/T gggccacttctctcagcag	1913
NTCP	7	Intron 2 + 5032	acacttggaaatcagacag C/C cagctttccacacagatca	1914
NTCP	8	Intron 2 + 5046	gcagagcagctttccacc A/T ggaatatacaattatgtg	1915
NTCP	9	Intron 3 + (8-21)	gcctcaatggacagtagta T/T 12-15 aagaaggctcactctgt	1916
NTCP	10	Intron 4 + (484-495)	taataaacccagaataaag A/T 10-13 gattctcaactctagtac	1917
NTCP	11	Intron 4 + (728-754)	tgcatttaacacaaattt A/T 25-27 caggacattcaaccactt	1918
NTCP	12	Intron 4 + 747	taaaaaaaaaataaaaa A/C aaaaaacaggacattcaaa	1919
NTCP	13	Intron 4 + 1339	ccccagtggaacacataat C/A aagcacagtattttctgg	1920
NTCP	14	Intron 4 + 1545	accagcagaagagagata C/C atcaattgggggttggaggg	1921
NTCP	15	3' flanking + 559	caggaataatagtttctgg C/A taccagtttggcaaatgtc	1922
PEPT1	1	exon 1 + 25	ctgcaagagcagctctccc C/T ggcaggtcgcagggccctg	1923
PEPT1	2	Intron 1 + 88	cagggcccgagagggcccaa C/A ggtaccgagcggcggagagc	1924
PEPT1	3	Intron 1 + 106	aggggtaccgagcggcggcga A/T gceggggccaccgaaagccc	1925
PEPT1	4	Intron 1 + 248	cagaglltgcattctggccc C/A ccgcccctggggcacatgta	1926
PEPT1	5	Intron 1 + 326	tggagcggagcggagccccc C/A gggtagcggcagggcccgca	1927
PEPT1	6	Intron 1 + 1238	tttagcatttccagcagatc C/T aatccgagggctgttagag	1928
PEPT1	7	Intron 1 + 3001	tttatactctggagagag C/T gtcagataagaaaagacgcc	1929
PEPT1	8	Intron 1 + 5673	ttggagagtgccatcagccac C/C gggcagagggacagagggcctt	1930
PEPT1	9	Intron 1 + 5679	agtgccagcagcggcgcca C/G agggcagagggcttctcacag	1931
PEPT1	10	Intron 1 + 5917	aaattcacaataatgacttc C/T ataagaaggctcttlaaag	1932
PEPT1	11	Intron 1 + 5966	ctaggcattttagaccttcta C/T aatctgcccctagtacaag	1933
PEPT1	12	Intron 1 + 9255	tggtcattttagggccttctc A/G gctatgatttttagatagtt	1934

遺伝子名	No.	存在位置	配列	配列番号
PEP1	13	Intron 1 + 10278	catgaccatagagcggga a/g aacacgcccgtatagacag	1935
PEP1	14	Intron 1 + 20251	aaagaacccgtattat c/t agtattgcaatgtgtggg	1936
PEP1	15	Intron 1 + 20509	aaacacccctcagatit c/a gcttctatagatagcaacc	1937
PEP1	16	Intron 1 + 20532	ttctaaatagatcaacc g/c taccacagttacattagat	1938
PEP1	17	Intron 3 + 55	agacggaagtgccatac c/a atctcctacttggttccc	1939
PEP1	18	Intron 5 + 1720	atccctctttctggaaa c/a aataagctacaaagaacc	1940
PEP1	19	Intron 5 + 1790	gctatgtttatgtttcc g/a gattgaattatagatgg	1941
PEP1	20	Intron 5 + 1860	agttcatttgaatcac g/a ctcacatctctgacatgac	1942
PEP1	21	Intron 5 + 1943	agggcacatgaggaacg g/a gaaagagagacatctac	1943
PEP1	22	Intron 8 + 1478	tgcttcagatcttagat a/g calgaatagaccgttttc	1944
PEP1	23	Intron 8 + 1898	ttaaatattagtataaag a/g aacataacatcaatctt	1945
PEP1	24	Intron 10 + 388	ttaalagttaacattt c/t gatttctlaaanaaacatc	1946
PEP1	25	Intron 11 + 985	atccataagttacagta c/t tggcctglatagaagatca	1947
PEP1	26	Intron 11 + 1022-1045	ctcaacagggtagattt c/t 20-24 gattcaagaatctcacatc	1948
PEP1	27	Intron 11 + 1320	tgtagccatctgacatg c/t aattctgactttctata	1949
PEP1	28	exon 16 + 107	tgtagagaaagtagacatc g/c ccaatgctcaglaagla	1950
PEP1	29	exon 18 + 6048	ttgtttgtttgtttttt t/a gttgtgtgtttgtttt	1951
PEP1	30	Intron 18 + 6141-6142	tcacttcacccctcgcccc c/t aggttcaagaatattatc	1952
PEP1	30	Intron 18 + 6141-6142	tcacttcacccctcgcccc ggttcaagaatattatc	1953
PEP1	31	Intron 18 + 6241-6242	tattttatagagagaggg c/t ttaccatattggccagcc	1954
PEP1	31	Intron 18 + 6241-6242	tattttatagagagaggg ttaccatattggccagcc	1955
PEP1	32	Intron 18 + 12102	gtgggaatctagtaagc c/t cgttggatctgctgcagat	1956
PEP1	33	Intron 18 + 12203	gacctgaatttaattag c/a catttctctgacacata	1957
PEP1	34	Intron 18 + 12307	gaaggtaaatattctt a/g cactctgagatgacata	1958
PEP1	35	Intron 20 + 79	tcacaacacttagacata a/g tatgatttaactagatgat	1959
PEP1	36	exon 23 + 1348-1370	tcattttctttttttt c/t 1018-23 gaaacagatttttctt	1960
PEP1	37	exon 23 + 790	cccatltagatcttctcc a/g tcacaagaattgtattt	1961
PEP1	38	3' flanking + 2	aaataattctgtcttaa c/a cctaagttatcatatct	1962
EPHX1	1	Intron 1 + 110	tcaaaaatgtcttctag c/t ttctatgcaaaaatattg	1963
EPHX1	2	Intron 1 + 143	aaatatgtgagacttc c/a ctgctgagccagtcacca	1964
EPHX1	3	Intron 1 + 1097	aatccagaagagataga t/g tgaagattcaagggtagaca	1965
EPHX1	4	Intron 1 + 1717	ttccaagacagagaggg g/c gctgctggggcgtgtttgc	1966
EPHX1	5	Intron 1 + 1772	aactgatcttctctcc c/t tctggcttaacttccatg	1967
EPHX1	6	Intron 1 + 2054	gaatgtgacagggacact a/g tggacacagaagaattat	1968
EPHX1	7	Intron 2 + 1414	atttccaaatctgttggg c/t gtaactgaacacttggaaa	1969
EPHX1	8	exon 3 + 174	tacccctacttcaagacta g/a attgaaggtagtttgcata	1970
EPHX1	9	Intron 3 + 6583	ctgtcaatactatagagg g/c ggcgggggacataagggtag	1971
EPHX1	10	Intron 4 + 34	agaaatttcaataacgtccc g/a tccctccagaaggtagggcc	1972
EPHX1	11	Intron 4 + 63	aagatgtgacccatgttcc c/t accaggtctcttctggcgc	1973
EPHX1	12	Intron 5 + 154	gcagtgcttggagacattt g/a ctggatcttcttctgtgta	1974
EPHX1	13	Intron 5 + 276	tcttggaccagctctggaa t/c agcccttgacagacatctccc	1975
EPHX1	14	exon 6 + 130	gatatgagactctctgacc c/t gtaagagaaggatttcta	1976
EPHX1	15	Intron 8 + 206	ggtgttggcttccggggc g/a cctcatatcccttcccagt	1977
EPHX1	16	Intron 8 + 353	tggccctcccaaaaagaa a/g gggccctcatctgagggagag	1978
EPHX1	17	3' flanking + 708	aggttgcagactcatgactc a/g ggccttgaagaagttgagagag	1979

遺伝子名	No.	存在位置	配列	配列番号
EPHX2	1	5' flanking - 523-522	aaagtcactgagatagcccc (U) ccccccgcgcgcacacacag	1980
EPHX2	1	5' flanking - 523-522	aaagtcactgagatagcccc ccccccgcgcacacacag	1981
EPHX2	2	5' flanking - 522	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	1982
EPHX2	3	5' flanking - 521	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	1983
EPHX2	4	5' flanking - 516	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	1984
EPHX2	5	5' flanking - 515	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	1985
EPHX2	6	intron 1 - 74	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	1986
EPHX2	7	intron 3 + 72	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	1987
EPHX2	8	intron 4 + 473	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	1988
EPHX2	9	intron 5 + 276	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	1989
EPHX2	10	intron 8 + 8	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	1990
EPHX2	11	intron 9 + 1573	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	1991
EPHX2	12	intron 10 + 207	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	1992
EPHX2	13	intron 12 + 911	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	1993
EPHX2	14	intron 12 + 2425	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	1994
EPHX2	15	intron 12 + 2460	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	1995
EPHX2	16	intron 12 - 281	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	1996
EPHX2	17	intron 12 - 268	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	1997
EPHX2	18	exon 13 + 50	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	1998
EPHX2	19	intron 13 + 1739	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	1999
EPHX2	20	exon 14 + 33	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	2000
EPHX2	21	intron 14 + 314	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	2001
EPHX2	22	intron 14 + 878	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	2002
EPHX2	23	intron 14 + 948	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	2003
EPHX2	24	intron 15 + 259	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	2004
EPHX2	25	intron 16 + 459	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	2005
EPHX2	26	intron 16 + 545	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	2006
EPHX2	27	intron 16 + 985	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	2007
EPHX2	28	3' flanking + 12	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	2008
EPHX2	29	3' flanking + 374	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	2009
EPHX2	30	3' flanking + 544	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	2010
COMT	1	5' flanking - 1287	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	2011
COMT	2	5' flanking - 1217	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	2012
COMT	3	5' flanking - 503	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	2013
COMT	4	5' flanking - 425	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	2014
COMT	5	5' flanking - 277	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	2015
COMT	6	intron 1 + 12058	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	2016
COMT	7	intron 1 + 12070	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	2017
COMT	8	intron 1 + 18831	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	2018
COMT	9	intron 2 + 832	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	2019
COMT	10	intron 3 + 90	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	2020
COMT	11	intron 3 + 425	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	2021
COMT	12	intron 3 + 671	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	2022
COMT	13	intron 3 + 676	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	2023
COMT	14	intron 5 + 75	aaagtcactgagatagcccc 1/C ccccccgcgcacacacaggt	2024

遺伝子名	No.	存在位置	配列	配列番号
COMT	15	Intron 5 + 310	accagacacacagggcagaaa C/A ggcacagggccacagggagatg	2025
COMT	16	Intron 5 + 346	aga tgggttggggaagggccc C/A ctctggcccgagcttctct	2026
COMT	17	Intron 5 + 3023	aagcagcccccctctcctca C/A gccctagccattgtctctct	2027
CAMT	1	Intron 1 + 429	ctcgaagaacttgactcag C/A agacagctgtccccgggtg	2028
CAMT	2	Intron 5 + 1411	ggcaccgtgctcctcctccc C/A accagagagccagcggccccc	2029
CAMT	3	3' flanking + 626	cactgaactctctgctctca C/A agagagccgctctctgtct	2030
PNMT	1	5' flanking - 367	aagagtgaaatgcttgcgg C/A ggcctggaagaagagatggg	2031
PNMT	2	Intron 1 + 35	ctgagcagcagggacacaa C/A gctctggggagtgaaagca	2032
PNMT	1	5' flanking - 211	cagagcgatgacagcgtt C/A gcttlaaagatttccctccg	2033
PNMT	2	Intron 1 + 5409	aataaactgataatag C/A acatttcatgttggcctagt	2034
PNMT	3	Intron 2 + 2561	cacttgcttggacagaa A/C agaagccctacagagaaag	2035
PNMT	4	Intron 2 + 2895	caacagaatgtagaaaa A/C ctccagagaaaatttaagtt	2036
PNMT	5	Intron 2 + 3977	accagattggagtglaaa C/A ttatgcatgatagttcatt	2037
PNMT	6	Intron 2 + 5296	ttacatagtgagttggag C/C cccagattttatttctct	2038
PNMT	7	Intron 2 + 13317	caaccctcagatttctag C/A tggatgggtccctataaca	2039
PNMT	8	Intron 2 + 14682	gtagatgacgaatgagttc A/Δ gggagattttaaatacccta	2040
PNMT	9	Intron 2 + 15406	gtctatgattcatgctcc C/A tctaaccagctgtatcccta	2041
PNMT	10	Intron 2 + 28943	atgtaacttaacttcaggt A/G tatcaatctcttgaatgt	2042
PNMT	11	Intron 4 + 49	cagaagaagacttllcaga A/G tatataataatgaatact	2043
PNMT	12	Intron 4 + (1942-1943)	ttggaaaaatttaaggta A/Δ tcttctatggccacttcca	2044
PNMT	13	Intron 4 + 2405	ccctgacacagagataa C/A ctcatgctttatttagtcca	2045
PNMT	14	Intron 5 + (80-81)	ccctgatttgaagaagctt A/Δ alataatttctctat	2046
PNMT	14	Intron 5 + (80-81)	ccctgatttgaagaagctt atataatttctctat	2047
PNMT	15	Intron 5 + 235	cttctttgggaanaatg C/C ctgtctctctataatgaa	2048
PNMT	16	Intron 5 + (702-703)	lacttaccatgattttag A/Δ acacacagactctgtcttc	2049
PNMT	17	Intron 5 + 749	lacttaccatgattttag acacacagactctgtcttc	2050
PNMT	18	Intron 5 + 1101	ttacacagacccactt C/G aacacataatgtcacaat	2051
PNMT	19	Intron 5 + 1137	gtagcagcctatcttgat C/G atattcataatcacaga	2052
PNMT	20	Intron 5 + 1348	acagaaaaatattgtag C/A gaatacaattcatgaga	2053
PNMT	21	Intron 5 + 1673	cagaagaaggagtaaga C/G tcaaatcagtttagcttt	2054
PNMT	22	Intron 5 + 2022	atttatttgggcttcta C/A gctctctctcctaagctta	2055
PNMT	23	Intron 5 + 2285	tgctacttlaacttctaaa C/C atccagagtaaatatggag	2056
PNMT	24	Intron 5 + 4159	taccagttggcccgacacc C/A tcttatagagtttaaat	2057
PNMT	25	Intron 5 + 4501	aatgattccaaaattacta C/G tcatgttttcttcaata	2058
PNMT	26	Intron 5 + 5251	cacacacacacacacaca C/G caaatggaagacagcacaga	2059
PNMT	27	Intron 5 + 5802	gaaaagaaattctgctta C/A atcaltgtaaaaaaaggt	2060
PNMT	28	Intron 5 + 6189	tcaatttccacttctcta C/C agcatactgtcagttacct	2061
PNMT	29	Intron 5 + 6297	gtcttggcttctcttctag A/A taatttagatctgggaactt	2062
PNMT	30	3' flanking + 458	tgctactctcagaact C/A tataagcacagagctcatct	2063
PNMT	31	3' flanking + 993	ctgaaaaagacagagacc C/A ttatcatcactatgctac	2064
PNMT	32	3' flanking + 1793	gtggagacagagatttag C/A ctgtatatttgccttata	2065
PNMT	1	5' flanking - 228	ataatttctcagagctc A/Δ atgctctctctgcttaca	2066
PNMT	2	Intron 1 + 44	cccactaatgtgactatcata C/C aratagagttcagggcagc	2067

遺伝子名	No.	存在位置	配列	配列番号
NNMT	3	Intron 1 + 149	ggataaacaagaatattggt a/g taggaattccacagtttaca	2070
NNMT	4	Intron 2 + 158	agataggccattgtgttc c/a ttgtagtaattgtgtatg	2071
NNMT	5	Intron 2 + 433	gcttgagccatccaaacctta i/c agaacttgcttgagtgatg	2072
NNMT	6	Intron 2 + 10826	atcatctgcttgagtgatg c/t agttctgttgtaactcaag	2073
NNMT	7	Intron 2 + 13630	atttctgaggaagaatcca i/c ggtagaagacagctgctgtag	2074
NNMT	8	3' flanking + 71	ggctcagtggttgtagccca a/g tagttcactaagacggag	2075
PEMT	1	Intron 1 + (297-299)	attgtctgagactcagaggt tgt/a cctgttgatcttgagatt	2076
PEMT	2	Intron 1 + 817	tcatgagccctgaaggcac a/g tcttgccccaagcagcttc	2077
PEMT	3	Intron 1 + 830	aagcagctcttgcccaa g/a cagctcttaactcagcttct	2078
PEMT	4	Intron 1 + 1035	gagttctgaaagagctaa i/c accabttagtttttgaaga	2079
PEMT	5	Intron 1 + 1573	agtggcagggagagctaac c/t ggtgtgtgaggggtggct	2080
PEMT	6	Intron 1 + 1759	gattttcttaagaagaaa a/g gaagaacatcacacatcac	2081
PEMT	7	Intron 1 + 2768	gcatttctgtctcacagcc c/a gggcaccctcagatctag	2082
PEMT	8	Intron 1 + 2785	ggcctgggagcctccagat i/c caaagaaagctccagtag	2083
PEMT	9	exon 2 + 162	agctcagagactctctgac c/t atgttggttagctcttctc	2084
PEMT	10	Intron 2 + 4598	ccgtgggtttttttttt i/a cttcatttttgggttctg	2085
PEMT	11	Intron 4 + 39	actgtcagagagagatc c/t cactcttgtagggccac	2086
PEMT	12	Intron 4 + 1317	acctctccagctggcccca g/a cctctgacatgggctctg	2087
PEMT	13	Intron 4 + 1355	ctggagcagagctgacagcg a/c agtgcctgacatctctggcg	2088
PEMT	14	Intron 4 + 5925	gtccagagccttgagcccta c/t gtaggagctcagctctcca	2089
PEMT	15	Intron 4 + 6028	ggcagtggttcaagagcag c/c atgagctcctctctcacc	2090
PEMT	16	Intron 4 + 6078	atctgacctctggagact c/t accggcttgcgcatcac	2091
PEMT	17	Intron 4 + 6089	cgcagactctctgagctt a/g tggcatcaccccccagat	2092
PEMT	18	Intron 4 + 6379	tcaggctcctctctctat c/a cctctcacccctgctctc	2093
PEMT	19	Intron 4 + 7339	tgtagaagatctctccaga c/t ggcagatgcatcagggctca	2094
PEMT	20	Intron 4 + 7619	ctctctcagatgctctcag a/g gagaagaagcatctacag	2095
PEMT	21	Intron 4 + 8858	ggcagtggtgtgtgtgtgta i/g gtatgtgggtgtgtcatgt	2096
PEMT	22	Intron 4 + 9029	ttcttgaccagaaagcctg c/a tctctgcccagggcctctg	2097
PEMT	23	Intron 4 + 9056	ggcagggcctctctacttg c/t gggaaagctgagctgagctg	2098
PEMT	24	Intron 4 + 9512	cggagctgggagagacatt a/g ctctgtgtgtgtgtgtgtgt	2099
PEMT	25	Intron 4 + 9523	agcagatctactctgtgttc i/c gctggcactggcctgtgtgt	2100
PEMT	26	Intron 4 + 9622	ggcaaatctacacaaagt g/a tctgagacgggtgagctca	2101
PEMT	27	Intron 4 + 10776	ccattctgggtctctcttgg g/a aggttgaaatgaaatctcatg	2102
PEMT	28	Intron 4 + 10912	ctctccctacttctctcaga g/c atcacacaagccttcagga	2103
PEMT	29	Intron 4 + 11590	ggacacttgccctgatacaga c/c atgtgtgtgtgtgtgtgt	2104
PEMT	30	Intron 4 + 12090	ggccagggcaccctccagag g/c ctgaatccaccatgtccagc	2105
PEMT	31	Intron 4 + 12263	taccgctctccagatgga g/a cggagctgctcatggacttca	2106
PEMT	32	Intron 4 + 12448	ctctgtccctctctctctct g/a tagtttctgggtgaagatc	2107
PEMT	33	Intron 4 + 12730	tggacacagctgcctcacc c/t gggccagagcctgtgtgttc	2108
PEMT	34	Intron 4 + 13240	gggctcagggcagcacacagg i/c cccagtagaccctgtctctt	2109
PEMT	35	Intron 4 + 13494	tccgtggaaactaagaatgg i/c acctcctctgagagtgaggac	2110
PEMT	36	Intron 4 + 13817	agctctcctctctctctctg a/g cagatcttgagagctctggcc	2111
PEMT	37	Intron 4 + 14773	cgccctctgtctctctctct c/t ctatgctctctctctctctg	2112
PEMT	38	Intron 4 + 14951	gtccctgagggccctccacc g/a aagcctgggggtgcccctaca	2113
PEMT	39	Intron 4 + 16896	gctgtgactgtcttggagag i/c gggcttggcgggcttggtag	2114

遺伝子名	No.	存在位置	配列	配列番号
PENT	40	intron 4 + 19439	ccaggagccttgaagcagc C/A ggggcttcaaccacac	2115
PENT	41	intron 4 + 19557	atttgcagcatgicacat C/T cctttcataatgaagcag	2116
PENT	42	intron 4 + 20051	acagcatcgaagagaccac A/G calctgcacacgcatlgaat	2117
PENT	43	intron 4 + 20816	tgacatcttgagcttccat C/T agccactttagtgcagctg	2118
PENT	44	intron 4 + 21196	ggcttgcaggccctgggat C/G atcgtacacggcttttagtgc	2119
PENT	45	intron 4 + 21528	acaggtagggagccggctc C/T ggaagtgccggctttagc	2120
PENT	46	intron 4 + 21596	ccgtctccagctgcttgc C/T gtagcagaagtgctccacat	2121
PENT	47	intron 4 + 22672	agcttccacgtccttctg C/T tgaaggagagggccggctc	2122
PENT	48	intron 4 + 22713	lctaagctgtcttcttctt A/T ctgaagaccacacaccttct	2123
PENT	49	intron 4 + 23010	tgcgggagcggcggagggga C/A ggcgggtgtgttccccaaat	2124
PENT	50	intron 4 + 23588	gtcagagcccttgcacccc C/T gcagcgaagttctggcgga	2125
PENT	51	intron 4 + 23627	gacacgtcccttgcagcaga C/T ggtgggtgggagcccttcc	2126
PENT	52	intron 4 + 23941	tgagggttggagcttaca C/A agagagtgagctcacaggg	2127
PENT	53	intron 4 + 24091	gacaccttcatctgtcagc C/T ctgaagacaccccttgcctt	2128
PENT	54	intron 4 + 25348	cagccagttggaatctac C/A tagatgaagcatctcagc	2129
PENT	55	intron 4 + 25603	taagcagttgacatgac C/A tgaagaatctccacagca	2130
PENT	56	intron 4 + 31540	cctcaggtggcagagac C/T gtgagagcatgcaacgtgc	2131
PENT	57	intron 4 + 31637	gtggcttgggagccagagc C/A gtaggggcttcaagtgctg	2132
PENT	58	intron 4 + 31642	ctgggagccagagagctga C/A gctcgggagcatgagtgctca	2133
PENT	59	intron 4 + 35593	ggaggagctggaagagctg C/A agcttcaaggtgtgtttgt	2134
PENT	60	intron 4 + 35647	actttagcaccacccagc C/A tgtcgtgcagtgagggagac	2135
PENT	61	intron 4 + 35862	tccagtgatgctctctcc C/T cgtctcagcagagcactcag	2136
PENT	62	intron 4 + 35882	ccgtctcagcagcactca C/T cggcagaggtggctagactc	2137
PENT	63	intron 4 + 37141	ccacagccgagatccctga C/G acttctcagctgcagggctg	2138
PENT	64	intron 4 + 38862	ggagagaccacatccagca C/G caagagcagcagatgacctag	2139
PENT	65	intron 4 + 38872	acctcagacagcaagagagc C/T catgccaatgggtccagcag	2140
PENT	66	intron 4 + 39140	atgtctcaatctctctccc C/T ggaatcttaggcacagctc	2141
PENT	67	intron 4 + 39635	cagcccccagagcagatggg C/T cctctcagcagggagcagggc	2142
PENT	68	intron 4 + 39713	actcttagcatctgctctcc C/T tctcttcttccagggagcga	2143
PENT	69	intron 4 + 40435	ccgtgtgtgcttggagacc C/A gaggcagacagagggagcct	2144
PENT	70	intron 4 + 47485	acaatgactgttgagacct C/T gaggcagctgtgtcacgtgc	2145
PENT	71	intron 4 + 48131	actggggagctctgaatccc C/A cctctcagtgagcagtgagagc	2146
PENT	72	intron 4 + 48558	cacagtgtaactgttaggc C/G acagccacatcttgcggag	2147
PENT	73	intron 4 + 48702	gaaatggagagagcttggga C/A gcaaaagcagagagagcaga	2148
PENT	74	intron 4 + 50302	gcagtgcatagggagagagc C/G attcctcagagtgagagc	2149
PENT	75	intron 4 + 54102	ggccgcctctctccagagcc A/T tgggctctctcagcatctt	2150
PENT	76	intron 4 + 54220	ccagggacacatcttctcc C/A ccaagctcttcttctgctt	2151
PENT	77	intron 4 + 54371	ggacataatgtagcagctgg C/A tgcatagtgtgtgtgtctccc	2152
PENT	78	exon 5 + 79	tggctctactctctttagc C/G tccacctctctctctgagc	2153
PENT	79	intron 5 - 6796	ggaggaagtcagcttcttac A/C gtagtgagctctcagcttct	2154
PENT	80	intron 5 - 6636	ttttctctcaactttttg C/G attcagagcagaggtgtgtgc	2155
PENT	81	intron 5 - 6448	gttggccagctctgacag C/A acctcgggagcagctctctg	2156
PENT	82	intron 5 - 5218	ggagccttggttgaaagag C/G ttacgacacaggtcttagag	2157
PENT	83	intron 5 - 4824	ggacagccgggggtttaggc C/A gctcatalgaagagggagag	2158
PENT	84	intron 5 - 4249	tcaccagatgtattctctgc C/A ggcagagttccttgggtagcc	2159

遺伝子名	No.	存在位置	配列	配列番号
PEMT	85	intron 5 - 4230	gagcagatgctcttgggtat c/ cactggcgggtccatgag	2160
PEMT	86	intron 5 - 4182	gagagtaggggtggggag c/a cacttaggacaggagctg	2161
PEMT	87	intron 5 - 3369	caggtggccctctctt c/c tggcctgggtgtgtggccag	2162
PEMT	88	intron 5 - 2625	caggaagctgggcccctgaa c/ agcctggccttggccac	2163
PEMT	89	intron 5 - 1200	attatgagcatggagaa a/ gcacattggcacacat	2164
PEMT	90	intron 6 + 606	gcttggtagccctccaca a/g tggcctggatggcagca	2165
PEMT	91	intron 6 + 1229	ttggcagggaggggag c/a gaggcagagggtcggat	2166
PEMT	92	intron 7 + 716	atggagatgcttccccgg c/g gggcagaggacctggctt	2167
PEMT	93	intron 7 + 1537	cctggggacgcaagacc c/a cctcagaggacatcagcca	2168
PEMT	94	intron 7 + 1718	ggcttcaggtgtctgac c/ ccccgcatgtaggaccca	2169
PEMT	95	intron 7 + 2695	ggcttggggacctggac c/ cttcttagaagacagcctt	2170
PEMT	96	intron 8 + 140	cgaggctccaggtcagag c/ ggccatggtagcttacaag	2171
PEMT	97	3' flanking + 179	tacttagagggctcaggag c/ tgcctggccttctctgac	2172
PEMT	98	3' flanking + 394	gatgactatcatctctaa a/g tgaatggccttctctgac	2173
ALDH1A1	1	intron 1 + 564	cattattctcagcaggt c/c tggccttggcagcagatg	2174
ALDH1A1	2	intron 1 + 710	gttcggagtagctctgaa c/ tttggccttctcactgct	2175
ALDH1A1	3	intron 1 - 3868	gccttttatccagata c/g agcctaaactcttctctg	2176
ALDH1A1	4	intron 2 + 2933	taagtagctatactatatt c/g gtagatatactatactata	2177
ALDH1A1	5	intron 2 - 1646	caatgatgaactgaagc c/ gcaaatatgcactglatag	2178
ALDH1A1	6	exon 3 + 54	caagcttttcaactggatc c/ cctggcctactatggatgc	2179
ALDH1A1	7	intron 3 + 157	taggccttcaactgaat c/g attcacaatagatgctgc	2180
ALDH1A1	8	intron 3 + 339	tgagcttctcagaaagat c/a ttaggcttctcagcattt	2181
ALDH1A1	9	intron 3 + 655	agcagttagatgagtcagag c/a ataatatagttggggagag	2182
ALDH1A1	10	intron 3 + 735	gaagcctatttactataac c/a accatttattactcaatat	2183
ALDH1A1	11	intron 3 + 863	gcagataggttaactaaag c/a accatttattactcaatat	2184
ALDH1A1	12	intron 3 + 1757	agatcacaaatttctcta c/a ttcacaaattcctcagcaca	2185
ALDH1A1	13	intron 5 + 90	ttcttaaacagagagag c/a ttatgtattgtttaaagtg	2186
ALDH1A1	14	intron 6 + 213	caggaagcacaacacaaag c/c ttgggtcaaacagctcaact	2187
ALDH1A1	15	intron 6 + 1323	tttgaattaaatttata c/ t tgaacttttaactttta	2188
ALDH1A1	16	intron 7 + 638	gcaagaagaagtgaggag c/a atactgaccatgcacaaaa	2189
ALDH1A1	17	intron 9 + (1462-1463)	aatggaattctagtgtttt tt gttgattattatctatc	2190
ALDH1A1	18	intron 9 + (1462-1463)	atggaattctagtgtttt gttgattattatctatc	2191
ALDH1A1	19	intron 9 + 1757	tgatcgaatttagtttct a/g taatgaatagatccagtg	2192
ALDH1A1	20	3' flanking + 40	aatccacttattactctc c/g gaggcttcaagtgctata	2193
ALDH1A1	21	5' flanking - 716	tttaatacaagtttgggt c/g acagtgatttctctgca	2194
ALDH1A2	1	intron 1 + 314	caggaatcttctctgag c/g cagggcagaggagactgca	2195
ALDH1A2	2	intron 1 + 314	cggtccagtcgcccggg c/g aggcctcgagacccgttag	2196
ALDH1A2	3	intron 1 + (664-675)	tttgaactgagacttac tt 11-13 atacgacattgacatctt	2197
ALDH1A2	4	intron 1 + 1370	gcatacagcttagagttt a/g ttatatagggtctcaacc	2198
ALDH1A2	5	intron 1 + 1557	ggtagcttttcagattta a/ ttggagcttctccagttc	2199
ALDH1A2	6	intron 1 + 1934	tcagctctttagtagact c/g taattttcttaagacagca	2200
ALDH1A2	7	intron 1 + (1971-1980)	agcatatggagacagcta tt 9-11 aaacgtgaagcagaagct	2201
ALDH1A2	8	intron 1 + 2295	tactgtaagcaatagtta c/g tgtttttgtcttgctaac	2202
ALDH1A2	9	intron 1 + 2387	ttggaccctcataagatga c/ t tacttaataataatgacag	2203
ALDH1A2	10	intron 1 + 2841	aggaatgctcttttaaac c/ agatgggtgttgaatcagagag	2204

遺伝子名	No	存在位置	配列	配列番号
ALDH1A2	11	intron 1 + 3035	gacatttataatttttgtata A/G ctagattataggaaacac	2205
ALDH1A2	12	intron 1 + 3319	aaagattatgtttttttt Y/Δ ctagatcgtatataatag	2206
ALDH1A2	13	intron 1 + 3474	tgtctttttttttttatcat Y/C taacttctgttttttctgggg	2207
ALDH1A2	14	intron 1 + 4186	cttcaaacctttacttaa C/C attgtctgttttggcctaaa	2208
ALDH1A2	15	intron 1 + 4222	catatattgtcagcaac A/G calgtatagagacttca	2209
ALDH1A2	16	intron 1 + 4254	aggacttcagttttttt Y/Δ aaatctttttcaactat	2210
ALDH1A2	17	intron 1 + 4397	cccttcacacacacacccct A/G ttttaccatgttgaaattac	2211
ALDH1A2	18	intron 1 + 5935	aactcaggttgcataaga Y/C gtttctgttttttttaagtag	2212
ALDH1A2	19	intron 1 + 6206	ttttgaagccctctagca Y/G tttttttttttttttttta	2213
ALDH1A2	20	intron 1 + 9559	agataatttgatatt C/T actctgtctgtctgtatagat	2214
ALDH1A2	21	intron 1 + (9631-9632)	tataaagaatttcaaga AAGG ccttttttttttaaacctc	2215
ALDH1A2	22	intron 1 + (9631-9832)	tataaagaatttcaaga ccttttttttttaaacctc	2216
ALDH1A2	23	intron 1 + 12731	ctgaatagaaaccttttag Y/A gtaccttgcagagcagtaga	2217
ALDH1A2	24	intron 1 + 13442	caatgtcatagaaacacgc C/A gaattcaaaattttcatat	2218
ALDH1A2	25	intron 1 + (14173-14176)	tctaaagaataaataaata AAA/Δ gagaataatagtttaagat	2219
ALDH1A2	26	intron 1 + 14586	actcatatttggctcaag C/G cttctcaaccttagatat	2220
ALDH1A2	27	intron 1 + 14711	ttgtttcaaacctctttca A/G ctttagaatatataatagg	2221
ALDH1A2	28	intron 1 + 17258	gtttgacattttacttcta A/G ttacactgaagaatgtcagtt	2222
ALDH1A2	29	intron 1 + 17258	gaagaacacatagaagaac U/G-11 aaccttcaaacatattga	2223
ALDH1A2	30	intron 1 + 18277	alcagtacaatgtgttgggc A/G tacacacttaatttaaat	2224
ALDH1A2	31	intron 1 + 18734	taatacaaatatttgaagc A/G ttactatttaaaatacaaa	2225
ALDH1A2	32	intron 1 + 19081	ctttgacacactctcat Y/A taagtcgtgttaagatgag	2226
ALDH1A2	33	intron 1 + 21514	ttatcacctcaacttttaa C/T gaattttttttttttttt	2227
ALDH1A2	34	intron 1 + 21732	aatcaggataagggagttc C/A ttttttttttttttttttt	2228
ALDH1A2	35	intron 1 + 21865	catttttaaatgtgttcta A/G taagacttgcattgttaagt	2229
ALDH1A2	36	intron 1 + 26282	legcaatgttttaaaatgt C/T tttttaggacttttttcca	2230
ALDH1A2	37	intron 1 + 27805	taagaagaagaataaaaa A/Δ ctatcttgagactttgcagg	2231
ALDH1A2	38	intron 1 + 28204	agatgactctcccaaggaa Y/C tgcacacttccagacaglac	2232
ALDH1A2	39	intron 1 + 28321	tcactctatttttttaact C/G cttcttaaatgtgtgtttaa	2233
ALDH1A2	40	intron 1 + 49478	ttttttagactttttttaa Y/C cggggtatcagataatcttc	2234
ALDH1A2	41	intron 1 + 49834	gaataaagaataggagcat C/T ggttaagaccatttttccct	2235
ALDH1A2	42	intron 1 + 50351	gccttcaatttttctcatgt C/T tatagaagaataaaccttgc	2236
ALDH1A2	43	intron 1 + 51181	gactgactgtttcataagt C/G agaatttttttttttttttt	2237
ALDH1A2	44	intron 3 + 654	tttttaccatagtttttc C/T gtaacacttgcagctttgact	2238
ALDH1A2	45	intron 3 + 654	tttaacctttttagtaaaa C/A gaatcttctagaacacagag	2239
ALDH1A2	46	intron 3 + 668	gtataagggaatctttcagaa C/T caagaagaatagtagagacc	2240
ALDH1A2	47	intron 3 + 1273	catactcttctgttctttt C/T ccttcttcttctatagcca	2241
ALDH1A2	48	intron 3 + 1743	tttttaccatagaaaggg Y/A gttttaggtagaagaattc	2242
ALDH1A2	49	intron 3 + 2891	ccacacttaaatagattcc C/T gtttttaaacacttcaact	2243
ALDH1A2	50	intron 3 + 2919	ttcacatataactcattgt A/G gttttttaggacttagac	2244
ALDH1A2	51	intron 3 + 3054	ctaggacttagaacaactg C/A caatctatagaaatttttta	2245
ALDH1A2	52	intron 4 + 290	ttgaaggttctggagactta C/C tatctctcatttcttcttc	2246
ALDH1A2	53	intron 4 + 380	catttgccttagattaggtgc Y/C ggggttagtagtagagggca	2247
ALDH1A2	54	intron 4 + 461	ccttctcccttcttgaaca Y/C ataagatctacttctttggaa	2248
ALDH1A2	55	intron 4 + 461	gatttaggctgatttttagt C/T tcttttttaatttttttct	2249

遺伝子名	No	存在位置	配列	配列番号
ALDH1A2	55	intron 4 + 506	tcctatatttcgaagcc G/A tgaattactttcataatc	2250
ALDH1A2	56	intron 4 + 1952	ttggtccaccctaccgt C/G atttattatiaaaca	2251
ALDH1A2	57	intron 4 + 2079	ctctattagcctaaagla C/T ctggtttctttacttc	2252
ALDH1A2	58	intron 4 + 2519	ttggctcaagagctctt C/G cagggtctcaacagatg	2253
ALDH1A2	59	intron 4 + (2840-2851)	ttgtcttcgatactggc (T)11-13 cacagtgagctcgaatat	2254
ALDH1A2	60	intron 4 + 723	aatagatcaaatatacaaa A/T gatagattcagatccaa	2255
ALDH1A2	61	intron 4 + 7958	taaaatcgtttttatgta C/T taggtatataaanatttgct	2256
ALDH1A2	62	intron 4 + 8090	ctgaatttactatatta C/T agatgcttagctacata	2257
ALDH1A2	63	intron 4 + 12823	tgtagccctagctaaag C/T ttccaatagtagaacgt	2258
ALDH1A2	64	intron 4 + 12939	atgagctcgacttttaaga T/C ttgtctacatttcttcc	2259
ALDH1A2	65	intron 4 + 14935	ttatgtagagctctttta T/G aaatgagcttttaccctct	2260
ALDH1A2	66	intron 4 + 15321	scatttggctctcagaga C/T atatccaaatatacctatg	2261
ALDH1A2	67	intron 4 + 15412	ttcaagatttatttctgtt T/G ttttttttttttttttttt	2262
ALDH1A2	68	intron 5 + 1888	aatccaaactctacttt C/T tagtcaacaagatttatgc	2263
ALDH1A2	69	intron 7 + 9166	gaagactctttatcaaa G/A ataaagatttttaaaaa	2264
ALDH1A2	70	intron 7 + 9914	aagctgagaaaaactatag C/T ttcttcaacagatttcc	2265
ALDH1A2	71	intron 7 + 18942	tttggaggagaaactaaacc G/A tgacttctagttatctct	2266
ALDH1A2	72	intron 7 + 19820	ttccactctacttttagtt A/G agggaggtggcttctacag	2267
ALDH1A2	73	intron 7 + 19826	ccctatttagcttaggaga G/A ggccttctacattttag	2268
ALDH1A2	74	intron 7 + 19913	cgtgaatcattcaatattt A/G tttaaaataccagttgaa	2269
ALDH1A2	75	intron 7 + (20110-20111)	catgatttctctacta (ACTA) tctaaagctcaaatctcgc	2270
ALDH1A2	75	intron 7 + (20110-20111)	catgatttctctacta tctaaagctcaaatctcgc	2271
ALDH1A2	76	intron 7 + 21857	acatgaaatlaagaaagg A/T gaagaggagaagacagaga	2272
ALDH1A2	77	intron 7 + 21929	tacagcacagagctattt A/G actagtttactggatctct	2273
ALDH1A2	78	intron 7 + 23308	ggctttagcttgaacact C/T tgggttatacaagatcag	2274
ALDH1A2	79	intron 7 + 23554	ggactttagtgaacacagag C/T tggtagagttctctctcc	2275
ALDH1A2	80	intron 7 + (23701-23703)	catctgagatttgcttgig G/C/A ttaccagatttagtgggtgc	2276
ALDH1A2	81	intron 7 + 26479	gatacagaacatttggtt T/C atcctcatgatatcttcaa	2277
ALDH1A2	82	intron 7 + 26561	taaggcccaatgcagta T/C tgaatctccattacatit	2278
ALDH1A2	83	intron 7 + 26662	tttctttagcttccatca C/T gaactaaagctcttcca	2279
ALDH1A2	84	intron 8 + 76	tttatactccacttttgat G/A gacacatgacaagaatatt	2280
ALDH1A2	85	intron 8 + (700-711)	accatcattcagtgatgc (T)11-12 ccttccactgttccagc	2281
ALDH1A2	86	intron 8 + 724	tttttttccctccactgt T/C gccagcagagctcttcc	2282
ALDH1A2	87	intron 8 + 800	cagatttcttgattttcag C/A ccacttgaattttcagag	2283
ALDH1A2	88	intron 8 + 1251	gatttctgaaaaattgaga G/A gatctgcaaccttggagctc	2284
ALDH1A2	89	intron 8 + 1627	ggcccttcccaggaagaag C/A gtgagaacatgctgtttcc	2285
ALDH1A2	90	exon 9 + 141	tggagctggcacaagagcgc G/A tagtggagagctcttgcac	2286
ALDH1A2	91	intron 9 + 778	aacagctcggacagatccc T/C tgaacttggaaagtgtag	2287
ALDH1A2	92	intron 9 + 801	tagctttgaaagtgttagga A/G gtgagaggttggcttacttc	2288
ALDH1A2	93	intron 9 + 868	tctgaagcctgtgtactt T/C atgagcttggagagagccac	2289
ALDH1A2	94	intron 9 + 1338	aatttttgccttttttact A/G tcaatacaacttgcctaagtt	2290
ALDH1A2	95	intron 10 + (1227-229)	ctatctcttatgatttatta T/A/G gccaaagacaatcagaat	2291
ALDH1A2	96	intron 10 + 316	ctaaatgtgggtcacttggga T/C gtttaaccagagagagaatc	2292
ALDH1A2	97	intron 10 + 368	ctttacatctgtgcaagaga G/A ggaacagaggaacatcagcc	2293
ALDH1A2	98	intron 10 + 660	gtaaacttgcatttgaattgt C/A gaaacaggttaaggaatga	2294

遺伝子名	No.	存在位置	配列	配列番号
ALDH2A	99	Intron 1 + 104	tgaggaa taccaaaggaac C/A aaggttcacacagaaaggg	2295
ALDH2A	100	Intron 1 + 229	aaattctaaagaataacc A/G tgcagtcagattatgtct	2296
ALDH2A	101	Intron 12 + 117	catatctcaaacattt C/T gtagagacatctactata	2297
ALDH2A	102	Intron 12 + 691	gataggagatcactctga A/G ctgaaaaatctggaaaacc	2298
ALDH2A	103	Intron 12 + 1934	catctgtctagatctcatg C/T ttgtttgtttgtctct	2299
ALDH2A	104	Intron 12 + 1973	ctacttaccocaaacatg A/T ttctctttcttaatgacc	2300
ALDH2A	105	Intron 12 + 2722	ccagatgactcagatatac C/A tcatctgctcagaccacag	2301
ALDH2A	106	Intron 12 + 3855	taacttgaagcacacataat C/C gtaggtttctgactctga	2302
ALDH2A	107	Intron 12 + 4185	ttctttaagcgaatgaac C/C atacagacaggaagacagcc	2303
ALDH2A	108	Intron 12 + 4991	acaggaacacttagacatgc A/G accatctccaccctcctc	2304
ALDH2A	109	Intron 12 + 5018-5019	ccacacctctctctggggg G agaaaaacacactactctcc	2305
ALDH2A	109	Intron 12 + 5018-5019	ccacacctctctctggggg agaaaaacacactactactctcc	2306
ALDH2A	110	Intron 12 + 5051-5052	actgtccaaagactaata A ctgaacagtgctgcttct	2307
ALDH2A	110	Intron 12 + 5051-5052	actgtccaaagactaata ctgaacagtgctgcttct	2308
ALDH2A	111	Intron 12 + 5300-5302	ttaaagttttaaaaactt C/T/Δ taaaactctactgagatg	2309
ALDH2A	112	Intron 12 + 5405	catccagactctctcttgc C/C caagtgataacgtgacctc	2310
ALDH2A	113	Intron 12 + 5435	aactgcatctctcctggact C/A cctctgactcactgacgc	2311
ALDH2A	114	3' flanking + 449	ttggcccggaacattt C/C caagtgataacgtgacctc	2312
ALDH2A	115	3' flanking + 597	acttggga tattcttgacc C/C atctggtttcttttaccca	2313
ALDH2A	116	3' flanking + 669	alagagacggagatcatca C/C gtcaggttcacgtctctga	2314
ALDH2A	117	3' flanking + 1122	cgtctcactcagctcctc C/G gtacacccactcttggcc	2315
ALDH2A	118	3' flanking + 2214	tgacgtglaaaagaatc C/C gtaaatgtagcgtctac	2316
ALDH2A	1	5' flanking - 1425	cagttttagccacacatat C/T ggtaagcttgcctcctcg	2317
ALDH2A	2	5' flanking - 1379	ccattaccccttccagg C/T ctacgtctgactcaccagc	2318
ALDH2A	3	5' flanking - 1270	aacttaccctctatcacc C/A ctatccagaagacacagc	2319
ALDH2A	4	5' flanking - 1214-1213	acggagctctcaaacagga GGA aataagagacccccctccc	2320
ALDH2A	4	5' flanking - 1214-1213	acggagctctcaaacagga aataagagacccccctccc	2321
ALDH2A	5	5' flanking - 1103	gcacagcttttgacagat C/T cgtgctcctgcttctgttc	2322
ALDH2A	6	Intron 1 + 986	gcttaacttctccacctt C/G gcttctctgttttctct	2323
ALDH2A	7	Intron 1 + 1462	gtacagatttcaaatatc G/A tatatagaaccagacata	2324
ALDH2A	8	Intron 1 + 1661	ctctgtcttgggggtct G/A caacttctgactttaaagc	2325
ALDH2A	9	Intron 1 + 2360	aaagga tagagctctctt A/G attagagggctcttctt	2326
ALDH2A	10	Intron 1 + 2516	tgaaaacattctcttga C/A tttagcttagtgcctgttg	2327
ALDH2A	11	Intron 1 + 2624	ctgaacacactacacac C/T gctctctctcatctctc	2328
ALDH2A	12	Intron 1 + 3255	tttctcttcttcaaaag C/C cctctctcttctgctcact	2329
ALDH2A	13	Intron 1 + 3643-3656	acttcagagtttlltggg U12-14 anallctatcaactttaa	2330
ALDH2A	14	Intron 1 + 4265	ccaaagcctctctttaa C/C atgacattaaagaacatt	2331
ALDH2A	15	Intron 1 + 5187	caaatagaataagacatcac C/T taagctcttagcatllga	2332
ALDH2A	16	Intron 2 + 43	ctctaaagtattcaattatg C/T ataccaaagaataagaaa	2333
ALDH2A	17	Intron 2 + 127	caagggcttggctagctg C/C gaatggcagatggcttca	2334
ALDH2A	18	Intron 2 + 1285-300	agaaaaagtttcttctt U16-17 atcaattattggacctga	2335
ALDH2A	19	Intron 2 + 778	agtgacagatagcttgg A/G ttatctctgcccagat	2336
ALDH2A	20	Intron 2 + 1216	actcggtagagctactctg A/C ctgctctctcactcctc	2337
ALDH2A	21	Intron 3 + 81	accatggatatggaaaaa A/C galcacggtctgttctt	2338
ALDH2A	22	Intron 3 + 236	gtcagcttcttgacaaat C/G gtgtctcttaggcagttgag	2339

遺伝子名	No.	存在位置	配列	配列番号
ALDH1A3	23	Intron 3 + 1467	ggccgggtgtagagggagga c/ atctcttcttctgaccttga	2340
ALDH1A3	24	Intron 3 + 1726	ccacatgtcccccgggtgag A/G gtagctccctccagggtaa	2341
ALDH1A3	25	Intron 3 + 3777	gcacagaatagatggcccca A/G ttacgtctgtcattactgg	2342
ALDH1A3	26	Intron 3 + 3829	caagtcactggggcgttagc C/G tccgtgtctccaccttaag	2343
ALDH1A3	27	Intron 3 + 4299	tcactttccagcaccact C/A gccagcttggccagagagga	2344
ALDH1A3	28	Intron 4 + 84	agagcccccctgactgtt C/G cclagagcatttcccaac	2345
ALDH1A3	29	Intron 4 + 126	ccactctcttccaaatgt A/G ctcgaatcttcttctlaag	2346
ALDH1A3	30	Intron 6 + (290-291)	taagagatttccggggggg (C) tcaaccaagagagggccaaa	2347
ALDH1A3	30	Intron 6 + (290-291)	taagagatttccggggggg tcaaccaagagagggccaaa	2348
ALDH1A3	31	Intron 6 + 705	aacagctggatgtagccaa A/G ttccactttcttcttctga	2349
ALDH1A3	32	Intron 7 + 56	ggagcgttatattgaacc C/T gtagcgtttcttcttctga	2350
ALDH1A3	33	Intron 7 + 1107	gagctgttactctcttgg A/G gacagacatgcccgttga	2351
ALDH1A3	34	Intron 7 + 1610	aagagccacacagacacc C/G cctactggcgttcttgaat	2352
ALDH1A3	35	Intron 7 + 1820	caacttaagtgagagacct A/G agaccagagatcccaagag	2353
ALDH1A3	36	Intron 8 + 963	gagaaagacagagagagga C/T ataggctctcagagagaaa	2354
ALDH1A3	37	Intron 8 + 1824	accattctatcactaagc C/A tglccccaagatctatc	2355
ALDH1A3	38	Intron 8 + 2384	ccctctcttcccccctccc C/A tccatgacttggcagtag	2356
ALDH1A3	39	Intron 9 + 24	atccccctgggtgtgtgaa A/C caatgctgtcttctgaagg	2357
ALDH1A3	40	Intron 9 + 91	acctacaggttccctctcc A/G gaaggaatctcagaccttc	2358
ALDH1A3	41	Intron 9 + 219	actagagatagagagagag C/G gclattccagagagagag	2359
ALDH1A3	42	Intron 9 + 435	ccagagagagagagagctgg C/A cagaggaatgataccag	2360
ALDH1A3	43	Intron 9 + 1472	ttgcttllggagccagala C/T accgatttcttccagagaa	2361
ALDH1A3	44	Intron 9 + 2038	taacaaatgttctctacgg C/A ctctccagagagtgtagat	2362
ALDH1A3	45	Intron 9 + 2124	caaacaggtctctccagag C/A catatgccagagagagag	2363
ALDH1A3	46	Intron 9 + 2154	actacagagagagagagcttc C/G gtlggcgaagagagagag	2364
ALDH1A3	47	Intron 9 + 2197	cttggccctcagagag C/A gaagagagagagagagag	2365
ALDH1A3	48	Intron 9 + 2466	ttcttagtctctatgttc C/T ctctagaatgttctgtgtg	2366
ALDH1A3	49	Intron 9 + 3655	gattgctcagtgagatga C/T ggtttagtctctctctctg	2367
ALDH1A3	50	Intron 9 + 3954	gggtgcttcttctacatg C/G tcaatgagctgttctcaagc	2368
ALDH1A3	51	exon 10 + 88	tggaatgggggggctcagc A/G tgaagagagagagagagag	2369
ALDH1A3	52	Intron 10 + 8	teccaagagagagagagag C/A gggctgtgagcagagctacga	2370
ALDH1A3	53	Intron 10 + 307	ctctcgtattcttaacaa A/C ccgttccagagagagagag	2371
ALDH1A3	54	Intron 10 + 378	gtgggttttccagagatca C/A ttcaggaacctgtgagatca	2372
ALDH1A3	55	Intron 10 + 975	aatatgtgtctctctctc C/G cgttagttatagagagag	2373
ALDH1A3	56	Intron 10 + 1088	cagtgccagagagagagag C/T ctctccagatgactctgaag	2374
ALDH1A3	57	Intron 11 + 105	ttgtttacattgtatatt A/G taccagagagagagagag	2375
ALDH1A3	58	Intron 11 + 274	agggctcagtagtctctg C/G gteggccctgtctgtctg	2376
ALDH1A3	59	Intron 11 + 1088	cagtgccagagagagagag A/A ctctccagatgactctgaag	2377
ALDH1A3	60	Intron 12 + 96	ctccaatctgtgagacccc C/A tcccccagagagagagag	2378
ALDH1A3	61	Intron 12 + 1537	gggctgttggggccttt C/T tgggtctcttcttgaatt	2379
ALDH1A3	62	Intron 12 + 1660	gtccctctccacacagtc C/A tcttcttctgagagagag	2380
ALDH1A3	63	Intron 12 + 5642	tcctgtcagatctctctc A/C ctatctcccccagagagag	2381
ALDH1A3	64	exon 13 + 104	gggctctctctcagagag C/C gacgagagagagagagag	2382
ALDH1A3	65	exon 13 + 281	ataggttctctcagagag C/T atctctctctctctctctct	2383
ALDH1A3	66	3' Flanking + 743	gtgagagagagagagag C/A aaggaatttctctctctt	2384

遺伝子名	No.	存在位置	配列	配列番号
ALDH1A3	67	3' flanking + 1145	gcctccacgctaccaccac A/G cctcagagagagctatcca	2385
ALDH1A3	68	3' flanking + 1185	aacctagggtcttgagaatc T/C gggtagatttaccgcaaaa	2386
ALDH1A3	69	3' flanking + 1600	acaccacccctacaaatlg T/C tggagacttctcgttgscaa	2387
ALDH1A3	70	3' flanking + 1847	cagagcctctcgtctgccc C/G ggtctctgaaatgacagt	2388
ALDH1B1	1	intron 1 + 134	cttgacactgtagactctc C/T ccaagtcccttaaccatc	2389
ALDH1B1	2	intron 1 + 367	gcagttcccgagatagaga A/G ggtccggtctctccgctgt	2390
ALDH1B1	3	intron 1 + 405	tgtagtaactctataaaa C/T tgcctgctattcagagagata	2391
ALDH1B1	4	intron 1 + 2002	cttcaactaattcggaaca C/T tacactctgttttaatttca	2392
ALDH1B1	5	intron 1 + 2157	tggaaagctctaaagagat C/T ctgagacctctgttggggg	2393
ALDH1B1	6	exon 2 + 192	ccacagctcaacctaccac T/C ggggaggtctatgggacgt	2394
ALDH1B1	7	exon 2 + 255	ctgaaagacgcccgggaag C/T ctccgacctggggtcccat	2395
ALDH1B1	8	exon 2 + 329	gcgggctcggctctctgaac C/T cctggcagacctagtggagc	2396
ALDH1B1	9	exon 2 + 614	acttgcctccgctctcgcga C/T aggcacacctggtttatga	2397
ALDH1B1	10	3' flanking + 168	aaagtcacactgaagacc G/A tagaanaaaccttggttcc	2398
ALDH1L1	1	intron 1 + 252	ccagagccagagctggacc G/C ccagagctctggcggcgc	2399
ALDH1L1	2	intron 1 + 544	ctcaggctctctggagct C/T ccaactccaccacttgcact	2400
ALDH1L1	3	intron 1 - 6596	caaatitcttaagttca C/G taaccttgaagatatit	2401
ALDH1L1	4	intron 1 - 6513	caatlatggttattctagg G/A acatgllatagatagta	2402
ALDH1L1	5	intron 1 - 6478	atagttacttactagctt G/A catttaaatltgttccct	2403
ALDH1L1	6	intron 2 + 240	gtggcattaggctctggag A/G aggcctatagagaagccag	2404
ALDH1L1	7	intron 2 + 1326	gagagagagccgagagaga C/G agccagctcagtcagggccc	2405
ALDH1L1	8	intron 3 + 386	gtctactctacttccact G/A cccctctcttggcagcaca	2406
ALDH1L1	9	intron 4 + 271	ggcccttctaatagacaag C/C aagcttaagagcagagactg	2407
ALDH1L1	10	intron 4 + 356	taggatttattctctctc C/T ttactctgttgaattctctt	2408
ALDH1L1	11	intron 4 + 608	gtgctctgaagctgtctc A/G gtcatcttctctctctggg	2409
ALDH1L1	12	intron 4 + 664	ggtcacatggctctggcggc A/G gggcagctcagtcacctggg	2410
ALDH1L1	13	intron 4 + 785	gagggctctctggcctctcc C/G gaggacagagctggcaggagc	2411
ALDH1L1	14	intron 4 + 874	ccctggggggccttctctg T/G tgggcccagagctcttggct	2412
ALDH1L1	15	intron 4 + 1349	tccctcagctcttctctac C/A tgggcccagagctcttggct	2413
ALDH1L1	16	intron 4 + 1799	ctggagctggagagagagca C/A gttctctatctctggagatag	2414
ALDH1L1	17	intron 4 + 1815	ggcagagctctattctctagg C/A atagacaccacatgactctc	2415
ALDH1L1	18	intron 5 + 272	aaagccacagagagagataag A/G gtggaggttagggggcaaaa	2416
ALDH1L1	19	intron 5 + 301	tagggggcaaaactcagcc C/A tagtgcgagagcttccaag	2417
ALDH1L1	20	intron 5 + 343	caaggctgagggagagagtc C/A ggtctctggagcaatagcca	2418
ALDH1L1	21	intron 6 + 926	cctctctggccttctctgctt C/T gggggcttcttctccccc	2419
ALDH1L1	22	exon 7 + 41	gagctgaacacttcagccc T/C ggtgcccagggagagcgtt	2420
ALDH1L1	23	intron 7 + 305	cttagaatcagagagaacc C/T tccagggagagcttggatttca	2421
ALDH1L1	24	intron 7 + 837	gtccgagacaagccactagg C/T gtagtaccaccacactctt	2422
ALDH1L1	25	intron 7 + 866	cccagctgttctctctctc C/T ggcctaccagagtgaggcgt	2423
ALDH1L1	26	intron 7 + 884	tccagctctcagagatagag C/T gtggacagtagggggctggc	2424
ALDH1L1	27	intron 7 + 1118	aatgttcagagaatctatcc G/C aggcagtaagggcagagaa	2425
ALDH1L1	28	intron 7 + 1168	aaagtaaggttcagagaa G/A tctagcttggggcgtctccc	2426
ALDH1L1	29	intron 7 + 1451	cagggcaccacacacatctg T/C ccagagacctctcaagacag	2427
ALDH1L1	30	intron 7 + 1489	caggaalgcagaagagagca T/C taagtgctttaagagagagc	2428
ALDH1L1	31	intron 7 + 1579	tcagggtggggggagagta G/A gagagaccagctagacacac	2429

遺伝子名	No.	存在位置	配列	配列番号
ALDH1L1	32	intron 7 + 1891	ctggcggagctttagcttgc a/c gaagctccagacacattt	2430
ALDH1L1	33	intron 8 + 1632	tcagggttgcattgttcac t/c gtcacattcagagttccag	2431
ALDH1L1	34	intron 8 + 1799	gcacagctctctctagct g/c ttacccgtcagcccccctaa	2432
ALDH1L1	35	intron 8 + 1986	ggtagggggctggcctgt g/t cctgttcagaggaacgtcc	2433
ALDH1L1	36	intron 8 + 2002	ctgtgctctctcagaggaac a/g ctcagagacccctctctaggg	2434
ALDH1L1	37	intron 8 + 2627	aaagagagacacaggggtt g/t ttatgccaggggtttagaga	2435
ALDH1L1	38	intron 8 + 2646	gccttgcagaggggtttaggg g/a aactgttctatattggcct	2436
ALDH1L1	39	intron 8 + 2925	ctctcctctcattaggtcc c/g agactgaatcttcagaga	2437
ALDH1L1	40	exon 9 + 4	cagctcttcttgcagagtl g/t ttggcagcggatctctccc	2438
ALDH1L1	41	exon 10 + 109	cagctttagttaggaact g/t cgaggagacataagaggg	2439
ALDH1L1	42	intron 10 + (671-672)	tgccatttctctctctcga (a/c) gtcctctttagccacccctaa	2440
ALDH1L1	43	intron 11 + 8	cacgcttggagtgtagtg c/a aggcacagcaccctctctcc	2441
ALDH1L1	44	intron 11 + 447	atagggcaaaacagcctat g/a atagatcacacgtgaacat	2442
ALDH1L1	45	intron 11 + 601	ctaaatagatcatttagg a/g aggtatlaatgaagactcat	2443
ALDH1L1	46	intron 11 + 639	catctcaaaaggagagggg g/a aggttagggacacagacag	2444
ALDH1L1	47	intron 12 + 66	ctggcagtgccacgggggg g/a acttctgtggagcccttt	2445
ALDH1L1	48	intron 12 + 478	ctattaaaaaaaataaaa a/d tttaagccaggagagaagg	2446
ALDH1L1	49	intron 12 + 684	tcctggagatagagaggtg c/t gggcagatagccgagaaca	2447
ALDH1L1	50	intron 12 + 767	cgctaggggttcagagcca a/g attatggctggttcccaag	2448
ALDH1L1	51	intron 12 + 1014	tcataggttcagctccctt c/t gcaagccctcaattctaga	2449
ALDH1L1	52	intron 12 + 1359	ctgttctcctcagctcag c/t acagcagaggttggcttag	2450
ALDH1L1	53	intron 12 + 1734	gggttcagagctctctggg g/t tcatgagggccggccagcc	2451
ALDH1L1	54	intron 12 + 1901	ttcagagcttaactgaat g/a acaatagaatagctctgcaa	2452
ALDH1L1	55	intron 12 - 470	ggatagggcacatctcca t/c ctctggaatccagctcca	2453
ALDH1L1	56	intron 12 - 334	aaggcagcctcttgggcca t/c gacccctttgctctgag	2454
ALDH1L1	57	intron 12 - 325	ctcttggccatagccctt t/c gctgtctgcagcaagtggt	2455
ALDH1L1	58	intron 12 - 221	gaagaaagcggagagatc c/g aggaagagagagagagacag	2456
ALDH1L1	59	intron 12 - 4	ccgcttcccttccctctgg t/c caggttggcagatctctagg	2457
ALDH1L1	60	intron 13 + 34	tccaccagctctagcaca t/c gcagatggccagccatat	2458
ALDH1L1	61	intron 13 + 58	aactggccacccatataag a/g aacttcaagagagacacag	2459
ALDH1L1	62	intron 13 + 125	tcacactggtagcttggaa t/c gacactgttatttagcttgc	2460
ALDH1L1	63	intron 13 + 126	cacactgtgctctagaa g/a acactgttatttagcttgc	2461
ALDH1L1	64	intron 13 + 281	acctgcatccagagagctt g/g aggttgcagagagttcagtt	2462
ALDH1L1	65	intron 13 + 299	tcgggttggacagagltca a/g ttccgtgtataga tgcagagct	2463
ALDH1L1	66	intron 14 + 121	catltaaacacacacatcc a/g tgcctctcttagcactctgc	2464
ALDH1L1	67	intron 14 + 167	ggcaggaattgttataaga c/t ttgagacaattgtatttaa	2465
ALDH1L1	68	intron 14 + 205	taattccagtaacactgg a/c tcaatcagatccacgttggg	2466
ALDH1L1	69	intron 14 + 219	cactggatcagtaggtcca c/g ggttggaaacagagataaac	2467
ALDH1L1	70	intron 14 + 2275	tcctatctgtatgcatccg t/c cagactctgcttccagct	2468
ALDH1L1	71	intron 14 + 2431	agaaatgactgagatcaga c/g ctagaaggtccacgcccgg	2469
ALDH1L1	72	intron 14 + 2660	agccaagcattcttgggga c/t accaaaaaccttctctgt	2470
ALDH1L1	73	intron 14 + 2740	aacttcacccctcagctcca t/c gcagcttcccagagagagltca	2471
ALDH1L1	74	intron 14 + 2756	tccatgagcttcccagagag t/c gtcagagggcagagagaggg	2472
ALDH1L1	75	intron 14 + 2805	ccgcacagcagagagaa tggc t/c ccaagagagagagagagaggg	2473
ALDH1L1				2474

[illegible]

遺伝子名	No	存在位置	配列	配列番号
ALDH1L1	118	3' flanking + 1707	cgctggactgctccctagca G/A gcccacttataccagaaca	2520
ALDH1L1	119	3' flanking + 1709	gtggacttcccttagcagc C/T gccattataccagaaca	2521
ALDH1L1	120	3' flanking + 1745	acagaatgicatatcatcagc G/T gcttccgagttcccttctt	2522
ALDH1L1	121	3' flanking + 1843	ctgctcttagccacacagc G/A ggcgcgtcacactctccca	2523
ALDH2	1	intron 3 + 1766	aaatgatgctctcatctgc G/A agccccccttccctctctc	2524
ALDH2	2	intron 8 + 52	gaagatagccctggccact G/C tatgtgcttccagcagtc	2525
ALDH2	3	intron 8 + 69	ccgtgattgagctccagc G/A atctctgcccctccagagtc	2526
ALDH2	4	intron 9 + 5197	gtttctttagacttggctc G/A atttcccatgtcttctgtg	2527
ALDH2	5	intron 11 + 114	ggcttggctcagttcttc C/T ggttcagagtgtagtgcga	2528
ALDH2	6	3' flanking + 411	ggatattcttctgcttc C/T ctctgttgggtaaacagct	2529
ALDH2	7	3' flanking + (432-433)	tcctgtgtgggtaaacagct C/A tttttcagcatcttattt	2530
ALDH2	8	3' flanking + 488	ccaaatagaatgtgcttga G/T gtttcttccatlaattgt	2531
ALDH3A1	1	5' flanking - 758	ctccagcgggtgagggagg G/A ggaagggccttggtagaggg	2532
ALDH3A1	2	5' flanking - 308	agcttggaaagctggagag G/T tccatgccagctgaatcaa	2533
ALDH3A1	3	5' flanking - 294	gaagagcttccatgccagct G/A aatcaatcagcagccctac	2534
ALDH3A1	4	5' flanking - 3	gtccccttggctcttccc G/A ttccagagcccccagttacc	2535
ALDH3A1	5	intron 1 + 2323	actgtcttcttcttctgga C/T ctttggatgtttacaatc	2536
ALDH3A1	6	intron 1 + 2499	ccgalltgcctatctt C/T cgttattgttgcaggaat	2537
ALDH3A1	7	intron 1 + 2943	cagggcttagcagagcagc A/G gggccagggctctgaatga	2538
ALDH3A1	8	intron 5 + 72	cacacatgactgcactcat G/C ctgtggctcactctgagta	2539
ALDH3A1	9	intron 7 + 533	cgcttggggctcttgcgc G/A tccaactctgcttcttcc	2540
ALDH3A1	10	exon 8 + 36	cggagctggagcccccagctc G/C caetalecagaagagagatc	2541
ALDH3A1	11	intron 9 + (40-41)	gcctgctcttcttggccc G/A agggctgggacacatcacc	2542
ALDH3A1	12	intron 9 + 322	gcctgctcttcttggccc agggctgggacacatcacc	2543
ALDH3A1	13	intron 9 + 322	cacagtgtgagatgctctgg G/A acactttagacattggccac	2544
ALDH3A2	1	intron 1 + 39	gggttggggaactggccc C/T cgcgcgcacttctggactg	2545
ALDH3A2	2	intron 3 + 2491	tccgcaagaatattggac T/A gctgagttcttcatcagtt	2546
ALDH3A2	3	intron 3 + 2595	ttctgtacatcaacttga T/A ggtttagggcagcttcttctt	2547
ALDH3A2	4	intron 3 + 2775	taccgtttgccccttagca G/A ggttaattcttcaatact	2548
ALDH3A2	5	intron 3 + 3424	aggcacttctccacacccc G/A cgtctcatgcatcttctccg	2549
ALDH3A2	6	intron 3 + 3676	atgttagagattgctat G/A tttagcgttaggatttattt	2550
ALDH3A2	7	intron 4 + 481	tagaaataaagagttttag G/T ttctcttcttcaaatccgt	2551
ALDH3A2	8	intron 4 + 769	atccttcttataccttgaac G/A tcttgcagcagagcccaaa	2552
ALDH3A2	9	intron 4 + 796	agcagagcccaagccaca A/G ccaggagctcttaccgaa	2553
ALDH3A2	10	intron 5 + 254	attagtgtgcatatattt T/G ttittaaagaatttaaat	2554
ALDH3A2	11	intron 6 + 137	aattcttcttctggtatc C/T gttctttagcttcttctt	2555
ALDH3A2	12	intron 6 + 923	aggctaatgaattgtaag G/A aagggttattcttctttagc	2556
ALDH3A2	13	intron 7 + 331	tgttttctgatttaattc A/A caaggcatcttcaataaca	2557
ALDH3A2	14	intron 8 + 643	tttagaacatgactgcttc G/T ctctccacagtgagagaga	2558
ALDH3A2	15	intron 8 + 666	ctccacatgtagatgact G/A atcagctttttattcttc	2559
ALDH3A2	16	intron 9 + 2129	tgttttctttaaataaaa G/T atttgcatttggatttcaig	2560
ALDH3A2	17	exon 10 + (1894-1895)	tggcttcttcttcaataca C/A tctgttcaataataacala	2561
ALDH3A2	18	3' flanking + 31	gtatttgcacttttttt T/A ctcatlttaaatctttagc	2562
ALDH3A2	19	3' flanking + 106	gtgtgttgggttgggt G/A gtactatagtaaatagatt	2563
ALDH3A2	20	3' flanking + 1630	aaaagcacttggagaacaca A/G ttaatactgtcttaccgtat	2564

遺伝子名	No	存在位置	配列	配列番号
ALDH3B1	1	5' flanking - 1455	CTGCTGTCACACCCACACG A/ agcttgcacacatcccccac	2565
ALDH3B1	2	intron 1 + 464	catgaatgcttgcgaag A/G atcattcttgcattggact	2566
ALDH3B1	3	intron 1 + 2269	aaatgaatcacaacacaa G/C agccctcccccacgggca	2567
ALDH3B1	4	intron 2 + 1349	actggcttgcacaccc G/ agcttgcgcttctcaga	2568
ALDH3B1	5	intron 2 + 1829	tcgcttgcgaagccttc C/G ctcagccctcagctgcaga	2569
ALDH3B1	6	intron 2 + 2046	aaactcagcttgcctcag C/G caggagcagccctgcgcc	2570
ALDH3B1	7	intron 2 + 2939	aagcagcagcagacatgga G/A agatgcagacgaalga	2571
ALDH3B1	8	intron 3 + 7	tgcctcaaaccttgcagc C/ agccagcttgcagccgscag	2572
ALDH3B1	9	intron 4 + 36	gcccccttcgcttacccttc C/G ccgctgcagccctcagggcc	2573
ALDH3B1	10	intron 6 + (116-117)	attctctctctctctct C/Δ agccagcttgcagcagctc	2574
ALDH3B1	11	intron 6 + 263	cagacccctcattatgacc C/G agctgcgcccagcctcttag	2575
ALDH3B1	12	intron 6 + 1298	atagacagcttgcagctcca C/G ccttgcgcttgcagcctc	2576
ALDH3B1	13	intron 6 + 1411	gcaagggctcagacagaggg C/ agcagagcagcagggcttc	2577
ALDH3B1	14	exon 7 + 185	acctgcgttgcgcccagct C/ gtcctatcagccttgcag	2578
ALDH3B1	15	exon 7 + 339	tgcgggcatctgcggcttc G/A agcttgcgcttgcgggccc	2579
ALDH3B1	16	intron 7 + 249	ctagggctccagggctcagc C/A tcttaagatgaactccctc	2580
ALDH3B1	17	intron 7 + 277	atgaactccctccctccac C/ agctatccagagggctgla	2581
ALDH3B1	18	intron 7 + 498	gaccaaggtcggcgattct C/ tgcctccacacagcctcag	2582
ALDH3B1	19	intron 8 + 14	cagcagggctggggcttcggc C/ agcctgcggcagggctcaggg	2583
ALDH3B1	20	intron 8 + 49	caggagccagctggggcag C/ acaagtggtgcagcagaggg	2584
ALDH3B1	21	intron 8 + 111	tcaggacttgggttggttcg A/ ccttgcgcttgccttgc	2585
ALDH3B1	22	intron 8 + 3219	atcctagtggttcagc A/G agcttcagcagcactctgttc	2586
ALDH3B1	23	exon 9 + 33	gctgctccagctcagcag C/ aggggcttcttgcgacgaa	2587
ALDH3B1	24	intron 9 + 946	tccagggcccccagcttcag C/A cttcttgcgcttgcgccc	2588
ALDH3B1	25	intron 9 + 1067	agggctccagagcttgcg C/ cttcttgcgcttgcgccc	2589
ALDH3B1	26	exon 10 + 137	ccgcaatgcgcccagctt C/A aggaatgcgcttgcgcttgc	2590
ALDH3B1	27	exon 10 + 397	cgcctccagcttgcagc G/A aggtgcgagcagcttgcgagac	2591
ALDH3B1	28	exon 10 + 1198	ccttccagcttgcgctt C/ cttcttgcgcttgcgcttgc	2592
ALDH3B1	29	exon 10 + 1475	cagggttgcagcttgcgctt G/A tcttgcgcttgcgcttgc	2593
ALDH3B1	30	3' flanking + 15	ctgcgcaatcacttgcgctt A/G agaatgcgcttgcgcttgc	2594
ALDH3B1	31	3' flanking + 60	caacagagcttgcgacaa G/C ccttgcgcttgcgcttgc	2595
ALDH3B2	1	intron 1 + 98	agggaggggagatgcgctt G/A tgcgcttgcgcttgcgaggg	2596
ALDH3B2	2	intron 1 + 157	atggctgcaggggagcaggg C/G aggggcttgcgcttgcgagag	2597
ALDH3B2	3	intron 1 + 354	ttctgcagacacacagatt C/G agtgcgagggccaccagggctg	2598
ALDH3B2	4	intron 1 + 851	tatgacaggttcacaggg C/G cacttcttgcgcttgcgcttgc	2599
ALDH3B2	5	intron 1 + 894	ctcagcatctgcgcccagag C/G gccttgcgacacgttgccttc	2600
ALDH3B2	6	intron 1 - 463	aaagaaccttcagagctt C/G gtttagtccagagagggagag	2601
ALDH3B2	7	exon 2 + 61	ggcttgcagcttgcgagcag G/A agggcggcggcagcttgcgag	2602
ALDH3B2	8	intron 2 + 8	ggacttgcataagtgaggg A/G tgcgagatgggcttgcgagcag	2603
ALDH3B2	9	intron 2 + 23	ggggcttgcagagtgaggg C/G agcagagggcttgcgagcagct	2604
ALDH3B2	10	intron 2 + (180-181)	ttcacttgcagacactcaca A/ gccccttgcgcttgcgagct	2605
ALDH3B2	10	intron 2 + (180-181)	ttcacttgcagacactcaca gccccttgcgcttgcgagct	2606
ALDH3B2	11	exon 3 + 72	gcttgcagcttgcagagact C/G cagggcttgcgagagagag	2607
ALDH3B2	12	intron 8 + 375	ctgcagacttgcagcttgc C/ gtcgagcttgcagcttgc	2608
ALDH3B2	13	intron 8 + 453	aatcaccctccatgcgaccc G/A acccttgcgagagggcttgc	2609

遺伝子名	No.	存在位置	配列	配列番号
ALDH3B2	14	exon 9 + 33	atcttgagagagagagagagag C/A ggcagcttggagagagag	2610
ALDH3B2	15	exon 10 + 428	aggctctctactacacca C/T cctcccaattccagccctt	2611
ALDH5A1	1	5' flanking - 1303	ggaattatattaaccttact C/A ttactcttctgcatatgt	2612
ALDH5A1	2	5' flanking - 301	gtgaaaggtgacagcagtc C/T ggcagtgatctactgagca	2613
ALDH5A1	3	5' flanking - 221	ggtccctccagagagagag C/T ggcagtgatctactgagca	2614
ALDH5A1	4	5' flanking - 175	aggcggcggcggcggcggc C/G gagaagagagagagagag	2615
ALDH5A1	5	5' flanking - 174	ggcggcggcggcggcggc C/A agaaagagagagagagag	2616
ALDH5A1	6	exon 1 + 106	ggcggcggcggcggcggc C/C ggcggcggcggcggcggc	2617
ALDH5A1	7	intron 1 + 326	cttaacgggggggggggg C/A agaaagagagagagagag	2618
ALDH5A1	8	intron 1 + 551	gtctgacaaaataatttt C/G tttaattagctgagagag	2619
ALDH5A1	9	intron 1 + 555	gtacaaaaataatttttt C/A aattagctgagagagag	2620
ALDH5A1	10	intron 2 + 306	gttttgggtgttttttttt C/A aactgtttttgtacattt	2621
ALDH5A1	11	exon 3 + 107	ggagagattatccacacc C/T ggcagagagagagagag	2622
ALDH5A1	12	intron 3 + 201	gtgtgtgtgtgtgtgtgt C/T atccatttctaatgcttgc	2623
ALDH5A1	13	exon 4 + 42	atccacggagagagagag C/T ggcggcggcggcggcggc	2624
ALDH5A1	14	intron 4 + 2306	atcgtgtgtgtgtgtgtgt C/T ggcggcggcggcggcggc	2625
ALDH5A1	15	intron 4 + (334-2346)	tataaaccttggctcaca C/T -13 acttattatcttataagta	2626
ALDH5A1	16	intron 4 + 2456	tataagcttatttttttt C/A acttattatcttataagta	2627
ALDH5A1	17	intron 4 + 2501	ttgtgttttttttttttt C/G tctttaaagagagagagag	2628
ALDH5A1	18	intron 4 - (64-46)	atctattatttttttttt C/C cactgttttctgtttctct	2629
ALDH5A1	19	intron 4 - 27	ttcatttggtaaaatgttg C/C cactgttttctgtttctct	2630
ALDH5A1	20	intron 5 + (4621-4624)	tttgaatagaataactta C/T -13 tttgtttaaataatagag	2631
ALDH5A1	21	intron 5 + (4677-4678)	accagagagagagagag C/G acccagagagagagagag	2632
ALDH5A1	21	intron 5 + (4677-4678)	accagagagagagagag C/G acccagagagagagagag	2633
ALDH5A1	22	intron 7 + (432-443)	aaaaatagtgtaaaagg C/A -10-12 tgaacacacacacacac	2634
ALDH5A1	23	intron 7 + (3243-3244)	catctctgtgtgtgtgt C/T -13 ccccaacacacacacac	2635
ALDH5A1	24	intron 7 + 4987	tttttgaacacacacacac C/A -13 tgaacacacacacacac	2636
ALDH5A1	25	intron 8 + 2717	gataccttggagagagag C/T ggtgtgtgtgtgtgtgtgt	2637
ALDH5A1	26	3' flanking + 2711	catgtgtgtgtgtgtgtgt C/A agcagagagagagagag	2638
ALDH5A1	27	3' flanking + 2777	gtccatgtgtgtgtgtgt C/A aatgtgtgtgtgtgtgtgt	2639
ALDH6A1	1	5' flanking - 1303	ctctaacagagagagag C/C aagagagagagagagagag	2640
ALDH6A1	2	5' flanking - (1273-1270)	ggagataccacacacac C/T -13 tgaacacacacacacac	2641
ALDH6A1	3	intron 1 + 437	tgccatttctctctctct C/T cctacttctctctctctct	2642
ALDH6A1	4	intron 1 + 835	gttccacacacacacac C/T -13 tgaacacacacacacac	2643
ALDH6A1	5	intron 1 + 1294	atatcttctctctctct C/T gttctgtgtgtgtgtgtgt	2644
ALDH6A1	6	intron 1 + 1447	gagtcattgagagagag C/G aagatatttctctctctct	2645
ALDH6A1	7	intron 1 + 2536	agcttgcctctctctct C/T gttgagagagagagagag	2646
ALDH6A1	8	intron 1 + 2703	cagagagagagagag C/T aagagagagagagagagag	2647
ALDH6A1	9	intron 1 + 2802	gcacaaagcctctctct C/T tcttgaagagagagagag	2648
ALDH6A1	10	intron 2 + 2333	gttgtgtgtgtgtgt C/A ttttttgcagagagagag	2649
ALDH6A1	11	intron 4 + 138	gacttctctctctct C/G tctctctctctctctct	2650
ALDH6A1	12	intron 4 + 200	aagagagagagagag C/T aatcttctctctctctct	2651
ALDH6A1	13	intron 5 + 291	ggcagagagagagag C/A cctctctctctctctct	2652
ALDH6A1	14	intron 7 + 209	ccccgggtcagagag C/A ctcctcagagagagagag	2653
ALDH6A1	15	intron 8 + 287	gcctctctctctct C/T acaggtgtgtgtgtgtgt	2654

遺伝子名	No.	存在位置	配列	配列番号
ALDH6A1	16	intron 9 + 877	gatacaaaataaacaata C/A agacataatttggagagcaaa	2655
ALDH6A1	17	intron 9 + 885	aataaacaatacaacata T/G ttggagagcaaaagagtagaa	2656
ALDH6A1	18	intron 11 + 40	tttgccttctcttaaga A/C atttcttaagatalicag	2657
ALDH6A1	19	3' flanking + 520	cttgaagattttcttttag C/T cctctttatccacaatac	2658
ALDH6A1	20	3' flanking + 1026	cgttgttcagccttgctt T/C gaactctgaacctcagctaa	2659
ALDH6A1	21	3' flanking + 1035	cagcttgctcgaacctt C/C acctcagtgatccgcttc	2660
ALDH8A1	1	5' flanking - (837-836)	gcgaacatggttaataat (A/T) tcatccaatgtgtcttc	2661
ALDH8A1	1	5' flanking - (837-836)	gcgaacatggttaataat tcatccaatgtgtcttc	2662
ALDH8A1	2	5' flanking - 702	gggactgaagcccttgctt C/T agtatcacatgtttttg	2663
ALDH8A1	3	5' flanking - 642	ggcacttagaagaatgta G/A cagcactgtggcccggtt	2664
ALDH8A1	4	5' flanking - 84	atctctcagaagctcag G/T tgcctccacatctacga	2665
ALDH8A1	5	intron 1 + 5437	gcatttgtaaatggagcc T/C gttcttltgttctatagta	2666
ALDH8A1	6	intron 1 + (5836-5855)	gtgagaatccacttaaaaa (CAAA) 4-5 ataggtatgtgagagaccig	2667
ALDH8A1	7	exon 3 + 146	cactacaggtggggccccc C/T gtggagtcgttgatctctc	2668
ALDH8A1	8	intron 4 + 1033	agatcttttgcctagtac C/T ccagggcagggcaggatg	2669
ALDH8A1	9	intron 4 + 1037	cttttgctatgcaccca C/T ggcagggcagggagctcttc	2670
ALDH8A1	10	intron 4 + 1662	tcctctcgaagaccagac G/A tctgaatagatagatga	2671
ALDH8A1	11	intron 4 + 2046	agcttgggcatcttaacag A/C ctggacagataaactctt	2672
ALDH8A1	12	intron 6 + 1146	ttttcagaatgcagagact C/G cctgtctctctctcttg	2673
ALDH8A1	13	intron 6 + 1744	ttctctctctctctt C/T ttcttttttaacatgact	2674
ALDH8A1	14	intron 6 + 3802	tgagtgaaatctaacit A/T cigtatttagcttataa	2675
ALDH8A1	15	exon 7 + (1089-1098)	tacagtgagactgtcttt (A) 9-10 tctgcacaaacaaaataa	2676
ALDH8A1	16	3' flanking + 848	cicagtgagctcccttcac T/C ttaatcatttagtagaaa	2677
ALDH9A1	1	exon 1 + 121	actgtgggctatggccgg G/A tggtaggagaaatgtgtgt	2678
ALDH9A1	2	intron 1 + 67	ccggatctccggcacc C/G cgtttctctgtctcag	2679
ALDH9A1	3	intron 1 + 103	tgcagcttgacttgacac A/G agacagtagacagtggaagt	2680
ALDH9A1	4	intron 1 + 1818	gaattttgaaaaaaaaa A/A tcttctttaggttgcct	2681
ALDH9A1	5	intron 2 + 5691	tcaggacaggaagtaga G/A gtttcaatcttaaatlct	2682
ALDH9A1	6	intron 2 + 6398	atcaaacactgtctgat T/G atctgtctgaacctgcct	2683
ALDH9A1	7	intron 2 + 9677	ataccctgaatttggctt A/G ttcttttttttcttgcct	2684
ALDH9A1	8	intron 2 + 9991	gggagaagtagggaccctac C/T ctggcttctaaatcttcat	2685
ALDH9A1	9	intron 2 + 10198	ttgtcagaacactttgat A/G atcttaccatctatatacag	2686
ALDH9A1	10	intron 2 + 10256	ttagtagaacttttttt T/A gtaaggatggagaataatag	2687
ALDH9A1	11	intron 2 + 11382	catattcaatcttttatgt T/C ctttagaccanaaagaacca	2688
ALDH9A1	12	intron 2 + 11455	taaccctttagctcatat C/T agaccatctatgaattctt	2689
ALDH9A1	13	intron 2 + 12044	attaaagtgaagcttatt C/T tagtttaaaaattgagcag	2690
ALDH9A1	14	intron 3 + 334	ctatttaacactttttt T/A gacagtataaagtttcca	2691
ALDH9A1	15	intron 3 + 368	gtttcaaatgatatgt G/A adggttgtagggccttagga	2692
ALDH9A1	16	intron 4 + 191	ccctcagaagctttagtt T/A aggttgatcacatcatctc	2693
ALDH9A1	17	intron 4 + 557	tgaataaatgttaattgta A/G aaagcatctactgttaggaca	2694
ALDH9A1	18	intron 5 + 830	agttcaaatgattttagt G/C ttcaaggccttagttaccta	2695
ALDH9A1	19	intron 5 + 838	attgattttgagctcagg C/T ctatgtgacttaagatgcaa	2696
ALDH9A1	20	intron 6 + 120	agaagaattgacaaaatagt A/G caaagaatcccatgacct	2697
ALDH9A1	21	intron 6 + 2569	attaaatctctttaaata T/C ttttttgggagagagcac	2698
ALDH9A1	22	intron 8 + 1414	ccgatctcaaaaatagac T/G gggggtgagtgatgcacactg	2699

遗传子名	No	存在位置	配列	配列番号
ADH9A1	23	intron 9 + 554	aaagttcacattttttttt /Δ ataacttcattggtcaagagc	27000
ADH9A1	24	intron 9 + 2170	taalecacacattttttttt /Δ ctctacagagacatccacgc	2701
ADH9A1	25	exon 11 + 587	aaacacaaagacaagaaaa A/Δ cttgtctctttataagttc	2702
ADH1	1	(5' flanking region -55)	atcatctgtgagactggaat C/Δ aggtgtttatcaagcaaaa	2703
ADH1	2	(intron 1 268)	acatttgcgttaagcaata A/G ttattccaagctaatcag	2704
ADH1	3	(intron 3 443)	aalaga g/c gctacatgctat G/A gcgaataagcagaccittt	2705
ADH1	4	(intron 6 56)	tacaacttgaagatgcaat /G aggtcgcaaatatattgtt	2706
ADH1	5	(intron 8 74)	gtctacagaaaataaaaag G/A tggaaaggaagaaaatita	2707
ADH2	1	(intron 2 340)	ctatttttaaacctgcat /C ctctacaagacttaaatat	2708
ADH2	2	(intron 3 91)	aagcaaa tgaagagagaaaaag /G gcttcacagaagctaccgc	2709
ADH2	3	(intron 3 205)	atgatattacacctcaacc A/G ttatctaccagatctact	2710
ADH2	4	(intron 7 108)	acallgacagaagcaagt /C tgaacacaaatcaaaaata	2711
ADH2	5	(intron 3 1721 1723)	actgcataaaatttaaaa GAA/Δ ctgtgtttatctctccag	2712
ADH2	6	(3' untranslated region 2305 2306)	gttaagtttccaccctc AG/Δ ggaagagattgtcatitga	2713
ADH3	1	(5' flanking region -254)	tgaagaaagaaagacagaa C/G ttgagagagagagagagag	2714
ADH3	2	(intron 2 355)	taagcatctctatatat A/G caagacaaaattttaagat	2715
ADH3	3	(intron 3 32)	acactggaagacalgcctt G/A gttccactacacagaatag	2716
ADH3	4	(intron 4 6)	cgccttaaaaatgagtaag C/Δ ttctgagctgtttcttcac	2717
ADH3	5	(coding region 453 Thr 151 Thr)	agcacttctccagctac A/G gttgtgga tgaagaatgcagt	2718
ADH3	6	(coding region 815 Arg 272 Gln)	ttcgtttgaagtcacgtgc A/G gcttgcacacatggtatgat	2719
ADH4	1	(5' flanking region -482)	acagccaaagaccacagacc A/G tcaagctctggttcaagact	2720
ADH4	2	(5' flanking region -437)	catcaggtggacacaaaaga G/A tascctcttaccagctacia	2721
ADH4	3	(5' flanking region -234)	actcaagcatatgtgcacc A/G agtaca tgaanaaatltgt	2722
ADH4	4	(5' untranslated region -381)	ggaagttaaatggggatt C/G tggaggtagaanaatttcctt	2723
ADH4	5	(5' untranslated region -263)	ttcaataaaagaaaadaaa /A ttaaaaatcttggagctca	2724
ADH4	6	(intron 1 707)	ttattttgaatttaaaaat A/G taattttagagctagaanaaa	2725
ADH4	7	(intron 5 619)	tcaaaagggactcacat /C ggaatctcaacctgcttatt	2726
ADH4	8	(intron 5 1755)	tttacacacaaatttacia /C taataaaaattttaaaaaal	2727
ADH4	9	(intron 5 3425)	actgaactctggagaata /C altaagaatcactacgaaca	2728
ADH4	10	(intron 1 1181 1189)	ggaatacttaatacacctg 019-11 caagaaataaaaatgtaat	2729
ADH4	11	(intron 5 2828)	tccagtcgaagtcacttaa A/Δ ttccagagattgttcttc	2730
ADH4	12	(intron 7 151)	tttgttgtcagttttttt /Δ ctctacagcttttaaatctt	2731
ADH5	1	(5' flanking region -115)	taactctgttaagtttaac G/A g/a ggaagccctttccgcaca	2732
ADH5	2	(5' flanking region -114)	aacgcgtgaagtttac g/a G/A ggaagccctttccgcacaaa	2733
ADH6	1	(intron 3 249)	tgaactgcacttgaagta C/A aaatagacacaaaattatg	2734
ADH6	2	(intron 6 1072)	taacctctactgtatgc A/G tcactttctcaacagcagct	2735
ADH6	3	(coding region 885 Val 295 Val)	gtctgtatggtttggagt G/A ttgcctccacagtttcaact	2736
ADH6	4	(intron 7 1292)	gttgaagaactctccctact C/A ccgtctgtgtgtcttgaatt	2737
ADH6	5	(intron 7 1616)	ctatcagaataatccga /C agaacactaagcagattacg	2738
ADH7	1	(5' flanking region -528)	ttctcaaacacagaagttt /C acttaactttctatacttaa	2739
ADH7	2	(intron 1 361)	tcagtagcagtgctgcact C/Δ cctcctagatgttcaatggga	2740
ADH7	3	(intron 3 183)	aacctcaacttttgaagcc A/G aaccttaccgtgtttataaa	2741
ADH7	4	(intron 4 76)	tgaattgaatttaatttac G/A tgaatllgaltatcaaca	2742
ADH7	5	(intron 6 615)	tggcagagctaaagagact /A ggaanaatagaataaagcca	2743
ADH7	6	(intron 8 532)	aggtctaacacataaccaca /C ttgata tccattgtactat	2744

遺伝子名	No.	存在位置	配列	配列番号
ADH7	7	(intron 8 651)	gcctctattatttcagla c/a gacacaaatttcctattt	2745
ADH7	8	(intron 8 727)	tteagatccctgaagccag c/a tattattttaccatttta	2746
ADH7	9	(intron 8 1207)	tcctccatttggtcagcc i/c acagatcalatattaga	2747
ADH7	10	(intron 8 1691)	tcctctatttcattgccac c/a ctaattgctttaaltcagtc	2748
ADH7	11	(3' untranslated region 1364)	aattacattttagagcta i/c aattgatacttttagaaaa	2749
ADH7	12	(3' untranslated region 1498)	gataatgaatgatctctc i/c agaglaaattoacttca	2750
ADH7	13	(3' untranslated region 1584)	aaacattttagagttaa c/g ttgattacattttgaatc	2751
ADH7	14	(3' untranslated region 1818)	aataaacaalagagctaga a/g tcaatatacatatctca	2752
ADH7	15	(3' flanking region 865)	tacataaagaataataac c/t aagaagaalaaacacattt	2753
HEP27	1	(5' flanking region -191)	tcagactctgtcttact a/t aagtttgttaalgaccaa	2754
HEP27	2	(5' untranslated region -163)	gaaccatcaattccatca c/a atttctgacttttaagag	2755
HEP27	3	(intron 1 1941)	aaatttaccctaacagctc c/c acicctctccacttctctt	2756
HEP27	4	(coding region 289 (Ala 97 'hr))	ttgtgtccacagtgaggag c/a ctgaagaccggagagctg	2757
HEP27	5	(intron 4 1070)	tgctcagttcacagatca i/c gactcttttctgaaactg	2758
HEP27	6	(3' flanking region 362)	ggcttctgtgtctctcatt a/g ctgaacttggccctctcctg	2759
UGT1A1	1	(5' flanking region -1337)	ctcttctgtttagactca a/c tcaatcagacaaatttcccc	2760
UGT1A1	2	(coding region 211 (Gly 71Arg))	ccctgttctacatcagac c/a gacattttacaccttgaag	2761
UGT1A1	3	(intron 1 2925)	gcatttggagaaggaanac i/g aatagaagcctaactaaa	2762
UGT1A1	4	(intron 1 3442)	agacttggcttttccagat c/t agcttcagtgtaagatggg	2763
UGT1A1	5	(intron 1 3512)	taagtaaacatttaccac c/t gctcagaagaagaactlga	2764
UGT1A1	6	(intron 1 3665)	tcctctacaaccacaaa i/c ccacatagctgttggggagg	2765
UGT1A1	7	(intron 2 15)	caacagtaagaagattca i/c accatggctcatactatt	2766
UGT1A1	8	(intron 4 574)	agattaaactccaattia c/t alaaaagtgcataatag	2767
UGT1A1	9	(3' flanking region 125)	tatagaggttaccacaca c/t gcttctattgggtgtacatg	2768
UGT1A1	1	(5' flanking region -1602)	ataacatctcttcagagaa a/c cttaatggaaataactca	2769
UGT1A1	2	(5' flanking region -1480)	tacagattatcttgggat c/c ggaagcttgaagaagacat	2770
UGT1A1	3	(5' flanking region -1406)	atttcagagattattaac a/t tgaaggagatcctctg c/t tt	2771
UGT1A1	4	(5' flanking region -1388)	acataaagaagatcactcig c/t ttatcagacataatgat	2772
UGT1A1	5	(5' flanking region -935)	aaattalcaatctcttgg c/a cagtgattcttttcttctg	2773
UGT1A1	6	(intron 1 535)	catleaicaagctatttat c/t calctaaagcttalliaalt	2774
UGT1A1	7	(intron 1 642)	tatatatcatglttatoc a/c ttatcacacataattctctca	2775
UGT1A1	8	(intron 1 1448)	aggctcttaccagcaatc c/t acatagcagctctgctgg	2776
UGT1A1	9	(intron 1 2000)	gacacattagcttcttct a/g cagatctctgtctctaaaca	2777
UGT1A1	10	(intron 1 3118)	cttaaatctttaaagaa i/g cattgcaacaaatttataic	2778
UGT1A1	11	(intron 1 3191)	ataatagacacactccca a/t gttacttctctcagctaga	2779
UGT1A1	12	(intron 1 3770)	atccagagataatttact c/t catttaagagtagatca	2780
UGT1A1	13	(intron 1 4584)	tgattgttagaacttctta a/c aaactctctagatcatcc	2781
UGT1A1	14	(intron 1 4854)	lactctgcatgttgaala c/a cctatcacttctgtctctcc	2782
UGT1A1	15	(intron 1 -19146)	ctgttaaaattctcatcaa c/t ggcacatagtttaaaataa	2783
UGT1A1	16	(intron 1 -19085)	tagacaagacccttttca a/c aacagatttagaataatggt	2784
UGT1A1	17	(intron 1 -18346)	atggcaatattttagaat c/a ttaacttcccaataatgata	2785
UGT1A1	18	(intron 1 -18218)	tatcatatttttaactia i/g agatagactagcccttaatt	2786
UGT1A1	19	(intron 1 -17937)	ctcttaataattgagctca c/t catacttattcagactalc	2787
UGT1A1	20	(intron 1 -12585)	ttccacagaggaagatca a/g cagaggaaatttttctct	2788
UGT1A1	21	(intron 1 -11430)	aacaagggtttatttctta c/g aattcttea tggcttagagctc	2789

遺伝子名	No.	存在位置	配列	配列番号
UG12A1	22	(intron 1 -10761)	tttaaaatagcatgattt t/g caactttttaaactatac	2790
UG12A1	23	(intron 1 -381)	aaactccctctctc c/t ttccagcccccactctac	2791
UG12A1	24	(intron 1 -329)	ttctctctctctc a/g tctctctctctctc	2792
UG12A1	25	(intron 1 -41)	tttctccagcaaac a/t aagtaatttcccatcca	2793
UG12A1	26	(intron 2 263)	caacttgatagctt g/c gggacagaaacacatcat	2794
UG12A1	27	(intron 2 454)	agaaagccatgaaatag c/c cagggtttttaggtttaat	2795
UG12A1	28	(intron 2 554)	aaaacttttttagt t/a t agttagttttaggtttctga	2796
UG12A1	29	(intron 2 1113)	ctccaggcagctctag t/a t gtttattatagaataaat	2797
UG12A1	30	coding region 922 (G1308A/g)	gtttctgtgtttctt c/g a gataatgatacaaacctt	2798
UG12A1	31	(intron 3 -217)	aagcttgaagtaata a/t c caaacataatatact	2799
UG12A1	32	(intron 3 -194)	aaactaatatactt g/c a tagactattagacaagact	2800
UG12A1	33	coding region 1171 (Val391Ile)	acggatccctatgctt g/a t tcccatgtttgctgacg	2801
UG12A1	34	(intron 5 1546)	tttttaaatccagaact a/g g/a ttatgtgtattcttcaaa	2802
UG12A1	35	(intron 5 1547)	tttlaaaatccaac a/g g/a ttatgtgtattcttcaaa	2803
UG12A1	36	(intron 5 2505)	taattgacttttaata c/a t acatgttgtataaactata	2804
UG12A1	37	(intron 5 2539)	tagacttatacaagttt a/g gttgtcagcaatttgttca	2805
UG12A1	38	(intron 5 4009)	gaatccagctggaactt c/a t tccagacacaaacaaat	2806
UG12A1	39	(intron 5 4311)	atcacacacgtctt c/a t tccacatacagatgtt	2807
UG12A1	40	(intron 5 4516)	actttttatgtctactt g/c a tcatctgttgttaagcata	2808
UG12A1	41	(intron 5 4717)	tccaaatataatctt c/a a ccttaactatgaccttaaac	2809
UG12A1	42	coding region 1524 (Gln508Gln)	gctaatttttgtctata a/g g tttgttgttttctctca	2810
UG12A1	43	3' untranslated region 1683	aaggagtttcaaaaac a/c t tccatctgttttccaaa	2811
UG12A1	44	3' flanking region 685	aatttagaataattt a/c t tttlaaaatttttagtca	2812
UG12A1	45	(intron 1 -18967) (-18965)	ctccatgattgattt a/t t/g ggttctggtgttactgt	2813
UG12A1	46	(intron 1 -18862) (-18803)	aatacatttccctt c/a t tcttctggtgttactgt	2814
UG12A1	47	(intron 1 -17483) (-17447)	aaacttagaacctt c/a t tcttctggtgttactgt	2815
UG12A1	48	(intron 1 -10860)	atcaatgcaactttttt t/g gtaatggcagattagaaca	2816
UG12A1	49	(intron 2 528 538)	ctgttagaacaattgtt a/g t ttttttagtttgaat/taag	2817
UG12A1	50	(intron 2 1514 1533)	tgtgtgtgtgtgtgtt g/t g-11 ttttttaagaataatatac	2818
UG12A1	51	(intron 5 916 917)	acttataatataat a/t t gtcataataatagctttagt	2819
UG12A1	52	(intron 5 1163)	caatattatatactttt t/g c tccatcttactctgttcc	2820
UG12A1	53	(intron 5 3819 3838)	agacagacagacacaa c/a c tcaacataataaactct	2821
UG12A1	54	(intron 5 4785)	tatcttcaatgaataaaa a/t caaaattgtctaatcttctg	2822
UG12B15	1	(5' flanking region -277)	ccgaacagcagcagctt c/a acttccactgttttcaaca	2823
UG12B15	2	(intron 1 670)	catcaagaataataggcc a/t aattaggagagacacata	2824
UG12B15	3	(intron 1 775)	ctaatatataaactt a/c aatgaaccaagacata	2825
UG12B15	4	(intron 2 2183)	cagagtttccatgttggc c/t agcttggcttgaactctg	2826
UG12B15	5	(intron 2 2430)	tatttcaagaataagact c/g t tcccaaaagtatcaag	2827
UG12B15	6	(intron 2 4806)	aaaaatttccatagctt c/t c/g c/g tttctatcttagat	2828
UG12B15	7	(intron 3 129)	ctaatatctcagactt t/c tcaa g/a caaaactatag	2829
UG12B15	8	(intron 3 424)	caatacaataacagat t/c aaaaaacttgaatgcat	2830
UG12B15	9	(intron 3 493)	ggc t/a gtttttcttccatg c/t attgaatagatctatttag	2831
UG12B15	10	(intron 3 905)	ggcctctgataatgctat c/a caagtttttcttgaacac	2832
UG12B15	11	(intron 3 1036)	tcaatgactttgtgtgtac t/c agacatgataatgactgct	2833
UG12B15	12	(intron 3 1544)	aataaatalataggttatt c/g taatttgcctcttttttatt	2834

遺伝子名	No	存在位置	配列	配列番号
UGT2B15	13	(intron 3 5550)	gctgtgaatcaatgctg /c/ tctgttgacacgtaccca	2835
UGT2B15	14	(intron 3 5720)	tttttaagaattatttt /c/ tgggaattttccctcaggg	2836
UGT2B15	15	(intron 4 134)	atcaaatlaactactttat /g/ ttattttccagcttagta	2837
UGT2B15	16	(intron 5 6627)	ttttatgttgatatttt /c/ attttcttcagctataaa	2838
UGT2B15	17	(coding region 1568 (lys23hr))	tttccaaacttccaaa /c/ azaaagaagaagaagaag	2839
UGT2B15	18	(3' untranslated region 1761)	ggatttaacgacttttag /c/ tgaattatttctgct a/t at	2840
UGT2B15	19	(3' untranslated region 1779)	ag c/t tgaattatttctgct a/t atgatttttgaactgaaa	2841
UGT2B15	20	(intron 2 1980 1981)	agaagagtcagcaataag /c/ acaagaagaataaagacagct	2842
UGT2B15	20	(intron 2 1980 1981)	agaagagtcagcaataag /c/ acaagaagaataaagacagct	2843
UGT2B15	21	(intron 3 505 618)	ctagccagtagattttag /c/ ctgtctctctctctgactt	2844
UGT2B15	22	(3' untranslated region 1957 1968)	agataatttaaaaaag /c/ tacaacttttttttaaac	2845
UGT2B15	22	(3' untranslated region 1957 1968)	agataatttaaaaaag /c/ tacaacttttttttaaac	2846
UGT2B15	22	(3' untranslated region 1957 1968)	agataatttaaaaaag /c/ tacaacttttttttaaac	2847
UGT2B15	22	(3' untranslated region 1957 1968)	agataatttaaaaaag /c/ tacaacttttttttaaac	2848
UGT2B15	22	(3' untranslated region 1957 1968)	agataatttaaaaaag /c/ tacaacttttttttaaac	2849
UGT2B15	22	(3' untranslated region 1957 1968)	agataatttaaaaaag /c/ tacaacttttttttaaac	2850
UGT2B15	22	(3' untranslated region 1957 1968)	agataatttaaaaaag /c/ tacaacttttttttaaac	2851
UGT2B15	22	(3' untranslated region 1957 1968)	agataatttaaaaaag /c/ tacaacttttttttaaac	2852
UGT2B15	22	(3' untranslated region 1957 1968)	agataatttaaaaaag /c/ tacaacttttttttaaac	2853
UGT2B15	22	(3' untranslated region 1957 1968)	agataatttaaaaaag /c/ tacaacttttttttaaac	2854
UGT2B15	22	(3' untranslated region 1957 1968)	agataatttaaaaaag /c/ tacaacttttttttaaac	2855
UGT2B15	22	(3' untranslated region 1957 1968)	agataatttaaaaaag /c/ tacaacttttttttaaac	2856
UGT2B15	22	(3' untranslated region 1957 1968)	agataatttaaaaaag /c/ tacaacttttttttaaac	2857
UGT2B15	22	(3' untranslated region 1957 1968)	agataatttaaaaaag /c/ tacaacttttttttaaac	2858
UGT2B15	22	(3' untranslated region 1957 1968)	agataatttaaaaaag /c/ tacaacttttttttaaac	2859
UGT2B15	22	(3' untranslated region 1957 1968)	agataatttaaaaaag /c/ tacaacttttttttaaac	2860
UGT2B15	22	(3' untranslated region 1957 1968)	agataatttaaaaaag /c/ tacaacttttttttaaac	2861
UGT2B15	22	(3' untranslated region 1957 1968)	agataatttaaaaaag /c/ tacaacttttttttaaac	2862
UGT2B15	22	(3' untranslated region 1957 1968)	agataatttaaaaaag /c/ tacaacttttttttaaac	2863
UGT2B15	22	(3' untranslated region 1957 1968)	agataatttaaaaaag /c/ tacaacttttttttaaac	2864
UGT2B15	22	(3' untranslated region 1957 1968)	agataatttaaaaaag /c/ tacaacttttttttaaac	2865
UGT2B15	22	(3' untranslated region 1957 1968)	agataatttaaaaaag /c/ tacaacttttttttaaac	2866
UGT2B15	22	(3' untranslated region 1957 1968)	agataatttaaaaaag /c/ tacaacttttttttaaac	2867
UGT2B15	22	(3' untranslated region 1957 1968)	agataatttaaaaaag /c/ tacaacttttttttaaac	2868
UGT2B15	22	(3' untranslated region 1957 1968)	agataatttaaaaaag /c/ tacaacttttttttaaac	2869
UGT2B15	22	(3' untranslated region 1957 1968)	agataatttaaaaaag /c/ tacaacttttttttaaac	2870
UGT2B15	22	(3' untranslated region 1957 1968)	agataatttaaaaaag /c/ tacaacttttttttaaac	2871
UGT2B15	22	(3' untranslated region 1957 1968)	agataatttaaaaaag /c/ tacaacttttttttaaac	2872
UGT2B15	22	(3' untranslated region 1957 1968)	agataatttaaaaaag /c/ tacaacttttttttaaac	2873
UGT2B15	22	(3' untranslated region 1957 1968)	agataatttaaaaaag /c/ tacaacttttttttaaac	2874
UGT2B15	22	(3' untranslated region 1957 1968)	agataatttaaaaaag /c/ tacaacttttttttaaac	2875
UGT2B15	22	(3' untranslated region 1957 1968)	agataatttaaaaaag /c/ tacaacttttttttaaac	2876
UGT2B15	22	(3' untranslated region 1957 1968)	agataatttaaaaaag /c/ tacaacttttttttaaac	2877
UGT2B15	22	(3' untranslated region 1957 1968)	agataatttaaaaaag /c/ tacaacttttttttaaac	2878
UGT2B15	22	(3' untranslated region 1957 1968)	agataatttaaaaaag /c/ tacaacttttttttaaac	2879

遺伝子名	No.	存在位置	配列	配列番号
GS1M1	15	(intron 5 140)	actatcagcaatattctcca C/T gactcacaatgacatgcaac	2880
GS1M1	16	(intron 5 577)	ctgccacccatagaaaga A/G ctttctactttccctgagct	2881
GS1M1	17	(intron 5 645)	actctctgagatccaaagcc T/A gccagatctctggagctcc	2882
GS1M1	18	(coding region 519 (Asn 173 Lys))	caccatattatgaaccac C/C tctctgacaccttcccaaa	2883
GS1M1	19	(coding region 528 (Asp 176 Asp))	tttagcccaagatctcttga C/T gcttcccaaatctgaagaa	2884
GS1M1	20	(intron 7 2421)	cagcaccctgtagaattctt C/A taagttagctatttactct	2885
GS1M1	21	(3' flanking region 42)	atttctcttggcaatctac C/T cacactgctctgtctctct	2886
GS1M2	1	(intron 1 7)	agaacatccgacggtagac C/T agagctccctggagctgag	2887
GS1M2	2	(intron 1 45)	agagcagagggagcttggag C/T agagagagtgagacacg	2888
GS1M2	3	(intron 3 70)	gactgcatctctctccca C/C cttagagagtgtagatcag	2889
GS1M2	4	(intron 3 224)	agcagcccttggctctctt T/G tggccctgcatataggaag	2890
GS1M2	5	(intron 5 100)	ttgattctcttggtaggt C/A ttggtcttggctgacttaag	2891
GS1M2	6	(intron 5 341)	tcccttggtaggttctag T/G ctggctggcttcagagatga	2892
GS1M2	7	(intron 5 696)	accttagctagacacag C/T gctgatttggcatlltaca	2893
GS1M2	8	(intron 5 723)	tttgcatlltacaacttt A/G ctgagcagagaaagttctcc	2894
GS1M2	9	(3' untranslated region 1006)	ctcagcccgagctgtccc G/A tcttgatgagagagcagc	2895
GS1M2	10	(3' flanking region 139)	tttctctggagcatagaa C/T gcttgagaaattctgtctcc	2896
GS1M2	1	(5' flanking region -546)	agcagggccaccagcgc C/A gctcgaagccctgagcc	2897
GS1M2	2	(5' flanking region -321)	tgctgagcagccccc C/T gaggagtcacaaagggcag	2898
GS1M2	3	(intron 1 2890)	aaaatctctcacaaccca G/A gccagctcttcttggagga	2899
GS1M2	4	(intron 1 2895)	ctgcatcaaacacagccac G/A ctctgttggagagacacca	2900
GS1M2	5	(intron 2 255)	ttctcaacacgtgtctca A/G agcccttggcaactagtt	2901
GS1M2	6	(intron 2 1560)	cacacatglttaagccctg G/C agggcgagagttaaacaca	2902
GS1M2	7	(coding region 94 (Lys 32 Glu))	cttgaagagctgagctac G/A agacggagccatcaatctc	2903
GS1M2	8	(intron 4 297)	agaagagagatgtctctg C/T ctgtccctctggctcagag	2904
GS1M2	9	(intron 6 94)	tatctgaacacacctctcc G/A ctgcttggagcttgcagtt	2905
GS1M2	1	(intron 1 269)	ctcccgagctccagaaa C/G ttctcttctgctgcagct	2906
GS1M2	2	(intron 2 134)	ccccggcctctctctgtt C/T cccgcctctccgctcagcc	2907
GS1M2	3	(intron 5 438)	gtgtgtctcgttgcgtctgc G/A gtgtgtctcgttgcgtctgc	2908
GS1M2	4	(intron 6 162)	ccccctgtgagctccctag C/T ccccttggcttgcagatct	2909
GS1M1	1	(5' flanking region -103)	taagaatgtccagagct C/T gtgcccacatggagcaca	2910
GS1M1	1	(promoter region -1879)	ttataaatgtatttcaat T/G aaaccaactgttaattct	2911
GS1M1	2	(promoter region -508)	ctgagaccttgacagagag G/C gacatctgtacaaagcaat	2912
GS1M1	3	(promoter region -314)	cttgagatttttaacttct G/A cgaagtttttaaaacaact	2913
GS1M1	4	(promoter region -131)	ctcagcagggatggattact G/C taggcaggttaaatcagctga	2914
GS1M1	5	(intron 1b 36)	agaagaaggagaccatgca A/G aggatggcagcagcagagag	2915
GS1M1	6	(intron 1c 456)	ccccctggagacgttctcac C/T tatccccacttcccagctc	2916
GS1M1	7	(intron 1c 719)	ggcccaagcatctctctat A/G gccacagagcttccagtgag	2917
GS1M1	8	(intron 1c 985)	cgagtaaatttttctaccc G/C ttatgttttagagtgatctct	2918
GS1M1	9	(intron 1c 1428)	gtaaagggaaaggcgttcc T/A caactgagagtggaagatc	2919
GS1M1	10	(intron 1c 2914)	ctctaaggttgctgtctcaga T/G gcttggcttgcctcagctctc	2920
GS1M1	11	(intron 1c 4274)	attgtagatgatttaacaag G/T tgaagaagtagtgcacata	2921
GS1M1	12	(intron 1c 4276)	tgtatagattacaagg G/T atgaagtagtgcacataat	2922
GS1M1	13	(intron 1c 4767)	gcttctctctcagacatt C/T ccaattatcttccattcc	2923
GS1M1	14	(intron 2 2379)	tttccaatttcaattatata G/C tatcttcaacccaagattt	2924

遺伝子名	No	存在位置	配列	配列番号
UGST1	15	(intron 2 2167)	tttaactatagaagctctt /G ctctcttctgtttgattta	2925
UGST1	16	(intron 2 2974)	tcactcagctcaactct C/T gggctcagtaetctccaa	2926
UGST1	17	(intron 2 3083)	aaaaatttataataggg /G actccctatgltccaggg	2927
UGST1	18	(intron 2 3106)	tccttatgtccagctg A/G tcttaattcttgggtcaa	2928
UGST1	19	(intron 3 1495)	gtcaacatggcccttacc G/A tctctcttgcacaatag	2929
UGST1	20	(intron 3 1703)	ttctcttcaagaagctc /C gtacagatacttagacaaa	2930
UGST1	21	(intron 3 2628)	ttttgaagacattitaga G/C agagctttccagcatc	2931
UGST1	22	(intron 3 2557)	tcagcatctctcttcca /C ttttaatttagatttttt	2932
UGST1	23	(intron 3 2731)	atcacataggaacatta A/C cttaaaacttaaggaatat	2933
UGST1	24	(intron 3 3032)	agagcatcttagaataatt C/A cctttaaagtagagaataa	2934
UGST1	25	(intron 3 3045)	atatactctttaaagata G/C agaatatcttctctgaa	2935
UGST1	26	(intron 3 3289)	gggttatagtttcccc /A cctcccccccaagaccga	2936
UGST1	27	(intron 3 3976)	ggaaactggggactgttt C/T cctgaagacagctcctaaa	2937
UGST1	28	(intron 3 4288)	ccattctattgtcaacgg G/A taacacagggcttagaatgg	2938
UGST1	29	(intron 3 4298)	tgtcaacttgcataacagg C/T gtgaagtggcaattgttt	2939
UGST1	30	(intron 3 4479)	attagaggtagcaatatct /C gtatgcttggggagaatc	2940
UGST1	31	(intron 3 4519)	tttaataaagaatgtatt C/T tgtctttcttctccatct	2941
UGST1	32	(intron 3 4817)	attctatagaagaagaa C/T gtaagcacaatagatttc	2942
UGST1	33	(intron 3 6077)	tttgaatttagtctttaa /C agttatcttttccacag	2943
UGST1	34	(3' untranslated region 603)	gggttaaccatttgaata /C tagcatctccaatactcgt	2944
UGST1	35	(3' flanking region 147)	tattttcttctctctct C/T tgtttcttttctctaaa	2945
UGST1	36	(3' flanking region 237)	cagacagtttctctataa C/T agacattctccaataact	2946
UGST1	37	(intron 1C 904 923)	tgcattatcttctgtaatt W16-19 ggcaaatatccaatttg	2947
UGST1	38	(intron 1C 3433 3434)	cccttcaactagacaaa GA gagacacataaagtgtac	2948
UGST1	39	(intron 1C 5146)	cccttcaactagacaaa GAGacacatttaattttac	2949
UGST1	40	(intron 2 552 563)	actattcaatttttttt Y/Δ ggaaggagagacagcttc	2950
UGST1	41	(exon 3 172 173)	cccagcatlataagaataac W10-12 aatctcaatgttgggaagg	2951
UGST1	42	(intron 3 152 158)	tagcatttggcagaagagaa AA/Δ tgcagaagatcttccaa	2952
UGST1	43	(intron 3 2198 2200)	agaaaactggatgtctgaaa TTGAA/Δ GTCCAA/Δ cactgcacttatagtgttg	2953
UGST1	44	(intron 3 2567 2568)	ggattttagattctccca CTA/Δ tcttctcgaccttccccc	2954
UGST1	45	(intron 3 2567 2568)	cccttccattttaaagta W gacttttttttttaccctct	2955
UGST1	46	(intron 3 2567 2568)	cccttccattttaaagta gacttttttttttaccctct	2956
UGST1	47	(intron 3 2571 2580)	tttccattttaaagtagac W9-11 cactctctctgttactcag	2957
UGST1	48	(intron 3 3288 3289)	ggattatagtttcccccc C tcccccccccaaaagacc	2958
UGST1	49	(intron 3 3288 3289)	ggattatagtttcccccc tcccccccccaaaagacc	2959
UGST1	50	(intron 3 4682 4683)	tcctctcagctctctatgt (GAGATGTTGGCTCAG) agtcatctctttagagac	2960
UGST1	51	(intron 3 4682 4683)	tcctctcagctctctatgt agtcatctctttagagac	2961
UGST1	52	(3' flanking region 1359 1360)	acacacacacacacacac CC/Δ tctctgaggttggcaact	2962
UGST1	53	(3' flanking region 1889 1891)	ttgaatagtttcttaactat ACT/Δ tttaactccaagaagactt	2963
UGST1	54	(3' flanking region -105)	tcctcagcttgccttggagc G/A gggcgttggcgttcttggct	2964
UGST1	55	(intron 1 277)	aggtctgtgagagaacag G/A tcttggaggttgaagtgttg	2965
UGST1	56	(intron 2 8030)	gggttatcacagccctc C/G accccacacacataaca	2966
UGST1	57	(intron 2 8499)	gtatggcaggttgggtctc C/T ggaagcctatagagatag	2967
UGST1	58	(3' untranslated region 468)	cccaactgtgaccagac /G gatgctctcttggaccacag	2968
UGST2	1	(5' flanking region -46)	gtacgacallcaagatcaak A/T agcccatattatcttccgt	2969

遺伝子名	No	存在位置	配列	配列 番号
WGS12	2	(intron 1 16)	ggcaccacagccgcctcct A/C cccctcctccagagggcgaag	2970
WGS12	3	(intron 1 204)	tccagggcgaagcagagac T/C gagaacattccagagattag	2971
WGS12	4	(intron 1 373)	ttacaaggttccaaagaaa A/T cggcctcctcttcaaacctg	2972
WGS12	5	(intron 2 -3245)	ccctcgatttgcacccctc G/A gccctccaaagctctggagc	2973
WGS12	6	(intron 2 -1998)	agcccgaggtggcggagca T/C gaggctcagagatcagagcc	2974
WGS12	7	(intron 2 -1640)	tgatttctcttcagatgcc A/G taatataagatagatattt	2975
WGS12	8	(intron 3 41)	acgtgtcttcaatagatgact A/G tgaacttcaaacattagag	2976
WGS12	9	(intron 3 453)	atcagagctcattgttcgag A/G tataaactttgccttcat	2977
WGS13	1	(5' flanking region -320)	acaaaagcccttaacagca A/C taatccattcacttcgga	2978
WGS13	2	(5' flanking region -355)	cgcttaaacgcctacagctg G/A ctctctcggggacaaattat	2979
WGS13	3	(5' flanking region -234)	cggggagtagatataat T/A ttgaaatagagagataa	2980
WGS13	4	(intron 1 74)	agccttgcagagcactcc C/T atattcagcctatcagac	2981
WGS13	5	(intron 1 682)	agaaaatgcccttccttatt G/C tgggtggcagacagagcc	2982
WGS13	6	(intron 1 832)	cgagtttcaagctatataa T/C agctcggggcagagtaagt	2983
WGS13	7	(intron 1 1919)	aatanaattccagttctt G/C tccctgcctctacagtacc	2984
WGS13	8	(intron 1 1991)	tgaaataggcacagagaaa A/G ttctactatcttcaaa tcc	2985
WGS13	9	(intron 1 4458)	ttctcattcccttccacata T/C agttgacttccacttccaa	2986
WGS13	10	(intron 1 4676)	tgaatacgaatgaattgt C/G ggggaatagttactttcat	2987
WGS13	11	(intron 3 278)	cagcatgacccattcaacc G/C atgtgacttccacagcct	2988
WGS13	12	(intron 4 423)	cttgccttttttgggggg T/G ggggggtggctcacagaag	2989
WGS13	13	(intron 4 506)	gtccagaagaanaanaag T/C ggggaagtggaagggagat	2990
WGS13	14	(intron 4 -162)	tcacgaattttattttcc C/T gactgaactaacttaatic	2991
WGS13	15	(intron 4 -130)	actlaacttccactaatg C/G ggggaagtagtggccaaa	2992
WGS13	16	(intron 4 -105)	ggagtagtggcgaataatc C/G aaattgttaacttttctga	2993
WGS13	17	(intron 4 -65)	aacatatgtgtaacacc C/T taggtttaaagaagtttg	2994
WGS13	18	(intron 5 105)	atccagacattgggagag G/C aaggcagcagattgcttga	2995
WGS13	19	(intron 5 197)	aaaaatcacaaaaattagcc G/A gattgtgtggctcacacttg	2996
WGS13	20	(intron 5 222)	tggttatgcacacctttagt C/T ccacttacttggagacttga	2997
WGS13	21	(intron 5 374)	ttctatcctactatatttt T/G ttcttgggaatttggaaaa	2998
WGS13	22	(3' untranslated region 517)	atgacttaccctttatttcca C/T ttacattttttttttaaata	2999
WGS13	23	(3' flanking region 166)	agctctatgtggtagtga G/T atatactatcctcacatgta	3000
SULT1A1/STP1	1	(5' flanking region -1597)	scagagtaagagagcactact C/G aagaagaagacgtgggggt	3001
SULT1A1/STP1	2	(5' flanking region -1491)	gagggatataattcatgaaa G/T tccaggaagaagtaagatt	3002
SULT1A1/STP1	3	(5' flanking region -1376)	cggtttcataatgttactgact C/T a/g taca a/g tgaatcttggatg	3003
SULT1A1/STP1	4	(5' flanking region -1375)	agtttataatgtactgact C/T A/G taca a/g tgaatcttggatg	3004
SULT1A1/STP1	5	(5' flanking region -1370)	catatttactgact C/T a/g taca A/G tgaatcttggatgaaacct	3005
SULT1A1/STP1	6	(exon 1B -65)	gaccttgcattcccccaca G/A caccacaaatcagccactg	3006
SULT1A1/STP1	7	(intron 1B 442)	gagccaccttgccttaggctt G/A tecttttgccttagtctg	3007
SULT1A1/STP1	8	(exon 1A -197)	gcctgggggttcccacagaaa A/G tggtagagacaaagggcctg	3008
SULT1A1/STP1	9	(exon 1A -159)	ctggcttgcagagagagacac A/C cagaaggttcttagaacttc	3009
SULT1A1/STP1	10	(exon 1A -95)	gagacttcaacaccttca T/C atctggcccttgcaccaca	3010
SULT1A1/STP1	11	(intron 1A 60)	ctggttttcagcccacccc C/T accactga c/g tggcttttgta	3011
SULT1A1/STP1	12	(intron 1A 69)	agcccgccc C/T gccactga C/G tggcttttgaatgctggcca	3012
SULT1A1/STP1	13	(intron 1A 174)	tctgaatggtagagagac G/A gcccctggcttggccctga	3013
SULT1A1/STP1	14	(intron 6 11)	catagaaggaggttagaccac C/G tctga a/t gcttccctccatg	3014

遺伝子名	No.	存在位置	配列	配列番号
SULT1A1/STP1	15	Intron 6 (7)	ggagctgagaccac c/g tctga A/ gcttccctccatctacacc	3015
SULT1A1/STP1	16	Intron 6 (35)	gaagcttccctccatctgac A/ cctagggcctggcaccctac	3016
SULT1A1/STP1	17	Intron 6 (71)	ctcacaggccaccacagg /c caccacgcccccccllgg	3017
SULT1A1/STP1	18	Intron 6 (108)	ttggaccctccacacagg C/A cc e/a gattcccatctgctct	3018
SULT1A1/STP1	19	Intron 6 (111)	ggaccctccacacagg c/a cc C/A gattcccatctgctctct	3019
SULT1A1/STP1	20	Intron 6 (270)	ctccctccacagggtatgc C/ accagggctacagctagg	3020
SULT1A1/STP1	21	Intron 6 (498)	tttctcttctgcatcag C/ aatcggcctccatcagg	3021
SULT1A1/STP1	22	Intron 6 (509)	aatccgagctccatcagg A/g gctctcgtctcagagacc	3022
SULT1A1/STP1	23	Coding region 600 (Pro 201 Pro)	ccctcctcctcagacc C/G aagaggagatcaaaagat	3023
SULT1A1/STP1	24	Coding region 638 (His 213 Arg)	gattctgagatttggggg A/G cctctccagaggagacc	3024
SULT1A1/STP1	25	Coding region 645 (Leu 215 Leu)	gagtttggggcactcct C/A ccagaggagaccctggactt	3025
SULT1A1/STP1	26	Coding region 902 (Gly 301 Ser)	gcttggaggaggcctctgg C/A gtcactcagaggaggtatg	3026
SULT1A1/STP1	27	Coding region 973 (Irp 325 Arg)	taaaatagaattggggcc /c gggaggtaggctcagctg	3027
SULT1A2/STP2	1	5' flanking region -547	tgttcttctggtctatg C/C atcaatctctctccacc	3028
SULT1A2/STP2	2	5' flanking region -423	tgtggctgacaggccag G/A accctggcaccctcaagac	3029
SULT1A2/STP2	3	5' flanking region -358	ctttcaggccctgctatc C/ ca g/ ctctctctccaatccc	3030
SULT1A2/STP2	4	5' flanking region -355	tccaggccctgctatc C/ ca G/ ctctctccaatccc	3031
SULT1A2/STP2	5	5' untranslated region -28	actcgggacaggaggccac A/G aggcaggtctccaaagact	3032
SULT1A2/STP2	6	Intron 1A (85)	ctactgctctctgagctc C/A ggcaggtcactcagctccc	3033
SULT1A2/STP2	7	Coding region 20 (Ile 7 Thr)	catgaagctatctcaggaca /c ctc /c cctccctcctgagct	3034
SULT1A2/STP2	8	Coding region 24 (Ser 8 Ser)	gagctcaacaggaaa t/c ctc /c cctccctcctgagct	3035
SULT1A2/STP2	9	Intron 2 (34)	ggcaccctctctctcagg /c ggcagctccctctggcca	3036
SULT1A2/STP2	10	Intron 5 (77)	cagcaaccctgctgagccac /c cctcggcctctcagctg	3037
SULT1A2/STP2	11	Intron 6 (684)	actgggctcagaggatcga C/C ggcctggtctctatgggtttt	3038
SULT1A2/STP2	12	Coding region 704 (Asn 235 Thr)	gttcaagagatcagagaaa A/C cctatagaccactacacca	3039
SULT1A2/STP2	13	3' untranslated region 895	gctctgagctgtagagagg /c tctggagctcactcagagg	3040
SULT1A2/STP2	14	3' flanking region 98	ctctccctctccagctctc A/ acttggcctgtttggagagg	3041
SULT1A2/STP2	15	3' flanking region 871	ccactgacttggggttgc A/C agcttgcagaggctggcaaa	3042
SULT1A2/STP2	16	3' flanking region 1006	ctctcccttggaggctcct /c taccgctgttggggcagcat	3043
SULT1A2/STP2	17	3' flanking region 1464	tcctgtagccagagcaagtt C/ t ggtgacctagagagagcccc	3044
SULT1A2/STP2	18	Intron 4 (728)	tcagcttctctcttggccaa A/ ccaagagatgacttggcctg	3045
SULT1A3/STM/ HAST	1	Coding region 843 (Ala 281 Ala)	cacttgcagtcggactatgc G/A gagaaga tggcaggtctcag	3046
SULT1C1	1	Intron 3 (2280)	gcaaatlttggattttta C/ t acagtcagggtttaccat	3047
SULT1C1	2	Intron 3 (3742)	ggagatctcacttctggca C/ t ttttttataatttctata	3048
SULT1C1	3	Intron 3 (4453)	ttcatagggttctcccca C/ t ttttttataatttctata	3049
SULT1C1	4	Intron 3 (5234)	gaaaagacacagagcagg A/G gactttgcagttcttctaa	3050
SULT1C1	5	Intron 3 (6175)	tggctggcagagaggtgag C/C agtctctcttctctctgccc	3051
SULT1C1	6	Intron 4 (205)	acatgaagcagagatccaga /c tgaattttggagagaaacta	3052
SULT1C1	7	Intron 4 (408)	ggctcaccctgtataacca C/C cacttttggagagcagagcgg	3053
SULT1C1	8	Intron 4 (429)	cacttggagagcagagcgg C/C gtagatcacaagatcagagag	3054
SULT1C1	9	Intron 3 (2106 2115)	tgcagtggtctgttttgg (110-1) gagacaaatctgctctgt	3055
SULT1C1	10	Intron 3 (4199 4210)	atggcagcctatatttggta (110-1) agagacagatttccatg	3056
SULT1C2	1	5' flanking region -110	tctgttaactacacagaa C/ t ggaaggctggaacggacc	3057
SULT1C2	2	Coding region 15 (Asp 5 Glu)	acactaatgcttaccaga C/G atgagagattttacatttga	3058
SULT1C2	3	Intron 1 (297)	gtagactgtttatttattt A/C ttcccaactaaggcccttat	3059

遺伝子名	No.	存在位置	配列	配列番号
SUL1C2	4	(intron 1 363)	gagtgatgaactagaagg /G aatcctgaagctcatttggg	3050
SUL1C2	5	(intron 1 2300)	ggctactatcagcagccac /T acctcagaagagatgacttc	3051
SUL1C2	6	(intron 2 455)	aagacttggagagcaataga /G aaaaaaaaaatcgtagaat	3052
SUL1C2	7	(intron 4 55)	caaatctcaaacacccca /A aagaagaatcttcttctt	3053
SUL1C2	8	(intron 4 11)	ctctcttcttaattgaaca /C tctcactctcttcaggat	3054
SUL1C2	9	(intron 5 1657)	cttctgttacttcttctt /C acttgctacaagaattctt	3055
SUL1C2	10	(intron 5 2082)	ctctacttagagatggagg /A gtccacacacacagatgaig	3056
SUL1C2	11	(intron 6 933)	agctactgaacctctccac /G taactgtatttcaaggagag	3057
SUL1ZAI	1	(intron 2 478)	ggactgggcttgtaacac /C tgccttactctgttgtat	3058
SUL1ZAI	2	(intron 3 382)	caaaccttctaattct /G tttctatctgtctcagaac	3059
SUL1ZAI	3	(intron 3 409)	ctgtctcagacatgac /G agacttagagatcactata	3070
SUL1ZAI	4	(intron 5 249)	agctggaaatcacagaca /T gcacacacacacactaatt	3071
SUL1ZAI	5	(intron 5 395)	agcatalaacacacagccc /A gcaaatltaacagcllta	3072
SUL1ZAI	6	(3' flanking region 33)	ttcttctttaaagttaaca /C gcttgccagagc a/g cggctgt	3073
SUL1ZAI	7	(3' flanking region 46)	gttaca g/c gcttgccagagc /G cggctgtcagccctgta	3074
SUL1ZAI	8	(3' flanking region 199)	ttacacagcacttgctc /G tctctgtaattccagacat	3075
SUL1ZAI	1	(intron 2 4162)	ttctccctctctccacct /T gcacacagatgaatcatal	3076
SUL1ZAI	2	(intron 3 819)	ggagcactcagctctggag /A ctggacttggaggtttgttg	3077
SUL1ZAI	3	(intron 4 3882)	ttccacgtctctctctggc /T agtggcctctctccctga	3078
SUL1ZAI	4	(intron 5 1780)	ctgcagaagggtctctt /T catctcagcagtaataagc	3079
SUL1ZAI	5	(intron 5 1814)	taatggctcagatggagc /A ttgtggggcatttagacag	3080
SUL1ZAI	6	(coding region 189 (Cys 263 Cys))	ccctctctcagaggtctg /T ggcacttggagaacacat	3081
SUL1X3	1	(intron 1 332)	ctgctctctcttacttg /T ctggctctctgacttggagc	3082
SUL1X3	2	(intron 1 1167)	taggaaggctcagagctg /A ttggctctctgctggcactca	3083
SUL1X3	3	(intron 1 2872)	catctcagatggagac /A agctcttgggcttgggctt	3084
SUL1X3	4	(intron 1 6242)	caccttggcttttaccac /G tggaaatatttaccgaa	3085
SUL1X3	5	(intron 1 6601)	gcttgggctcttgagagag /T gggagagagatggagagccc	3086
SUL1X3	6	(intron 1 6166)	agcttgaatggagcagact /T tcttggagacttggacccc	3087
SUL1X3	7	(intron 1 6905)	agcttcttcttcttctct /T catctcacaacttggccal	3088
SUL1X3	8	(intron 1 7464)	ggcagatcctcttagagac /A acatgaacacacagagagc	3089
SUL1X3	9	(intron 1 7833)	tgtctgggcttgggcttggc /A ggggagacttggctcagagc	3090
SUL1X3	10	(intron 1 8189)	caacttgggcttcttctt /T gcacacagagcttcttctt	3091
SUL1X3	11	(intron 1 8316)	ctctcacaagggcggagc /G tcttctcttggagcagagc	3092
SUL1X3	12	(intron 1 8617)	agacagaggttgggccaag /T caaggttggcggacttctcc	3093
SUL1X3	13	(intron 1 8631)	ggcaagcaggttggcggca /T ctctctggacttggcggcc	3094
SUL1X3	14	(intron 1 9493)	tttctctttagagcttctc /A tctgtctctgtctgagggc	3095
SUL1X3	15	(intron 1 10306)	caaggcgggagcctgaagc /T gaagtcttggggggggccag	3096
SUL1X3	16	(intron 1 11987)	tcatataatgaatgac /C acacttttgggaattttag	3097
SUL1X3	17	(intron 1 13085)	ctcttggcgggtgttga /A aggcataggccttagagctcl	3098
SUL1X3	18	(intron 1 13108)	ggcagccttagagcttctc /A ggttccacccacagacagc	3099
SUL1X3	19	(intron 2 700)	ggaccttggagctgtct /T gtaatcgttggcggggggc	3100
SUL1X3	20	(intron 2 818)	agccatagcttagcagc /A atcagcgttgggagggagc	3101
SUL1X3	21	(intron 2 1677)	actccacttctcttgaacc /T accttcttctctctctc	3102
SUL1X3	22	(intron 4 4954)	gcttccgagggcgggggg /T tggagagctcaagacatga	3103
SUL1X3	23	(intron 5 3632)	ccagcttacttccctcctag /T ggtcagagagacttctt	3104

遺伝子名	No	存在位置	配列	配列番号
SULX3	24	(intron 5 3662)	acatgatcttlaagcttc c/ gaggctcgaataaagaaa	3105
SULX3	25	(intron 6 1874)	tcgtatccagagctaac a/ g atggaagaattcilaacga	3106
SULX3	26	(intron 6 2133)	agaccgctcccaacttta t/ g ccacagctcagccctccct	3107
SULX3	27	(intron 6 2524)	ggaaggccagggctccctg t/ c gatgccagagcagctcact	3108
SULX3	28	(intron 6 2573)	agatcactcctcctcctg a/ g tttattaaacacctcgcca	3109
SULX3	29	(3' flanking region 12)	gttcaggcttcctcctg a/ g gtcttcctctgaggctag	3110
SULX3	30	(3' flanking region 445)	tcaaagctctctccctc a/ g tctctcgaagagagctcc	3111
SULX3	31	(intron 1 6418)	cctcctctttagtctgggg c/ Δ cagctcttccagctctc	3112
SULX3	32	(intron 5 2458)	cccttaaggaggatctc c/ Δ tctctgctctcagctcc	3113
TPST1	1	(5' flanking region -298)	accgcaccatgccact a/ c attttttgattttttt	3114
TPST1	2	(intron 1 3520)	agaaagcagaltatgtaa c/ g agtgcgtctagcaacaag	3115
TPST1	3	(intron 1 3610)	ggcagaagagaalagca a/ g clatlaaacacaaataat	3116
TPST1	4	(intron 1 20828)	tattctgtccactcctgca a/ g tggctcctcctcgaagctc	3117
TPST1	5	(intron 1 -6761)	aatacaactatctctga t/ c aattctagagggccagaga	3118
TPST1	6	(intron 1 -544)	tagacaagtaaatctta c/ t attcttagtcttattgctt	3119
TPST1	7	(intron 1 -526)	tacgttcttagtggtttag c/ t ttagcagtttccccaaca	3120
TPST1	8	(intron 1 -234)	tcaagacattatagca c/ t atgttcagctaacctttt	3121
TPST1	9	(intron 1 -48)	ttatagtggtttaagcag a/ g tttctaaaaatttaataa	3122
TPST1	10	(intron 2 -18944)	aaacattagacacgggaag c/ a ttaaaaaacttttagcttt	3123
TPST1	11	(intron 2 -18587)	tatctcaccataaacat a/ g tttccttaaacactagctacta	3124
TPST1	12	(intron 2 -18501)	ttagaagtaacttaatga a/ g gtccctgaanaacagagata	3125
TPST1	13	(intron 2 -159)	gaatgggatttccctcag c/ g ctgccacttgcctcttg	3126
TPST1	14	(intron 2 -19)	accttctgcttaactcac c/ a cctcttctgttttccagct	3127
TPST1	15	(intron 3 158)	tctcgggaagaagagctc c/ g ctctggagcttgttgattt	3128
TPST1	16	(intron 3 3779)	accagggcagctaccctcc c/ t ggcacaccaagtctcacc	3129
TPST1	17	(intron 4 292)	tgttatcttcatatgaac c/ t atgaatatttcagctgaaa	3130
TPST1	18	(3' untranslated region 1518)	gtctctgcatatctctaa t/ g gttttgagaacacgtctc	3131
TPST1	19	(3' flanking region 264)	accgtcttggcctgcatia c/ t cattttgtagtgaagtttct	3132
TPST2	1	(intron 2 578)	tcacctatctctcactcc c/ a aggaactcaggaatacctccc	3133
TPST2	2	(intron 2 789)	ctaaagcactctcagctc a/ g ttgctctctctgctcactt	3134
TPST2	3	(intron 3 2009)	cccagctggagtagtctg t/ c gtgatct c/ t gctcactgcaa	3135
TPST2	4	(intron 3 2017)	ggagtgtagtg t/ c gtagct c/ t ggcctcagcaccctccgc	3136
TPST2	5	(intron 3 2035)	ctcagctcactgcactccc c/ a cctcccgggttcagcagtt	3137
TPST2	6	(intron 4 104)	aatgtcagctctcacttc c/ t ggttcacatctgatttctct	3138
TPST2	7	(intron 4 379)	taaaataaactatttgg c/ t cctttctgctcttalaaggt	3139
TPST2	8	(intron 4 588)	tactcagcctgactctct c/ t ggcctaagccatctctcag	3140
TPST2	9	(intron 4 626)	caccctagctctctgagtag c/ t taggaactcaggtcagccc	3141
TPST2	10	(intron 4 718)	cccagcttgcttagagctc c/ g tggcgttagaggaagctccct	3142
TPST2	11	(intron 4 873)	gttagtgccttatttatac c/ a tttccattacagcttctagt	3143
TPST2	12	(intron 4 949)	caataattgaanaagggac c/ g cagcctcaggaagaagcttt	3144
TPST2	13	(intron 4 1033)	taagctcagcttttaggaa c/ a tctctgatttttaggaata	3145
TPST2	14	(intron 4 1051)	ggctgctcgaatttaggaa a/ g taacacagttatctgattgaa	3146
TPST2	15	(intron 4 1356)	gattcaacatcacaccac c/ t aacattacagctgaatgac	3147
TPST2	16	(intron 4 1707)	gtctcttaaaaggtgcttc c/ t ctgccccctggttgcctcag	3148
TPST2	17	(intron 5 215)	aagaccagctcagcaaac c/ a gtaaaccccgctcttacta	3149

遺伝子名	No.	存在位置	配列	配列番号
TPS12	18	(intron 5 341)	TTGGAGGCAAGGCTGGAGT C/A AGCTGGATCAGCCGCTTC	3150
TPS12	19	(intron 6 31)	GGACTTCATGGAGATCC C/A CTGCTCTGGGTGCCCCGG	3151
TPS12	20	(intron 6 273)	GTTCCTGACACTGGAGAC A/G GGCAGGAAGACACACATG	3152
TPS12	21	(intron 6 693)	AAAGGATTTTGTGACTT C/G GTAATCAAGATTTAAGAT	3153
TPS12	22	(intron 6 1635)	TCCTGGTAAAGATGGCC T/G TGAACAACATGAGTCTTC	3154
TPS12	23	(3' untranslated region 1147)	CTCCGCTTCAGATCC C/T GCAATGATCTCATGCCAA	3155
CS1	1	(intron 1b 6302)	AGAGCTCCGAGGAGGACT A/G TGAAGCTGATGATGATGA	3156
CS1	2	(intron 2a 1004)	GAATGAGCCCTCATCTCTA C/T AATATTTTAAAGATGA	3157
CS1	3	(intron 2a 1395)	ATGCTAAGTTACAGAGC T/C AGGAGGAAGGACACACCA	3158
CS1	4	(intron 1d 473)	CCAGGCTGAGTTGGTGG T/A GGGGCCCTCCATGGCTGCC	3159
CS1	5	(intron 2b 726)	CTATCTCCAGTGGCTCTC T/C GTCCTGTGTGATCCCTGCT	3160
CS1	6	(intron 2b 745)	CTGCTCCCTGTGGACCCG C/A TGGGGGCCACAGAGAGGCG	3161
CS1	7	(coding region 85 (Val 29 Met))	TCAGATTTCTGCTGCTG C/A TGTCTCTATCTGCTGCTCC	3162
CS1	8	(intron 3 308)	TCGCTGAGGTCAGAGTTC C/A AGACGAGCTGGCCACATG	3163
CS1	9	(intron 3 853)	TTTGTCTCTATAAATGGCA C/A TTTGATGGCCCAAGCTGA	3164
CS1	10	(coding region 198 (Asn 66 Asn))	GAGCAGTGAATCGGCGCA C/T AGCTCGCGGGGGAGATGCA	3165
ST1B2	1	(intron 1 80)	ACTGTTCATAAATCATTA C/T CATCTAATAAGTAAAT	3166
ST1B2	2	(intron 2 -352)	AACATTAATAGTATTTA T/C AGCAATGACAGGATATAA	3167
ST1B2	3	(intron 2 -85)	ATTACATAATCTCAAAAT T/C TGTGAAAGACTGGTGGCA	3168
ST1B2	4	(intron 4 460)	ATCTGACATTAAATAA T/C CTGAGTTT A/G TATATCCATA	3169
ST1B2	5	(intron 4 470)	TTAAAAA T/C CTAATTT A/G TATATCCATAAATAGTAAT	3170
ST1B2	6	(intron 4 518)	TTAAGATTGCTCATAT C/G TACTCTCTTGTGTACAA	3171
ST1B2	7	(intron 4 616)	AATGTTAATAATAGAT T/C TATCTGTTTGTAGTCCCT	3172
ST1B2	8	(intron 5 58)	CTGATCATCTGCTAAAGG C/A TGTATTTCTTCTCAACT	3173
ST1B2	9	(coding region 612 (Glu 204 Asp))	TATAGAACTCAAGAGGGA A/C ATCAAGAGATCATAGATT	3174
ST1B2	10	(intron 6 582)	AATACATCTCTCATTTAA C/A TGTCTGTTTGTGTGCTT	3175
ST1B2	11	(intron 6 3130)	AGATGATAAATATTTCAA A/T TTTAAAGCCCTGAATAAT	3176
ST1B2	12	(3' untranslated region 907)	TTTAAAGTCTAAATACA C/A ATCTGAAGAATAAGAAAT	3177
ST1B2	13	(3' flanking region 50)	TGATATCCAGTTTGTGCC T/G TGTATCTGAGTTTCCAAAT	3178
ST1B2	14	(3' flanking region 328)	TTGACCCAGGACACTGCT T/G CCATCTGCTGTACCAGATT	3179
ST1B2	15	(3' flanking region 446)	GTATTCAGATTGTGAAT C/A TTTTCTTATATCATCTA	3180
CHS11	1	(intron 1 3900)	GGCTGCCCCACTCCCA C/G TTAGGCCCTCAGGCCCTT	3181
CHS11	2	(intron 1 6520)	CTCCCCAGAGGAGCTGG C/T ACACAGGGGCTTGTGTAT	3182
CHS11	3	(intron 1 7963)	AAAACATCTATGGGGATTA C/T TGTGCTGATCTCAGATCA	3183
CHS11	4	(intron 1 9173)	GGCTCCACAGATCAGGCC C/A AGATGGAGGACAGAAATGCC	3184
CHS11	5	(intron 1 9701)	CCAGGAATCTGAATACAC A/G GCAATGACGGGACTACAGGG	3185
CHS11	6	(intron 1 12132)	ACAGATCCACAGACACCA C/A AGCAAGAGGGGAGAGACATCC	3186
CHS11	7	(intron 1 12465)	ATGACAGAAAGGGGCTTGG C/A CAATCTCATCATGAGATA	3187
CHS11	8	(intron 1 12561)	ATGCTCCCTGGTCCACTTC C/A CTTTGAATTTCAAGTAGTGG	3188
CHS11	9	(intron 3 529)	CCATGGTCTGAGGGGCTCT T/G CATGCTCAGGGGATTTGGGT	3189
CHS11	10	(intron 3 617)	AGAGACAGAGGAAGAAGGA C/A CACTTGGAGATCTGGCCGC	3190
CHS11	11	(intron 3 796)	AAGAGCTTCCCACTGCTC C/T AGAGTTAAATCTTGGGGTG	3191
CHS11	12	(intron 3 818)	CAGTTAAATCTTGGGTTC A/G AGGAATTTTGTTCACCTCC	3192
CHS11	13	(3' flanking region 762)	ATACTGTGACAGTTTACT C/T GTGTCTACATCTGCAGAAA	3193
CHS11	14	(intron 1 7874)	GTTCCTCCCTGGCTTCCCT T/A CATTTCTCATCTCATTTT	3194

通 话 子 名	No.	存在位置	配列 番号
CHS11	15	{3' flanking region 335-349}	cacatcaccacaccctggccta tt12-15 ggaattttagtagaagacgggg
CHS12	1	{5' flanking region -260}	agccggacagctccgcggggc g/a gtagacggggggcgcctccc
CHS12	2	{5' flanking region -56}	gccttggggacagccggcgc g/a ggcggcctcggagtcggcgc
CHS12	3	{3' flanking region 218}	agagtgaaacacatctttg t/a attctaaaggagaaaccaa
CHS12	4	{3' flanking region 383}	gcagacacatatttttgg t/c ctggggcctggcttcagaaaa
CHS12	5	{3' flanking region 952}	tacttgaaacattcttcagaa t/c gttatctatagagaagaat
CHS13	1	{5' untranslated region -294}	tcgaagctggccggccgc g/g gcagggcttccatccctccg
CHS13	2	{intron 1 96}	ggcttcaggggcgccggcca g/a atttgagggggagagagggg
CHS13	3	{intron 1 4467}	agaaagaaatggggcagagc g/g ggaagcaccagggaggaagatga
CHS13	4	{intron 1 4853}	ggaatgagcacctggcagctg a/g tccctggctcacccttcacag
CHS13	5	{intron 1 4965}	ttcacttcagagggagacaca g/c tgaccagagagcgaagtggg
CHS13	6	{intron 1 5046}	ggcgctgcatctttgttacc g/t ctggttcactccagtgct
CHS13	7	{intron 1 5300}	ctctttctcttaaggcct a/g aagagaatgacacaaatgcctc
CHS13	8	{intron 1 5354}	agccgtgagctccacagc g/a ggttgagggtggcccttgcc
CHS13	9	{intron 1 5428}	gacacctctcagcctctgt g/g tctattcccccacatctggc
CHS13	10	{intron 1 6555}	gagtggggactactggaaag g/c tcttgctctccttctg
CHS13	11	{intron 1 6990}	aaacacatggggctacccccc g/a tcccgacatgtagctacac
CHS13	12	{intron 1 7133}	ctgggggctctcttcacag t/g ttgatgtgtctagaaggcc
CHS13	13	{intron 1 7161}	gtctgaaggggccggcagaa t/c agaaatctagaacctggccg
CHS13	14	{intron 1 7189}	cagctcgaagacagtgctac g/a caccagagagatgaagaactg
CHS13	15	{intron 1 7316}	cttccatcttgcttgaggctc g/t tgggggttagcgtggccggga
CHS13	16	{intron 1 7967}	gacagaagaccccccaccag t/g gatctcggccctgtgacct
CHS13	17	{intron 1 11412}	gcttgacatcttgatctact g/t tgcactcactggcctttgt
CHS13	18	{intron 1 11591}	cccctgaaggcctctcagc g/a gtaactcattaccagcatg
CHS13	19	{intron 1 12541}	accacacagcatgaatggg g/c cagccccaccctggccgct
CHS13	20	{intron 1 12672}	gtagccacagctggggcctg c/c gggctcaggcatggcgaagg
CHS13	21	{intron 1 14809}	gaa t/gtagggatttgggct g/t ggccttaaggatgggtggga
CHS13	22	{intron 1 16161}	gatactggctcagcattgtc g/a ttgggactctttaaccacc
CHS13	23	{intron 1 16385}	tatttagcatggggttca a/c ctctctgtttttcaaaagg
CHS13	24	{intron 1 33638}	gacttgggcagctccttgg g/c catgaattcttgctctatgc
CHS13	25	{intron 1 35145}	agggagacgaagcctcact t/c gctggggcttgcctggcctc
CHS13	26	{intron 1 35340}	tgtgaagctttggccacag t/c ggtggcatggtttgcaccg
CHS13	27	{intron 1 35436}	ggcactcatgtagggcga t/c tgccttttttctctctt
CHS13	28	{intron 1 36150}	ccataaagagagctgggct g/t aggaagccagggagagcaga
CHS13	29	{intron 1 36194}	ggcttgggagagggcagcag g/a gtttggggcttcagcggggag
CHS13	30	{intron 1 37602}	ctgaagaacacacttaaaa a/t agaatagctcttcgaaagg
CHS13	31	{intron 1 37725}	gggttgcacaggaacatccc g/t gaccgga g/g ctgccttttca
CHS13	32	{intron 1 37734}	ggcgaatccc g/t gaccgga g/g ctgcctttcaccctctcc
CHS13	33	{intron 1 38208}	ggcatttagatgcacccc g/t gactlgggg t/g gcttccat
CHS13	34	{intron 2 255}	ctaacgcttgaagaattag a/g caagatacttaacatctgt
CHS13	35	{3' untranslated region 2202}	acacttcagagagccttg t/g ttacatcttgaggallatt
CHS13	36	{3' untranslated region 2569}	agggctcatctgggtaggg g/g caagagaagaatcacagatg
CHS13	37	{3' untranslated region 2717}	ctgaatcttccctctggggc g/t ctgggaagatattctctaa
CHS13	38	{3' untranslated region 2753}	cttaagcagaagatgcctgg g/a tggttgttccgggttta
CHS13	39	{3' untranslated region 2800}	gcttgggtcttcttctt g/t atgctgtgttttctttt

遺伝子名	No.	存在位置	配列	配列番号
CHS3	40	13 untranslated region (3283)	CGAGGCTCCAGCCTC /A/ TCTGTTCTCCAGCAAT	3240
CHS3	41	13 untranslated region (3327)	CTGCAATACGCCCC /C/ AATCAGAGGCTGCTAT	3241
CHS3	42	13 untranslated region (3787)	GTCCCATGAGAGCTCG A/G GGGCTGGAGCTGGAGAGG	3242
CHS3	43	13 untranslated region (3860)	GGCCCTAATGAGCAG /C/ AGCTTATCTCTCTCT	3243
CHS3	44	13 untranslated region (4915)	CGAGTGTGATAGAGCA G/A CTCTGTGATACACGCA	3244
CHS3	45	13 untranslated region (4993)	TAGCAATTTAGCTTT G/A TCTTGTGATACATGAC	3245
CHS3	46	13 untranslated region (5208)	ATTCATGTCATGATAC G/A AGACCCCTTAC G/A GATA	3246
CHS3	47	13 flanking region (281)	AGCAGAGTGTGGCCAG C/T GGTAGGGGCTGGGATG	3247
CHS3	48	13 flanking region (997)	ACCTTAAGTATTTGAG C/T GGTGCTGCTCCCACT	3248
CHS3	49	(intron 1 (22595))	CGGAGCAGAAAAAAA A/Δ GAATAAGAGAAAGAGCT	3249
CHS3	50	(intron 1 (35423-35424))	GCATCTCAGAGCTC A/Δ GATAGAGCA /C/ TGCCTTT	3250
CHS4	1	15' flanking region (-1092)	ATGAGCTTGTGCTCTC G/A CTGTGTGCTGCTGCTG	3251
CHS4	2	15' flanking region (-941)	CTCCAGAGAGAAACAGAA C/A GAGAGAGAGCACCAAT	3252
CHS4	3	(intron 1 (-150))	CAGGAAATGATGAGAG G/T ACTGTGCTGCTGCTGCT	3253
CHS5	1	(intron 1 (-144))	GGCTTGTGTTTACCA A/C GACAGTGTCTTAGCACC	3254
CHS5	2	(intron 2 (17))	CACGTAGAGAGCTCTCA /A/ TGTGCTGCTTGTCT	3255
CHS5	3	(intron 2 (139))	AATCCAGCACTTGGAGG C/A GGAATATGCTGATGATCA	3256
CHS5	4	(intron 3 (1829))	GACTGATGCTGCTATTA /C/ ATAGGACAAATATCATG	3257
CHS5	5	(intron 3 (2037))	AATGAACCAACACCA C/G TGCAGAGAGCAACAAAG	3258
CHS5	6	(intron 3 (2134))	AGCAGTAATATGTTTCC G/A TACAGGTGCAATTAGCAG	3259
CHS5	7	(intron 3 (2528))	ATGTAAGTTCCTGGT G/A CAGTATGATCATCTGCT	3260
CHS5	8	(intron 3 (2674))	GCCTTATCTAGAAAGCC A/G TTTCTGAGACTCAGCAGGA	3261
CHS5	9	(intron 3 (7039))	CTGTCTCCCGCCGACCT /C/ GGGACCCAGCCACTCTGA	3262
CHS5	10	(intron 3 (7211))	GTAGCCAGCAGACCCCA /C/ CCTCAATCCCATCTGAG	3263
CHS5	11	(intron 3 (7294))	GGAGCTCCAGTGGTGGT /C/ ACCCCACTCTTCTCAT	3264
CHS5	12	(intron 4 (108))	GCAGGCTCTGCTCTTCA G/A GGGCAATCAGGTGGAG	3265
CHS5	13	(intron 4 (402))	AGCATTGAAAGATACAGT /C/ GCATTGTAGCAGGTGGG	3266
CHS5	14	(intron 4 (547))	CTCTGCTCCGCTAGAGG C/G GAGGAGCAGAGTGAATC	3267
CHS5	15	(intron 4 (1142))	GGCCAGCTCTAGCTCC C/G CATGGCAGTCTGGATT	3268
CHS5	16	(intron 5 (1187))	CATGGCAGTATGAGGC A/G TGGATAGGCAAGAGGCC	3269
HNK-1S1	1	(intron 1 (139))	GTGTTGGCAGCTGAGA C/T CTCCTAGTTCGGAGTA	3270
HNK-1S1	2	(intron 1 (1020))	ACTGAGCAAAATCTCT /C/ CTCCTGAAATGAAATG	3271
HNK-1S1	3	(intron 1 (1091))	AGAAATTTGAAATACA G/A GCACTTGCAGTTATTCG	3272
HNK-1S1	4	(intron 1 (1971))	CTAATCTATTCAACATA C/T GAAACAGCATATTTGATT	3273
HNK-1S1	5	(intron 1 (2096))	ATTGAAATATTTTACC A/C AGAATCAATATAACTG	3274
HNK-1S1	6	15' untranslated region (-91)	CTATCATCTACAAAGAA C/A CAGAACTCAGTTCAAGG	3275
HNK-1S1	7	(intron 2 (-530))	AGTGGAGGAGGAGAGAG C/A TCAAGTTCATCTTCT	3276
HNK-1S1	8	(intron 2 (-466))	GCTACATCTGTCCAGCT C/T AGAATTTAATCAGCAG	3277
HNK-1S1	9	(intron 2 (-92))	ACGGAATATTTCTGAT A/T CTACTACTGAATCACT	3278
HNK-1S1	10	(intron 3 (152))	CATGGCTCTCTCTCT C/A TTACAGAGGTGAGGGAG	3279
HNK-1S1	11	(intron 3 (312))	CAGTGGCTTATCTCTG C/T AGCAGGCTCTCTGAGCT	3280
HNK-1S1	12	(intron 3 (1948))	TCTTTGATGATCAAGTT /C/ GTCTGAATTTTCTGCT	3281
HNK-1S1	13	(intron 3 (2140))	TTACCTTGGAGAGAGCAT C/T GAGAGGCTCTAATCTG	3282
HNK-1S1	14	coding region 187 (Leu 63 Leu)	AGAAGCATTTCTAGAA C/T TGAAGTGGACACAGG	3283
HNK-1S1	15	(intron 4 (581))	CCGATCTCTCTGCTG C/A ATGAGGAGTCTCTGGA	3284

通称子名	No	存在位置	配列	配列番号
HNK-1S1	16	(intron 4 615)	tcgaagggctctcacttc w/c taaccccaatcagactca	3285
HNK-1S1	17	(intron 5 71)	gattcttaaatgggtgt c/a tgggtctactgaatgtcac	3286
HNK-1S1	18	(intron 5 123)	accataaggacttgatgcc c/a tccagacagccgtgttttg	3287
HNK-1S1	19	(intron 5 121)	ataatttgggtctactta i/c gaaatttagcttccacagg	3288
HNK-1S1	20	(intron 5 867)	tgctccacacagctcgttg c/a tcaatcttgccacagtttg	3289
HNK-1S1	21	(coding region 444 (ile 148, 11e))	ccaggagcatttttccat i/c gaagagatcccgaacgt	3290
HNK-1S1	22	(intron 6 94)	ctgagttctgacttggcag a/g ttatcagaaggaccacagag	3291
HNK-1S1	23	(intron 6 247)	catgaagtgatcatctttt c/a ttatataaatttagcagca	3292
HNK-1S1	24	(coding region 695 (thr 232, 1hr))	agagagacccagacagagac c/g cggggatccagtttgaaga	3293
HNK-1S1	25	(coding region 870 (ala 290, 1ala))	gaacccctggagagcagatgc c/t ccaatcatcttaaaagagc	3294
HNK-1S1	26	(3' untranslated region 1110)	tcaaalatctttatagacc i/c ggggttaaccagagagat	3295
HNK-1S1	27	(3' untranslated region 1178)	ccacacccctcttttgaaga c/t gccggggtctccacagc	3296
HNK-1S1	28	(3' untranslated region 1393)	ggagatcatcacagagctta c/a gacccatttcttcaggtgt	3297
HNK-1S1	29	(3' untranslated region 1452)	tgaggtcttcttgctgctagc a/g ggggtgcttccacctact	3298
HNK-1S1	30	(3' untranslated region 1540)	gcaggagggctgctgagat c/c cagagacttttgcacalca	3299
HNK-1S1	31	(3' untranslated region 1696)	gggtgtgtgtgtgtgtgtgt c/a tccatttctcagaatccat	3300
HNK-1S1	32	(3' untranslated region 1829)	agggagggcttttttctact c/a agagggaggtgtcttgag	3301
HNK-1S1	33	(3' untranslated region 2211)	tcagagctggcgttctctg c/t c/t aacaaagtagcccttggt	3302
HNK-1S1	34	(3' untranslated region 2212)	ccagcagctggcgttctctg g/t c/t aacaaagtagcccttggt	3303
HNK-1S1	35	(3' untranslated region 1016)	cacacaaaggtgtgtgtgt c/t ggcctgagagcaccaggt	3304
HNK-1S1	36	(3' untranslated region 1152)	gcagcttctgtctatctaga a/g tctcagaagcagggacagc	3305
HNK-1S1	37	(3' untranslated region 1291)	gcagagacccctcagcagat a/g gtacgttaccagctgagc	3306
STE	1	(5' flanking region -605)	caggttcttaaaataat c/t gaaagtgatgtgttttac	3307
STE	2	(5' flanking region -536)	taaaatttcaggcttctct a/g agagtttaagcacaagagtt	3308
STE	3	(5' flanking region -231)	ctcttctccacacccctct c/t ggcagacttgggaattgaa	3309
STE	4	(5' untranslated region -64)	tcaggttgaagcttctct c/a gtatttgaagagataaac	3310
STE	5	(intron 1 69)	aaatataaataaataat c/a tattcaagctcttataaa	3311
STE	6	(intron 1 311)	caatgagaaataaagcag c/g aggtgagagagagagagat	3312
STE	7	(intron 1 655)	tctaagaagtaggagctat c/a agacccctatgtatctata	3313
STE	8	(intron 1 671)	ctatgagagacccctatgtat c/t tatalccacatagatctct	3314
STE	9	(intron 1 772)	aaaaggcaggttggagagat c/a agagggagagatagcagaaa	3315
STE	10	(intron 1 1715)	taaccatctgttgaacct a/g tcatittttagcgaagctatt	3316
STE	11	(intron 1 1928)	aaatgatacatallcaggaa a/g tcaaaaatctctactttaga	3317
STE	12	(intron 1 1953)	aaatctctacttagatacc c/t ggcataataatcaatgta	3318
STE	13	(intron 1 2087)	aaatttgaagaaatagaag i/g tctatggttttttttttca	3319
STE	14	(intron 1 2323)	tagetatagtagaagggtccc c/c ttatatacatagttgttaat	3320
STE	15	(intron 2 165)	tctattccatgacacaatt i/g ttacctgaacttgaatagt	3321
STE	16	(intron 2 1707)	ccatagaccacacatagac a/g taatatacatcagataaat	3322
STE	17	(intron 3 850)	gggtctatctcttcaagaa i/g ttatctttgtgtttacacac	3323
STE	18	(intron 4 1653)	agtaacaggttagtagataa i/c aataataacttaggccaacg	3324
STE	19	(intron 4 1899)	tacatgaacttagagaatca a/g gtagatcacacacacacaca	3325
STE	20	(intron 4 1930)	cacacacaaataaataat a/g cagaatgataaagaatttg	3326
STE	21	(intron 5 666)	tttgaatcagtagaacaa i/c tataaagaataaataatgt	3327
STE	22	(intron 5 982)	agcagaagcagacatttttg a/c ctacacacacatataat	3328
STE	23	(intron 7 368)	agattttatctctctctt i/c ttgagttgagaagaataagtt	3329

遺伝子名	No	存在位置	配列	配列番号
STE	24	(intron 7 447)	caccttcaagggaagtagg C/A aaaaaatagaatcaata	3330
STE	25	(intron 7 672)	aattctctcttgaacct A/T ctgtcattgaagtcaggaa	3331
STE	26	(intron 7 856)	tgtacagagacttaaaac A/G gtgtcttctgttgaacagg	3332
STE	27	(3' flanking region 218)	caectctcaatagtagg A/G ctacagacatgtcaacct	3333
NQ01	1	(intron 1 80)	agaagatttgaagaccttgg C/A cgaatttttcttcaact	3334
NQ02	1	(5' flanking region -434)	ttttcttgcacacaaacc C/G tcttctgttaaccggatag	3335
NQ02	2	(5' flanking region -406)	gtacacagatccagccag A/G gatggagcagagagcgca	3336
NQ02	3	(5' untranslated region -102)	tctctgccttcttactagg A/C gtgcgttgatctggaaagta	3337
NQ02	4	(intron 1 1919)	tccctcaaatagagcttagt T/C agtcacacagcttggacc	3338
NQ02	5	(intron 1 2004)	acaactacatgccacag C/G calatgaatgaacatataa	3339
NQ02	6	(intron 1 3391)	aaagcagagagcttggcagg C/T gcccttcccctaggcagg	3340
NQ02	7	(intron 1 3456)	caagggctcatctcagg C/A ggtcaacttcttctttag	3341
NQ02	8	(intron 1 3595)	actgcacagctttagtica T/C tcttgaagtggttctgtg	3342
NQ02	9	(intron 1 3596)	ctccctacgttttagttat T/C ctltgaagtggttctgtg	3343
NQ02	10	(intron 1 3598)	gccagctttaggttctc T/C tgaagtggttctgtg	3344
NQ02	11	(intron 1 3651)	ccctgcctttagagggatg A/G atgtaccttctccacatc	3345
NQ02	12	(intron 1 6036)	tgtgtgcagcttctcagat C/T cccagccttctgtcagc	3346
NQ02	13	(intron 2 14)	atggcagatgaattact A/G ttgtggagtaagacttttt	3347
NQ02	14	(intron 2 182)	gccagctgaagtgatataa C/T tcttgaattatctgttt	3348
NQ02	15	(intron 2 635)	cacctgtttagccttagg C/C ccatcctgcttctgctcca	3349
NQ02	16	(intron 2 685)	agtagcacccttccccacc G/A gcgtgacaaacaaatgt	3350
NQ02	17	(coding region 139 (Phe 47 Leu))	ctatttatagctatgac T/C tgaacccagggccacagc	3351
NQ02	18	(intron 3 36)	aaetctatattataaac T/C atcttattgttttacttt	3352
NQ02	19	(intron 3 728)	aacgtggcataaacacca T/C ctatggcdaaaagcagtg	3353
NQ02	20	(intron 4 1577)	tgccttcacaccccttcc C/T gacacaccccttcttacc	3354
NQ02	21	(intron 4 1832)	tccgcctccctcctggacc C/T gcttctcctcctgacccac	3355
NQ02	22	(intron 4 2583)	tgggtttagcacacacct C/T gtccctcctcctgacccca	3356
NQ02	23	(coding region 330 (Pro 110 Pro))	ctgtactgtttagcgttgc C/T gtccctcctcctgacccca	3357
NQ02	24	(coding region 405 (Ser 135 Ser))	atccagatctttagatc C/T ggttgcctcctgacccca	3358
NQ02	25	(intron 5 21)	gtatgtcttctttagaagg A/T tcaatataatatttagagg	3359
NQ02	26	(intron 5 253)	atggcaaacagagagagagg T/C caggtgtcaggtgacggagg	3360
NQ02	27	(intron 6 2435)	ccctcttaaatatttacc T/C gaatggatataacagggtgt	3361
PTG3	1	(5' flanking region -47)	ggaaagaaagaaagaaagaa G/A gggagagaggttctgtctta	3362
PTG3	2	(intron 2 243)	taacccagagcctcagcag A/C agtccacacttcttagaatc	3363
PTG3	3	(3' flanking region 282)	agcagggccagcccttggcc G/A ctactccttgggccccacc	3364
PTG3	4	(5' untranslated region -93)	tccgagagatagagggcc (C/G)T G cagacaatagttagccctg	3365
PTG3	5	(3' flanking region 525 626)	ctctcagggcccccctt (T) ccattacttcttgggtccc	3366
PTG3	5	(3' flanking region 625 626)	ctctcagggcccccctt ccattacttcttgggtccc	3367
PTG3	6	(3' flanking region 770)	tcccttgggtccccccttacc C/Δ tctataaccccttctcagc	3368
NDUFA1	1	(5' flanking region -1437)	aggctataaatctctatta T/A acctacttgaagctttttaa	3369
NDUFA1	2	(intron 2 3071)	ataaagatcatagcatat C/A ttgaaggagacagacttct	3370
NDUFA1	3	(3' flanking region 1218)	aactcatgtatataagca A/G caccacataatcacattcca	3371
NDUFA1	4	(3' flanking region 1411)	ggattgtccatccctttagt C/T ggcaatgaccccttctcttt	3372
NDUFA1	5	(3' flanking region 1411)	ggattgtccatccctttagt C/G ggcaatgaccccttctcttt	3373
NDUFA2	1	(intron 2 1087)	aacatacaaaaatagccagg A/G t a/g tggtagcgggaccccttcta	3374

遺伝子名	No	存在位置	配列	配列番号
NDUF-A2	2	(intron 2 1089)	catcaaaaattagccgg a/g t A/G tggccggccacttataat	3375
NDUF-A2	3	(intron 2 1356)	ttcccgaaacacccattg t/c ggcatacagaatcagcaa	3376
NDUF-A2	4	(3' flanking region 467)	catagccatcaggtcagcc c/t actcagagggcattccc	3377
NDUF-A2	5	(3' flanking region 744)	ggagcagggccctcggcca c/t agccctggcaglaagcagg	3378
NDUF-A2	6	(3' flanking region 838 839)	tatagctacagaalga aaacatacaaatagctia	3379
NDUF-A2	6	(3' flanking region 838 839)	tatagctacagaalga aaacatacaaatagctia	3380
NDUF-A3	1	(intron 2 2656)	tcctcctgcctcccttgc c/a cacttatcttcccttccc	3381
NDUF-A3	2	(coding region 241 (Low 81 Val))	agggccacagctggagatgg c/g tgaagaacatgtgagacct	3382
NDUF-A3	3	(3' flanking region 1019)	tccttaccctgacatgaccc a/g gctcggagcccccagctccct	3383
NDUF-A5	1	(intron 3 2155)	agacatgacatgactacg c/g aacataaggttcccttagaaa	3384
NDUF-A5	2	(intron 3 2493)	ggcatatgctagtcttctc c/t gtcctaatlcaatcatat	3385
NDUF-A5	3	(intron 3 2712)	acaatllgacagctgtcac c/t taacacagcttttttcgaa	3386
NDUF-A5	4	(3' flanking region 1296)	aggatataaaggtatgac a/c atttgctatgtgttcttc	3387
NDUF-A5	5	(intron 3 30 31)	aagtcagttttgtgtcttg (catttgcgtatcag) tgaacatttaaccacaaaa	3388
NDUF-A5	5	(intron 3 30 31)	aagtcagttttgtgtcttg tgaacatttaaccacaaaa	3389
NDUF-A5	6	(intron 3 427 428)	atttgatagcagtttaaaaa ac/Δ tctagactgctgattctatc	3390
NDUF-A5	7	(intron 3 4733 4734)	tataggaaatttaaaataa ta/Δ ggaatltgaacattcagtt	3391
NDUF-A5	1	(5' flanking region -1148)	tttaataattatagttta c/t gtccttctttttgtatagct	3392
NDUF-A6	2	(5' flanking region -363)	actaccaaggagccggccgg c/a cagccggalagcagagacct	3393
NDUF-A6	3	(coding region 26 (Ala 9 Val))	ggggagcggcgtccggcaag c/t tacttaccgcccagacct	3394
NDUF-A6	4	(intron 1 1318)	attcagcagtttgaacact a/g atgttgcctggcagaatc	3395
NDUF-A6	5	(intron 2 562)	agtlaaagatctgaagat c/g tcaagaatgatttaccctga	3396
NDUF-A6	6	(5' flanking region -861)	cgtlaaaa tgggggtactctga II) agtactactgacctatga	3397
NDUF-A6	6	(5' flanking region -861)	cgtlaaaa tgggggtactctga agtactactgacctatga	3398
NDUF-A6	7	(intron 1 1251 1278)	tgtagggagttactgtagca gt/12-14 ttcgggtgctgctatcaca	3399
NDUF-A7	1	(5' flanking region -731)	accacaaaggtctatcaa a/g ggggtgctctcttggcacc	3400
NDUF-A7	2	(5' flanking region -434)	aaagggaaccatcagaaccc c/t gtaataaaatagaatctagg	3401
NDUF-A7	3	(5' flanking region -395)	gtcccggtatccggctggc a/g ggggttggggcagggtagag	3402
NDUF-A7	4	(5' flanking region -100)	agaggagtcagctctctcgg c/a agagagctttatagagactt	3403
NDUF-A7	5	(intron 1 92)	tcacctctctctcaagcgg c/a acccttcgctctcccgaa	3404
NDUF-A7	6	(intron 1 133)	ctcctgggaaccccccagct a/c gt c/g acccttcagcccgga	3405
NDUF-A7	7	(intron 1 136)	cttgggaaccccccagct a/c gt c/g acccttcagcccgga	3406
NDUF-A7	8	(intron 2 89)	tcctttagacccctgaaag c/t agggctgacatcctgctacc	3407
NDUF-A7	9	(coding region 196 (Pro 66 Ala))	ggcccgaggaaatctgtgccc c/g ctccatcatcatctgctg	3408
NDUF-A7	10	(intron 3 4203)	ggcttcaaccccttggggccc t/g cctccatcatcctccctccc	3409
NDUF-A7	11	(intron 3 4604)	gggcttctgtactcgggg a/g ccaaaagtgggaaggagga	3410
NDUF-A7	12	(5' flanking region -1353 (-1360))	aggatccagggtcccttgcct cagatgcct/Δ asacttggcgaagagaag	3411
NDUF-A7	13	(5' flanking region -1233 (-1234))	agccttgatccacactct c/t/Δ ggaacttctttcttaataa	3412
NDUF-A7	14	(intron 2 4142 4143)	cattttgactgaggtgac ag/Δ gggccacagcggggccatg	3413
NDUF-A8	1	(intron 1 -75)	tttggttctctattcttgc c/t cccataggttaagctgaga	3414
NDUF-A8	2	(intron 2 790)	caaacctagacaaaggtgc c/t ctltatcagaagtgagcag	3415
NDUF-A8	3	(intron 2 900)	ttcaggagataaagctct g/a attctcagagcctgagatgg	3416
NDUF-A8	4	(intron 2 3837)	ggaetgtcttgaagtag a/g taagaatagtactacata	3417
NDUF-A8	5	(intron 2 3942)	tcattgttttgcagaagat c/t cccctaacccagctttctt	3418
NDUF-A8	6	(intron 3 -66)	ggagagacccagagagcgc a/g ttgatgtttacagattcttc	3419

遺伝子名	No.	存在位置	配列	配列番号
NDUFAB	7	13' untranslated region 570	tttttttggaccagaataa A/G gatgggtcgtggccacac	3420
NDUFAB	8	13' flanking region 367	gtcacaaggaggccctcc A/G agatagaagtcagaactt	3421
NDUFAB	9	13' flanking region 771	attctttttctactactagg C/T tctttctccactctgact	3422
NDUFAB	10	13' flanking region 1053	aaagaaagacactctctctga T/A ctgcataggccgtctctga	3423
NDUFAB	11	13' flanking region 1190	gattcttaagaaataa C/T actttttttgcatlittt	3424
NDUFAB	12	(intron 2 449-453)	tcatttgcatgactactaa G/A/M/Δ aaaaacttaactgtctaat	3425
NDUFAB	13	(intron 2 455-459)	tcatactactttagttaa A/M/Δ ctgaactgtgtaattttagg	3426
NDUFAB	14	(intron 2 707-708)	tcatttggaaagactctca A/ ccttgctgtaccataaagg	3427
NDUFAB	14	(intron 2 707-708)	tcatttggaaagactctca ccttgctgtaccataaagg	3428
NDUFAB	1	15' flanking region -807	gtagctctttttagaaca T/G gcagatctcaaggtagcc	3429
NDUFAB	2	15' flanking region -769	accagatttaagaaaaat T/C acaagcattctcctagaga	3430
NDUFAB	3	15' flanking region -353	ccacccctatttggllct C/G tctccacilltccctcctg	3431
NDUFAB	4	15' flanking region -322	ttccctctctcttctcc C/T ctcttctctctctggccc	3432
NDUFAB	5	(intron 1 447)	atcatatagacacaaaga A/G agtaataatcacaaaca	3433
NDUFAB	6	(intron 1 1039)	ggcttgatctcagcttag G/A caagaattaggagtgittag	3434
NDUFAB	7	(intron 1 4010)	aatgtatcaaaagagattc T/G tattctgccaalagaaga	3435
NDUFAB	8	(intron 3 49)	gcaaaatataaattactaag G/A tcatitttaggaagtagg	3436
NDUFAB	9	(intron 3 107)	aatcttccagaaaggac C/T aaggatccctctgtccca	3437
NDUFAB	10	(intron 3 1183)	atctctgtaataattctac A/G aattatttetaatcccttta	3438
NDUFAB	11	(intron 3 1395)	atctctgllcttctccct C/T agtlltlllgllccactlgl	3439
NDUFAB	12	(intron 3 2363)	agaaatagctcaaaaggc C/T ccaactaacactagtcttta	3440
NDUFAB	13	(intron 3 2508)	gcatitgaattccctagga A/C agtctactgttccctgttg	3441
NDUFAB	14	(intron 4 551)	atttataaattcttctag A/C ctggggctcttattcaact	3442
NDUFAB	15	(intron 4 850)	attgttagaagaaagcag C/T aagactgtcaactttttaa	3443
NDUFAB	16	(intron 4 879)	gcagagctgtcaactttttt A/I aaaaaataattttagcttaa	3444
NDUFAB	17	(intron 4 893)	tttttaaaaaataattt A/G ccttaaaaaataaaaaat	3445
NDUFAB	18	(intron 4 1090)	atcattctgtttaaagtt T/C aagtagtgtaatttcagta	3446
NDUFAB	19	(intron 4 1188)	accaatctttttattttt A/I tcttcaaaaacttttaatt	3447
NDUFAB	20	(intron 5 161)	gggtgtgtgtaagllttaa C/T gllttatgatttccctct	3448
NDUFAB	21	(intron 5 373)	cittctacccttctccag C/I agtgglltllgtccacitct	3449
NDUFAB	22	(intron 5 457)	gccaggaagaagctctatc A/C cacagcttattgtctctt	3450
NDUFAB	23	(intron 5 3113)	gatttttctctcttcaat G/A taagcttcccttaaaataa	3451
NDUFAB	24	(intron 5 3339)	cttaactcaaaacagattt G/A ttggattttgttttagctg	3452
NDUFAB	25	(intron 6 414)	tatagtttctcttttccag G/C aattacataatgtttaga	3453
NDUFAB	26	(intron 6 518)	cittctatttctttagc T/C tgaatgctatttcttata	3454
NDUFAB	27	(intron 7 974)	ggattatgctacttgaana A/G tacttgaatagcgtgatta	3455
NDUFAB	28	(intron 8 368)	acattatatttatttaggata T/G caaatctctccagagctg	3456
NDUFAB	29	(intron 8 954)	gcatacatagttatataag T/C ctagaataagaattacaalc	3457
NDUFAB	30	(intron 8 1253)	tctcttgaattttagata G/I gtactacacatttctcatc	3458
NDUFAB	31	(intron 8 1608)	gaanagaagaatgataaat G/A accaaatctctgaagaaa	3459
NDUFAB	32	(intron 8 11930)	ctacaataatttctaagt C/I gtaatcataagaatagataa	3460
NDUFAB	33	(intron 9 1998)	tgtttttcaagcctttaaac G/A gcttggaacacctgtgctca	3461
NDUFAB	34	(intron 9 2238)	ccagcttctggagagctga A/G gggagagatcactttagcc	3462
NDUFAB	35	(intron 9 2885)	acagcgtctgtcttctctgc A/G gtttctataggctagcttac	3463
NDUFAB	36	(intron 10 801)	tacactaaagtgtctcttac G/A ttattacttgaagaagtggtt	3464

遺伝子名	No.	存在位置	配列	配列番号
NDUFA9	37	(intron 10 910)	tcagacttcagatggta c/c gataaggaatgcgcgcgt	3465
NDUFA9	38	(intron 10 1180)	aaaactgagtagagagccc g/a tgcagaaaaagagccgt	3466
NDUFA9	39	3' flanking region 554)	gtccacacttaagaaalia y/g aactcttaagaagttctt	3467
NDUFA9	40	5' flanking region (-1129) (-1128)	taacagtagagagcaagata tt/c gatgagaacagccaagatt	3468
NDUFA9	40	5' flanking region (-1129) (-1128)	taacagtagagagcaagata g/l gaggagaacagccaagatt	3469
NDUFA9	41	5' flanking region -341)	tggtttt c/g ttctcaatt y/d cccctgcttctgccc c/t c	3470
NDUFA9	42	(intron 4 594)	attcaacttttaccccc y/d aagattaacatagttatt	3471
NDUFA9	43	(intron 10 356 375)	taacttccttcacagctcct g/a gaaagaggttgcagttt	3472
NDUFA9	44	(intron 10 379 381)	gaaactttgcaactttctt cct/y/d tcttcttaacclactcca	3473
NDUFA9	45	(intron 10 384 387)	tgtagcagtttctctctc tt/c/d ttaacclactccagtcagg	3474
NDUFA9	46	(intron 10 436 437)	ccatttcccctaaatag ttctttt/aaatttc) ctttttcaagttatccac	3475
NDUFA9	46	(intron 10 436 437)	ccatttcccctaaatag c/c ctttttcaagttatccac	3476
NDUFA9	47	(intron 10 485 496)	gccacatccaatggtcagtt ttccagggctttt) ctcagacctatgcatg	3477
NDUFA9	47	(intron 10 485 496)	gccacatccaatggtcagtt ggcgctt) ctcagacctatgcatg	3478
NDUFA9	48	(intron 10 519 520)	gacctatgcatgctgcctg ggcgctt) ctcagacctatgcatg	3479
NDUFA9	48	(intron 10 519 520)	gacctatgcatgctgcctg c/c ctcagacctatgcatg	3480
NDUFA9	49	(intron 10 558 559)	gatgcaaaaataaataaaa ttactataccaataaccacatc	3481
NDUFA9	49	(intron 10 558 559)	gatgcaaaaataaataaaa tactataccaataaccacatc	3482
NDUFA10	1	5' flanking region -1734)	tcaccltgaactgttact y/c tcttgaacatttaccctt	3483
NDUFA10	2	5' flanking region -1492)	aaaacatcccacaaacagg y/c tctgagaagttacgtctgcg	3484
NDUFA10	3	(intron 3 370)	agaactgcatgctgcctc g/a aacagagatgtaagtcga	3485
NDUFA10	4	(intron 3 2485)	ttctatttttttttttc g/a aatcactatcatttaca	3486
NDUFA10	5	(intron 4 236)	ctgtaagcagattgagc c/y ctcagacctatgcatg	3487
NDUFA10	6	(intron 4 1742)	ttctgcatctctctgattg c/y tctgagaagttacgtctgcg	3488
NDUFA10	7	(intron 4 2090)	gactgaggaagaagatca y/c ctgtaagttacgtctgcg	3489
NDUFA10	8	(intron 4 3054)	caactaatatactactgaa a/c cggataaag c/y agcltga	3490
NDUFA10	9	(intron 4 3056)	ctacgaa a/c cggataaag c/y agcltga	3491
NDUFA10	10	(intron 4 3377)	gtcacatttaaatgctcct g/a ttctactctgtatgtag	3492
NDUFA10	11	(intron 5 46)	agaactcttatttgaag y/c agatcagacctatgcatg	3493
NDUFA10	12	(intron 8 1465)	gcaacgtccttcttctgta c/y agcctcatalccagctg	3494
NDUFA10	13	(intron 8 1809)	cttgagagcagagagagc c/a agggcactatcttctctc	3495
NDUFA10	14	(intron 8 1226)	gttgtagatgtagtggggc a/g tctcactctcggcttgcag	3496
NDUFA10	15	(intron 8 1319)	atcttcttcttctctgc c/a tctgtcagaccttgaatcct	3497
NDUFA10	16	(intron 8 1386)	ccataatccttactgagc c/y tcttcttctcctgctgacc	3498
NDUFA10	17	(intron 8 1386)	ccagccacttgaatgctt c/a catttctgacatttctta	3499
NDUFA10	18	(intron 9 183)	ttctgtgtggaagctg a/a aagtcctcagatgacagccc	3500
NDUFA10	19	(intron 9 8028)	ggagacattccacagaccl c/a tcaattatagacagagaggt	3501
NDUFA10	20	(intron 9 10742)	ctggagagagagagagagc c/g agtgcagcagcagctgggt	3502
NDUFA10	21	(intron 9 13908)	cacattgtatgtaacacag c/t ct g/t gaattgacgtctgaga	3503
NDUFA10	22	(intron 9 13911)	attgtatgtaacacag c/t ct g/t gaattgacgtctgaga	3504
NDUFA10	23	(intron 9 14054)	tttcaactatgagaacct a/g tcaataaattttaaagcag	3505
NDUFA10	24	(intron 9 14184)	tggttctgttggagacagc g/a agagatagacagacagaggt	3506
NDUFA10	25	(intron 9 16487)	cttgaagcttgaatcttct c/a ctgaagcttgaatcttctt	3507
NDUFA10	26	(intron 9 16779)	ggcagagctgacgctttag g/a ttctcagacattcagacc	3508
NDUFA10	27	(intron 9 17663)	ttccaataaccacagagc y/g tgcagatttttgaagctcct	3509

遺伝子名	No.	存在位置	配列	配列番号
NOUF10	28	(5' flanking region (-1658) (-1659)	gtataattgtttaactaga (G) 9-1 ttcataaaccaaggtataaa	3510
NOUF10	29	(5' flanking region (-1355) (-1334)	cgtatccatttgaaggac (A) 15-21 tgcataagaacaagaacaaa	3511
NOUF10	30	(intron 1 46-61)	tggcgggtggcaggggtgc ggggtggggggggg/△ gacagatccacatcctccc	3512
NOUF10	31	(intron 4 2486)	ctcactggacatttttttt 1/△ aatttaatttttaaaattt	3513
NOUF10	32	(intron 7 1600 1601)	cacttcacatcagcttga (A) cgggtgactttctctccca	3514
NOUF10	32	(intron 7 1600 1601)	cacttcacatcagcttga cgggtgactttctctccca	3515
NOUF10	33	(intron 9 1054)	ggcgtctctttctccct A/△ tctgtctttgacacgtg	3516
NOUF10	34	(intron 9 8161 8172)	tttctgcctttctggagcc (1) 10-12 aagtttgaataatgtgttt	3517
NOUF10	35	(intron 9 8646 8647)	aattcccatgtgtctt (1) cgttagacattttaaccia	3518
NOUF10	35	(intron 9 8646 8647)	aattcccatgtgtctt cgttagacattttaaccia	3519
NOUF10	36	(intron 9 16503 16523)	aattcccatgtgtctt cgttagacattttaaccia	3520
NOUF10	37	(intron 9 17905 17936)	cctt c/a cttgaagctgactgt tcccttcttgaagctgtgtgt/△ gtccaaataatgttgcataaga	3521
NOUF10	37	(intron 9 17905 17936)	cctt c/a cttgaagctgactgt tcccttcttgaagctgtgtgt/△ gtccaaataatgttgcataaga	3522
NOUF10	1	(intron 1 8451)	cagcaccctgttagggctt c/a ggaatctgaagatgctcata	3523
NOUF10	2	(intron 1 8455)	ggacagggcattctgcagac c/a ctgacaaatttttagtggcag	3524
NOUF10	1	(5' flanking region -1439)	ttaaaatttgaattttttt c/a cc c/a ggcacagctgtctcacc	3525
NOUF10	2	(5' flanking region -1436)	aagttgactttttttt g/a cc c/a ggcacagctgtctcacc	3526
NOUF10	1	(5' flanking region -213)	ggcggatggaacatctctac A/c aagaaggcccaacacggccg	3527
NOUF10	2	(intron 1 6288)	ggcggatggaacatctctac A/c aagaaggcccaacacggccg	3528
NOUF10	3	(intron 1 -1581)	ctctggacacatctctac A/c aagaaggcccaacacggccg	3529
NOUF10	4	(intron 1 -1487)	cctctgaacatctctac A/c aagaaggcccaacacggccg	3530
NOUF10	5	(intron 2 556)	ttgtctggacatctctac c/a atagataagctctgaatca	3531
NOUF10	6	(intron 3 467)	ggcggatggaacatctctac c/a atagataagctctgaatca	3532
NOUF10	7	(intron 3 497)	atagataagctctgaatca c/a atagataagctctgaatca	3533
NOUF10	8	(coding region 397 (tyr 133 His))	atagataagctctgaatca c/a atagataagctctgaatca	3534
NOUF10	9	(intron 1 213 215)	attagcattctaaacgtt c/a atagataagctctgaatca	3535
NOUF10	1	(intron 1 68)	cctgaacatctctgaacatctctac c/a atagataagctctgaatca	3536
NOUF10	2	(intron 2 266)	ggcggatggaacatctctac c/a atagataagctctgaatca	3537
NOUF10	3	(intron 1 4480 4481)	ggcggatggaacatctctac c/a atagataagctctgaatca	3538
NOUF10	3	(intron 1 4480 4481)	ggcggatggaacatctctac c/a atagataagctctgaatca	3539
NOUF10	1	(5' flanking region -3)	tcttagggctgtgtgtgt c/a atagataagctctgaatca	3540
NOUF10	2	(intron 1 425)	ttgttattctgtgtgtgt c/a atagataagctctgaatca	3541
NOUF10	3	(intron 1 470)	ttgttattctgtgtgtgt c/a atagataagctctgaatca	3542
NOUF10	4	(intron 1 502)	ttgttattctgtgtgtgt c/a atagataagctctgaatca	3543
NOUF10	5	(intron 1 557)	ttgttattctgtgtgtgt c/a atagataagctctgaatca	3544
NOUF10	6	(intron 1 5218)	ttgttattctgtgtgtgt c/a atagataagctctgaatca	3545
NOUF10	7	(intron 3 1371)	ttgttattctgtgtgtgt c/a atagataagctctgaatca	3546
NOUF10	8	(intron 5 414)	ttgttattctgtgtgtgt c/a atagataagctctgaatca	3547
NOUF10	9	(intron 10 812)	ttgttattctgtgtgtgt c/a atagataagctctgaatca	3548
NOUF10	10	(intron 11 233)	ttgttattctgtgtgtgt c/a atagataagctctgaatca	3549
NOUF10	11	(intron 11 283)	ttgttattctgtgtgtgt c/a atagataagctctgaatca	3550
NOUF10	12	(intron 11 585)	ttgttattctgtgtgtgt c/a atagataagctctgaatca	3551
NOUF10	13	(coding region 1251 (Arg 417 Arg))	ttgttattctgtgtgtgt c/a atagataagctctgaatca	3552
NOUF10	14	(intron 13 5159)	ttgttattctgtgtgtgt c/a atagataagctctgaatca	3553
NOUF10	15	(intron 14 250)	ttgttattctgtgtgtgt c/a atagataagctctgaatca	3554
NOUF10	16	(intron 14 550)	ttgttattctgtgtgtgt c/a atagataagctctgaatca	3555

遺伝子名	No.	存在位置	配列	配列 番号
NDUFS1	17	(intron 4 2429)	CTGAAATACAAATATAC C/ GGGTGGTGGCATGGCT	3555
NDUFS1	18	(intron 14 2530)	TTACAGTGGCGAGATAC C/ CCATCGCTCCAGCTGG	3556
NDUFS1	19	(intron 14 2659)	ACCATTTAATTTTACAT T/C GAAATACAGCAGTTATGAT	3557
NDUFS1	20	(intron 16 150)	AGAAACATGATTCAGAAA C/ AGGAATTCAGGTTACAGTG	3558
NDUFS1	21	(intron 18 279)	CCTGTGGCAATTTATGG T/C GATTTCCAAAGTGGCAAA	3559
NDUFS1	22	(3' flanking region 182)	CTGGGTAATTAATTA T/A AATAATAGTAACTAG	3560
NDUFS1	23	(intron 12 3226)	AAATGATGCTGCTTT T/Δ ACATTTGTAATAGTAAT	3561
NDUFS3	1	(5' flanking region -194)	CTGCGCAAGGACTAGGA C/ CACGCTCCACGACTTC	3562
NDUFS3	2	(intron 1 46)	CGGGTCAGCCGCGGG T/C GCCAGTGCAGAGAGCTCT	3563
NDUFS3	3	(intron 6 -439)	AACTGTATCAATGACT C/ A CTTAATCTAGACTGAA	3564
NDUFS3	4	(intron 6 -280)	GGTGGTGGAGCTGCTT C/ A GAGCTCTGATGGGAGTG	3565
NDUFS4	1	(5' flanking region -439)	AACGGAATACGCCCTGCT C/ A GAGGCTTGCAGAGTAACT	3566
NDUFS4	2	(intron 1 1829)	GAAGAAATCTTAATCCA C/ GGAAGCGTTTITTAATCT	3567
NDUFS4	3	(intron 1 2057)	ATTAATGGGAAATCTCAT C/ G TAAATCTATTTATGTA	3568
NDUFS4	4	(intron 1 -521)	TTCTTTAATTTAT T/ G TCTCCATTTGTAATGGG	3569
NDUFS4	5	(intron 3 -1259)	ATAAATATGATATATTA C/ A TACTAATATACGACATA	3570
NDUFS4	6	(intron 3 -1174)	ATAATATATATAGGAA T/C CTCAGATAGCAACCTAGGT	3571
NDUFS4	7	(intron 4 10682)	CAAAATAGGCATAACT A/C CTACCAAGCACTACAAGT	3572
NDUFS4	8	(intron 4 12299)	TTTCTATATATATATGG A/ T ATAGCTATAGATATCTCT	3573
NDUFS4	9	(intron 4 12560)	ACCAATAGGTTATATGCA C/ A GCTATCTTTTATATAGA	3574
NDUFS4	10	(intron 4 18801)	GGAAAGCTGTGGCCAG T/C GTATCGAAACCTCTGTAT	3575
NDUFS4	11	(intron 4 19888)	TCGACAGCTGGAGAGCA A/G GGGCTGTTTTCAGTACC	3576
NDUFS4	12	(intron 4 20178)	AGAAAGATAGTATATCT C/ A TCTACTTACCATCTCTAA	3577
NDUFS4	13	(intron 4 23016)	CTACTCTGAAGTAAGGT T/A ATGTTGACAAGTAATTA	3578
NDUFS4	14	(intron 4 23124)	ACTCTTTGGGATGGAGT T/A CCAGCAGTGGGAATGTAAT	3579
NDUFS4	15	(intron 1 766)	TGATGATTTTTTTTT T/Δ GGCCTATTAACCTCCAT	3580
NDUFS4	16	(intron 1 1261)	TTCTCTCTTTTTTT T/Δ GAGATACATCTCCTCTGA	3581
NDUFS4	17	(intron 4 19744 19745)	CTCATTTAGGTCTGCTGG T/Δ AGTGGGTTTGTGGCAATC	3582
NDUFS4	17	(intron 4 19744 19745)	CTCATTTAGGTCTGCTGG T/Δ AGTGGGTTTGTGGCAATC	3583
NDUFS5	1	(intron 1 388)	CCAACATAGCCAGCTCT C/ T GCTGTAATCTCCGGCTGT	3584
NDUFS5	2	(intron 1 -13082)	ATGAGCGGATATACCA C/ A TGCATCCAGCTGGGCAAC	3585
NDUFS5	3	(intron 1 -12905)	GTTCACAAAGGACTCCA C/ T AGTAGAGAGATTCTGT	3586
NDUFS5	4	(intron 1 -12554)	ATTCTACACCTCAACT T/ G AAGTATACACCTTAAAG	3587
NDUFS5	5	(intron 1 -12561)	TTCTACACCTCACTTAA C/ A ATATAACACCTTAAAGT	3588
NDUFS5	6	(intron 1 -10551)	ACCAATGATATAGTGGG C/ G GGGTGGTGGCAGGTGCTAT	3589
NDUFS5	7	(intron 1 -10065)	CCGATGCTCTGGTCTCAG C/ A ATAGACCTTTCTCTTGA	3590
NDUFS5	8	(intron 1 -8871)	TCACCACTGTCTGATATA T/C AGGACCGCAGCTTCTCTT	3591
NDUFS5	9	(intron 1 -7312)	AAATCTTGGCTCTAGAAT C/ T GCTCAGTATGATATAAT	3592
NDUFS5	10	(intron 1 -6827)	AACCTGCTCTCCGATC A/G CCTATCTCTCTCTCAGC	3593
NDUFS5	11	(intron 1 -6725)	AGTAAAGCGGTTTACCC C/ A TGTAGCCAGCAGTCTG	3594
NDUFS5	12	(intron 1 -6631)	AGGCTAAGCAGCTACCC C/ A GCTAGACCTTCTCTATA	3595
NDUFS5	13	(intron 1 -6531)	CCCAAGCTCTCCATATA A/G ACAATATATATATCTG	3596
NDUFS5	14	(intron 1 -6346)	GAACAATCTTACTATA T/C CCTATAGGTACAGCTAAG	3597
NDUFS5	15	(intron 1 -6327)	ATCCATAGGTACAGCTGA C/ C GACTTAATCAGAAAGGAG	3598
NDUFS5	16	(intron 1 -6122)	TAGCTTGTCTTTACTAT C/ C GTTCTCTCAATACACCC	3599

退位子名	No.	存在位置	配列番号
NDFUFS5	17	(intron 1 -2512)	acaactctaaatgcaatt /C/ tccagatcaaatggcctta
NDFUS5	18	(intron 1 -1945)	ttaaacccttlaaatllc G/A caalltcacaccttaggia
NDFUS5	19	(intron 2 75)	tttttttttttttgagac G/A aagcttactcttctctcot
NDFUS5	20	(intron 2 148)	ctataacctgcgtcccag G/A ttacggcatatcgctacct
NDFUS5	21	3' flanking region 150	cagattcacatgatctctot C/C ccttagcctccaagttagct
NDFUS5	22	(intron 1 (-10682) (-10681))	aataaacactaaacaaac A/TΔ gtagctctcttttagasgg
NDFUS5	23	(intron 1 -10267)	caaggtaactaccctgaaaa A/Δ gaagagaagaacaatcac
NDFUS5	24	(intron 1 -2069)	accagacagatctccctta C/Δ ttgtttcttgtggcaaga
NDFUS5	1	(intron 1 26)	gctccttgagatcacaga tgc A/C cctctccagccgacctc
NDFUS6	2	(intron 2 1076)	ggatcataatgtagagagg G/A gctgtctgtgtaggttgc
NDFUS6	3	(intron 2 1260)	caattctcagtaaatagctg /C/ ataaggtaagctcttctct
NDFUS6	4	(intron 2 1413)	caaagagctcatcgacat tgc C/T aaatggacatttcttccgt
NDFUS6	5	(intron 2 1568)	tggaagagggagatcttctc /C/ agatgtgagatgccgatalgt
NDFUS6	6	(intron 2 1692)	gaccttgctacagggagttt C/T ctggcatcagatgggtggtt
NDFUS6	7	(intron 2 6488)	tagcttaaatatattagcc A/G tcatgttcagatatccctga
NDFUS6	8	(intron 2 6563)	tttaacttlatlilaat G/A lccalgaalggggctgcltat
NDFUS6	9	(intron 2 6740)	aagagatltaaccctacatat C/T tta tcccaatcatltgat
NDFUS6	10	(intron 2 6832)	gcaaggagctattttacag A/T ggltggacatttactgtgt
NDFUS6	11	(intron 2 7054)	ttcacctccggagagcttgccc G/A tgtaaccctggagccggect
NDFUS6	12	(intron 2 7186)	ggctcaggctacaccttgagc /C/ gcgcacatlaaalacggga
NDFUS6	13	(intron 2 7225)	gaaggctatccgcgtcagtc G/A ccagttcctgggcttcagca
NDFUS6	14	(intron 2 7810)	cttccactc.tggggggggga C/T gctgtagaaggagacacaag
NDFUS6	15	(intron 2 11080)	ataactgttgagctgttct C/T ctlttgatitcatgttaaatc
NDFUS6	16	(intron 2 11637)	gggcagagacagatgtgtgtgt G/A gagaaagagggcstggcaag
NDFUS6	17	(intron 3 208)	ceaaaaacctcttaaatg /C/ gaagtgtatggcgagcatgtt
NDFUS6	18	(intron 3 1031)	ctagatgggctgtgggcacc C/T gscatgtccccctcttgacct
NDFUS6	19	3' flanking region 270	acttcagagacacaaagttgg G/C tcttaaggtgcatagttaag
NDFUS8	1	5' untranslated region -45)	agttgactctccctctccg A/C ttacatggctgtctgtggcaa
NDFUS8	2	(intron 1 163)	aggttgacagcgggagcgccc /C/ cttagggcgtatggccgcc
NDFUS8	3	(intron 3 123)	tccttagccttggttccact /C/ ttaaatgattaigtatg
NDFUS8	4	(intron 5 -305)	aggcagagcagcggcggcac G/A glegctcaccttgtaalc
NDFUS8	5	3' flanking region 491	ggcccttgacttggccttggct G/A cagccacatctcttctctg
NDFUS8	6	3' flanking region 693	ttcaacttatitcagtagt G/A aaaccagctccagagatga
NDFUS8	7	3' flanking region 1267	tttccagagatgaaccac G/A tcagagagtgccatggagcc
NDFUS8	8	3' flanking region 1362	cccttgcttcttctcttac C/T glegcttccagcgacttacc
NDFUS8	9	3' flanking region 1440	tgtagaagacggcctatggc G/A ccaacacacagttcccccac
NDFUS8	10	3' flanking region 1572	cagctccacagcttactact C/A gctgtgtggggcttagggat
NDFUS8	11	3' flanking region 783 784	caagagaccttaaccccccc C) atctacatcatcttccaaa
NDFUS8	11	3' flanking region 783 784	cagagaccttaaccccccc attacatcatcttccaaa
NDFUV1	1	(intron 3 670)	ctgggtggagttggggtagca /C/ ggaattgaagaccagctctt
NDFUV1	2	(intron 6 160)	tgctcggcggcccgagccttga C/G catgcatctctttgggaac
NDFUV1	3	(intron 9 27)	accacctcttgaatagacac G/A gagggttgggtggcatalcaagg
NDFUV1	4	3' flanking region 1111	tgtaggcttaggttcagcccc A/C atccagttccaaagccacc
NDFUV1	5	3' flanking region 1658	gaatgcggagatgctctgtg C/A gccaccacctatctccgggc
NDFUV1	6	3' flanking region 1713	gactctgggctggcgggttaca C/T ggggctggcactggatgaag

遺伝子名	No	存在位置	配列	配列番号
NDUFV1	7	(intron 4 - 214)	tggtatgaattttttttttt /Δ ecctcaaaatataagattt	3645
NDUFV1	8	(3' flanking region 772-774)	tgactcgggttcaggc /C/Δ ctgtaacacttggtttgaa	3646
NDUFV2	1	(intron 1 526)	ggaaatctggcgaataaa /C/ gatacaactaacctcga	3647
NDUFV2	2	(intron 1 5689)	tcttggatggtagtatgt /G/ tgaacacagaagaataca	3648
NDUFV2	3	(intron 1 14767)	ccaaatcagccagcagag /C/ gggcagaaggtaacaa	3649
NDUFV2	4	(coding region (129Val))	aggaatttgcataagacag /C/ta tgcataa tggacctggag	3650
NDUFV2	5	(intron 2 - 289)	cagaagatctactctctaa /G/ gaagctgataaacatttt	3651
NDUFV2	6	(intron 2 - 168)	tttacttggataatctt /C/ atcaaatgigtgtttagaca	3652
NDUFV2	7	(intron 4 677)	aaacacatactatttga /C/ tgaatgataatcacatacca	3653
NDUFV2	8	(intron 4 2795)	taagtacactttcaaaag /A/ gatttataatataalaga	3654
NDUFV2	9	(intron 5 102)	caactctcactctattg /G/ atcgtacttacttactagaa	3655
NDUFV2	10	(intron 7 5466)	tgataagagctttaagata /C/ caaatcctcagctttcaga	3656
NDUFV2	11	(intron 1 13562 13563)	tactttaaaatatactct /C/ ttattataagatacagctct	3657
NDUFV2	11	(intron 1 13562 13563)	tactttaaaatatactct /C/ ttattataagatacagctct	3658
NDUFV3	1	(5' flanking region -222)	cctcgcaccccccacac /G/ cccagcgcgcgcagggcac	3659
NDUFV3	2	(5' flanking region -111)	tggcccaaggagagacat /A/ gccctacttgggaatgcgac	3660
NDUFV3	3	(intron 1 137)	tggccgcctgacccctc /C/ ctggcctcagagctgaccc	3661
NDUFV3	4	(intron 2 152)	tatacagaacacagaacta /C/ aacagattttagaccaaca	3662
NDUFV3	5	(intron 2 6304)	ttcacagatgaggggttcc /G/ aaatttttgcagaagaagc	3663
NDUFV3	6	(intron 2 6433)	tgcctcgtcttcaatc /C/ tccagctctctgcttctga	3664
NDUFV3	7	(intron 2 6563)	ctttgaaaacagagacccc /C/ aggttacagatacagaata	3665
NDUFV3	8	(intron 2 9619)	actatctctggcagcag /G/ aagagccctctgcagac	3666
NDUFV3	9	(intron 2 9858)	agga tggcactctttaa /G/ agacatcgttttcttaac	3667
NDUFV3	10	(intron 2 11673)	cttggatgataagccctgt /A/ gtagcagcagcttcatata	3668
CG1	1	intron 1 + 85	ttatcagtaaggtggctc /G/ taactctttctctgttgg	3669
CG1	2	exon 3 + 68	gagccagatccgaatgt /C/ gtaggagctctgggggac	3670
TGM1	1	exon 2 + 179	tgcgaatatggcagaaga /C/ gactggggaccttgaacctc	3671
TGM1	2	intron 9 + 1594	acttaccactctgtctctc /C/ tccagggctctctcttca	3672
TGM1	3	intron 9 + 1933	cgcacactctgtacctgcc /C/ ccatctccagcagagacac	3673
TGM1	4	intron 10 + 54	tcaatcactgggtctctgt /C/ caacttccacctgactga	3674
TGM1	5	intron 10 + 420	aggaagccggggctgagcc /A/ ccttcaagacctcttgcctca	3675
TGM1	6	intron 12 + 101	ggagatcccgggggaagcc /G/ catgtaggagagcagagctc	3676
TGM1	7	intron 13 + 72	ggataagagactcagagtg /G/ ggcctagcctcagcagagcc	3677
TGM1	8	intron 14 + 1671	atctttaccacaccccca /C/ catggtagggaggttcttca	3678
TGM1	9	intron 14 + 1691	ccatggtagggaggttctt /C/ tcttaaggatccagagc	3679
TGM1	10	intron 14 + 2883	tcccggctctctcttctag /G/ gagctcagaacacacttcaa	3680
TGM1	11	intron 14 + 3158	ggaaacctctagaacacag /C/ tccagcraatggctttgcc	3681
TGM1	12	intron 14 + 3816	cagaataaaagtaggaag /C/ gagaagaaggttccgttag	3682
TGM1	13	exon 15 + 233	cttcaaggttgaacttacc /C/ atcccaagacatagagact	3683
TGM1	14	exon 15 + 369	ggagctagcttcttcttca /C/ tggggacagactactaata	3684
CPIA1	1	5' flanking - 1061	ctcccgagctctctctccc /C/ tgcgtacttgcagagcccc	3685
CPIA1	2	5' flanking - 1035	tgaatgaagccccccccc /G/ agccggggaaatgggttggct	3686
CPIA1	3	5' flanking - 1020	ggccgggcccggggaatgg /G/ cctctgggttgcctcgggg	3687
CPIA1	4	5' flanking - 947	cgcgccctccgggacagagg /G/ aggggggacggcccccag	3688
CPIA1	5	intron 1 + (1326-1334)	catctattgagaattgagcc /A/ 8-9 ccttggccttggattctctg	3689

遺伝子名	No	存在位置	配列	配列番号
CYP1A1	6	intron 1 + 1357	ctggcttggatttcttctgac t/c aagagctcaatctagctgg	3690
CYP1A1	7	intron 1 + 1590	ccactttcaaaagagata c/t atgtacagcagctggaaat	3691
CYP1A1	8	exon 2 + 160	gaatccacagggccatagg g/a ctggccttgatltggcaca	3692
CYP1A1	9	3' flanking + 1710-720	caccgagatttccagctc t/c 10-12 gaacgagcttccactgt	3693
CYP1A1	10	3' flanking + 834	gctcagcctcccaatagg c/t gggactacagggccctgcca	3694
CYP1A2	1	intron 1 + 103	gcttggcttaggttagggg t/c ctgagttccggcttggct	3695
CYP1A2	2	intron 2 + 371	cttccctgttccactcaa c/t clttctcttcttgaatlg	3696
CYP1A2	3	intron 4 + 44	atagcaggaagaacttga g/a accagattttgtttcag	3697
CYP1A2	4	intron 4 + 206	aagatgacatgggtataa g/c agggataatcatggcgca	3698
CYP1A2	5	intron 5 + 623-648	tggccaggttgcctgctgc t/c 22-26 catgaaatatagaaacat	3699
CYP1A2	6	intron 6 + 81	tccctctaggaacacttta t/c ataataagaaagggggacct	3700
CYP1A2	7	exon 7 + 181	ctggcattcttctatagca a/t ctggattctagcttccgcc	3701
CYP1A2	8	exon 7 + 295	cggtctgcttctcatalaa g/t taagaagacacacattc	3702
CYP1B1	1	5' flanking - 3659	tgtatcttggagaatcac g/a gttatcttctctgcatatg	3703
CYP1B1	2	5' flanking - 3149	tgcacacttaccacacta g/c ttcttctgatttttgatca	3704
CYP1B1	3	5' flanking - 1222	ggggagacacacccgcc g/a agcccttccgcttccctta	3705
CYP1B1	4	5' flanking - 375	ttccggagagacgtcag g/c gctgagagagagagagaggt	3706
CYP1B1	5	5' flanking - 265	ctgggacacccctggcccl c/t gattggaggttgcctatag	3707
CYP1B1	6	intron 1 + 129	tggccaggttctgtccca g/a attgcagagacgtttacgg	3708
CYP1B1	7	intron 1 + 319	tgaatgacacgttcttcc c/t tcttcccgagatggcac	3709
CYP1B1	8	exon 3 + 1799-800	agcttctggagatttttt t/c gactcaagactttaaaggc	3710
CYP1B1	8	exon 3 + 1799-800	agcttctggagatttttt gactcaagactttaaaggc	3711
CYP1B1	9	exon 3 + 1284	agtagtgggttctcaga g/t ttaataaallttaagta	3712
CYP1B1	10	exon 3 + 1398	tcgacaagaaataaaaaa a/Δ gccagcagcttttaatta	3713
CYP1B1	11	exon 3 + 1488	tcataaggttaaaaaaaa a/Δ gtcaccaaatatgaaat	3714
CYP1B1	12	exon 3 + 1564	ttgaataatattgctctt g/a taatatgaaattgaaag	3715
CYP1B1	13	exon 3 + 1762	ttgaattctattataata c/Δ aaatcttctttaaata	3716
CYP1B1	14	3' flanking + 2216-2226	agccaccttcttcttttc t/c 10-12 aaatttcttcttcc	3717
CYP1B1	15	3' flanking + 2230	tttttcttcttcttcttc a/Δ ttatcttcttcttcttaca	3718
CYP3A4	1	intron 2 + 1754-763	cacaaatgatttggggg t/c 9-11 acacaagcggaatcacat	3719
CYP3A4	2	intron 7 + 258	accataatcaacttctec c/t tctatggatttgcctattct	3720
CYP3A4	3	intron 7 + 894	tcttcatctctctctctag c/t ggtctctcttatacatabac	3721
CYP3A4	4	exon 9 + 32-33	ttcttcaacttctcttga a/Δ ctctcagaattcaaaagaa	3722
CYP3A4	4	exon 9 + 32-33	ttcttcaacttctcttga ctctcagaattcaaaagaa	3723
CYP3A4	5	intron 10 + 12	cccaatagggttagtgga g/a tacaaggagagagagaggg	3724
CYP3A4	6	intron 10 + 459	agacatgtaatttttttt t/Δ gaaaggttaacatcttctc	3725
CYP3A4	7	intron 10 + 608	agcccttctgaatctctcc c/t acitaaactctctccacac	3726
CYP3A4	8	intron 12 + 2467	tttttggcatttacttccat a/g gaatacaaaatatactctg	3727
CYP3A5	1	exon 1 + 69	ggaagctcacagacacag t/c tgaagaagaaagtgcccat	3728
CYP3A5	2	intron 1 + 955-956	tctggatgtagaggttcca a/Δ cctgtccatttaacttctac	3729
CYP3A5	3	intron 1 + 1126	tgttgatgtagaggttcca cctgtccatttaacttctac	3730
CYP3A5	4	intron 1 + 1145	tatggtttaaatttctat a/g tggtttaatttcttctt	3731
CYP3A5	5	intron 1 + 1543	ttcatggcttctggccac c/a gtagaggtctctcaagggc	3732
CYP3A5	6	intron 1 + 2366	cttatcttatatgctact g/a caccatttctctataacagg	3733
CYP3A5	6	intron 1 + 2366	cttatcttatatgctact g/a caccatttctctataacagg	3734

遺伝子名	No	存在位置	配列	配列番号
CYP3A5	7	Intron 4 + 1813	tggttcaatttttactcttc G/A tctcttcactccttgaagt	3735
CYP3A5	8	Intron 4 + 1887	aatcacataaagaagtg A/T ttgtgaagcaaggatattt	3736
CYP3A5	9	Intron 4 + 3384	gagttctccatttggct C/T acaagaanaagtcatttct	3737
CYP3A5	10	Intron 4 + 3415	agtcatttgcacttttca T/C tgaacattctcttcatcc	3738
CYP3A5	11	Intron 4 + 3760	aggaataacacatcgaagtc G/A cacacacacataaactlga	3739
CYP3A5	12	Intron 4 + 3885	acaaattcacttcagtgagca C/T tgcattagggctcttctgt	3740
CYP3A5	13	Intron 4 + 5061	taccctacttttcaaaaaa A/Δ tccacacatcagtcacatcc	3741
CYP3A5	14	Intron 4 + 5316	ccagatggcttggcttcccc A/T cttcccccccccaccat	3742
CYP3A5	15	Intron 9 + 77	gttcgaaatgtcaggaag C/T taltccaggaagatagaat	3743
CYP3A5	16	Intron 9 + 1791	aaattttattggaaaaag C/T ctacccatttttactaca	3744
CYP3A5	17	Intron 12 + 1408	atttaataaaaaaaaaa A/Δ cagaatccacagaatttg	3745
CYP3A5	18	3' flanking + 542	tgagaaaataatcatalgt T/C calctgccttcttllgaaga	3746
CYP3A5	19	3' flanking + 737	atgaacacttaataaaaat T/C gtcaattctcagttgatg	3747
CYP3A5	20	3' flanking + 804	ttttcttttttttttttt A/C ttctctctcttttctgaat	3748
CYP3A7	1	5' flanking - 1680	cccaagaacatagtgcttc G/A ggcacatctcggcacaca	3749
CYP3A7	2	5' flanking - 1191	tagaatactctcacttctt A/C aaaggagcctatttgcctt	3750
CYP3A7	3	Intron 1 + 1173	ccccatttcaatatacct G/A cttagcagttatcttaaac	3751
CYP3A7	4	Intron 1 + 1587	ttttcttcttgccttctca T/C tcttcttttttttcttctt	3752
CYP3A7	5	Intron 3 + 762	tccagtgcttgccttctcc T/C tcttcttttttttcttctt	3753
CYP3A7	6	Intron 7 + (1060 - 1069)	atggtttctgtttctcttgg 109-10 ctacagaagttcttccattc	3754
CYP3A7	7	Intron 11 + (592 - 594)	taagacaagttaggaggag AAG/Δ gaggaataatagaacaacaa	3755
CYP3A7	8	Intron 12 + 911	ccccctcatatcaataat C/T tctcattttttcttccatttaa	3756
CYP3A7	9	Intron 12 + 1137	gtctgtcagagaataa T/Δ atcagtccttttgaat	3757
CYP3A7	10	Intron 12 + 2147	tatttcagtaattttttt T/Δ acttgcattcttcttctt	3758
CYP3A7	11	exon 13 + 218	ttcatccatgtctgcata A/C ataacagggattctgtag	3759
CYP3A43	1	Intron 1 + 3579	tcatctcacttttttttt T/Δ ctcaaaatgacatctcac	3760
CYP3A43	2	Intron 2 + 2427	taagagaacttttttttt T/Δ ccttttttcttcttgcgtccag	3761
CYP3A43	3	Intron 3 + 3034	ttttatagactagagaga T/C tctaaattacaaatttctt	3762
CYP3A43	4	Intron 3 + 3433	agtcagataacttttttt T/Δ cataaaggaccacagtaagt	3763
CYP3A43	5	Intron 3 + 3504	catgactcatttccaaca T/C aacttttcatlttggcatag	3764
CYP3A43	6	Intron 4 + 2767	taagtaactttgaanaaa A/Δ ttgtaataagcaaaagact	3765
CYP3A43	7	exon 5 + 22	aaactttaaggacttttca G/A aaatccattggacttaag	3766
CYP3A43	8	Intron 12 + (1585-1584)	tactttgagcccttcttc A) ccaagtcacttcagtgtag	3767
CYP3A43	8	Intron 12 + (1585-1584)	tactttgagcccttcttc ccaagtcacttcagtgtag	3768
CYP4B1	1	5' flanking - 333	gaacatttcacatgctctgt A/T tgaagaacagtggttatta	3769
CYP4B1	2	5' flanking - 18	gaacagcttgaagcagagctca C/T atgaagcctatagcttga	3770
CYP4B1	3	Intron 1 + 341	tccaagcccttggatagta C/T atagaatataagcaatccall	3771
CYP4B1	4	Intron 1 + 542	ccctatggcttgcacagag C/T gtgacaccttcccagttta	3772
CYP4B1	5	Intron 1 + 2856	ggagcatttccacatagtag G/A tctcagctatatttctggc	3773
CYP4B1	6	Intron 1 + (2923-2938)	caacaaattgtgtgtgtgtg (C) 17-8 agaatgccagctccagatc	3774
CYP4B1	7	Intron 1 + 6086	tttggaaacttaagacttgg C/T cacatctctagtgtgtgac	3775
CYP4B1	8	Intron 1 + 6598	tttttggaggttggagagag G/A cccatagtaggaagacagct	3776
CYP4B1	9	Intron 1 + 6660	acctaaaggttctcattcttg A/G aggaagacagctcttggggg	3777
CYP4B1	10	Intron 1 + 7242	ccctggcttctcttactca T/C gtgagactgttccctttagt	3778
CYP4B1	11	Intron 2 + 107	gctgtgtacttaagttctgg C/G agctgaaggttcccacctac	3779

通位子名	No	存在位置	配列	配列 番号
CYP4B1	12	Intron 3 + 361	atgggtggtagtagagacaa C/A ggcctgaccagaagcctgt	3780
CYP4B1	13	Intron 4 - 492	aaagctttcacatctaa C/A atgtctctcttctgtc	3781
CYP4B1	14	Intron 4 - 315	ggaattactatatacacc A/G tggaggagagctcacacct	3782
CYP4B1	15	Intron 4 - 157	ctaccacctctctctgta T/C tccagacaga tgaaggcag	3783
CYP4B1	16	exon 5 + 22	acaagtggagagaagct C/T ggaaggaatctcttacc	3784
CYP4B1	17	Intron 5 + 125	ccaggagacttgcctgac C/A ggaagacagacttgcctat	3785
CYP4B1	18	Intron 5 + (287-289)	tcttaagcaatctctct C/T Δ acctctctttagcaggac	3786
CYP4B1	19	Intron 6 + 54	ggctggcttctctctctg C/T cctctatgcccctctcat	3787
CYP4B1	20	Intron 7 + (99-100)	agctttagcatctctccc TC tttctcagcaataataacc	3788
CYP4B1	20	Intron 7 + (99-100)	agctttagcatctctccc TC tttctcagcaataataacc	3789
CYP4B1	21	exon 8 + 114	tcttggttctctctgcat C/A ggcctgaccctgagacaca	3790
CYP4B1	22	exon 8 + 138	tatacctagcaccacagat C/T attctagagagagctcgc	3791
CYP4B1	23	Intron 8 + 247	agaagttgcaacaagagg C/T gataatttggctgaact	3792
CYP4B1	24	Intron 8 + 366	tatggggctgaacaggagctg A/G aacagctggagagccagtt	3793
CYP4B1	25	Intron 8 + 650	cttggcttggctacaca C/A cctctcttctcttgggt	3794
CYP4B1	26	Intron 8 + 844	tcatatgagaaatcccc C/A ccaggaggtatccagacaca	3795
CYP4B1	27	Intron 8 + 1767	tccattcaaaaatgllct C/T gtgtgtgtctggcagagat	3796
CYP4B1	28	exon 9 + 33	tatgcatgaagaagcttc C/T gctctaccaccctgtgccc	3797
CYP4B1	29	Intron 9 + 652	atgagagtgctgcatgac C/T ctctgctacgtggcagctgctc	3798
CYP4B1	30	Intron 9 + 774	cctgtctacaaactctgtt C/T tcccacaggaagcctgctc	3799
CYP4B1	31	Intron 10 + 33	tggctggagagctcagacag C/T gggggagactggagagctca	3800
CYP4B1	32	exon 12 + 224	ccagatggctcagctgttaa C/A ctcccaggcaccaccctcc	3801
CYP4B1	33	exon 12 + 270	ctggatggagagagctggg C/A ccccagctctcagggagct	3802
CYP4B1	34	3' flanking + 129	tctgtctcagctcagct C/A gctctcagctcagctcagct	3803
CYP4F2	1	Intron 1 + (145-146)	caaacctctggcacaactca C/A Δ gtagatcagctggccttt	3804
CYP4F2	2	Intron 1 + 193	tttaatgctctctctct C/T tttccattctaaagcttca	3805
CYP4F2	3	Intron 1 + 324	ccctctctacctcggcac T/C ggcctccctggcctctccac	3806
CYP4F2	4	Intron 1 + 367	tcccggaggtctctggacc C/T tttctggacctcagagatct	3807
CYP4F2	5	Intron 1 + 402	ggatctaccgctcactccc T/C ctgcccctgcagagatgtccca	3808
CYP4F2	6	exon 2 + 35	gctctctctggctggcctc T/C ggcagtgagcagcctccct	3809
CYP4F2	7	exon 2 + 166	caggttttcccaaaccccc A/G agaggaactggttttgggg	3810
CYP4F2	8	Intron 2 + 125	ggcagagaagcagagagggc A/G tcttactcattctctctct	3811
CYP4F2	9	Intron 2 + 440	ggccgctctccactctcac T/C acaccgaaggacactttct	3812
CYP4F2	10	exon 3 + 48	gttctgactcagctggggc C/T acctaccacagggctttaa	3813
CYP4F2	11	Intron 3 + 701	agacttcaacccagcttggg T/A cctttctctggcccctctg	3814
CYP4F2	12	Intron 3 + 742	cttccactgttggcgggc C/A aggcctgagcagggagatag	3815
CYP4F2	13	Intron 3 + 1020	gctttagcttctcactg C/A cttttctctatcaggtggcc	3816
CYP4F2	14	Intron 3 + 1039	gcctttctctatcaaggtgg C/A cttttctctatgctctcac	3817
CYP4F2	15	Intron 3 + 1040	gcttttctctatcaaggtgg C/G ttttctctatgctctcac	3818
CYP4F2	16	Intron 3 + 1920	ccactctgttaccctctgtt C/C ctgtttctctatgctctggg	3819
CYP4F2	17	Intron 3 + 1945	tgtctcatgtctggggctg T/A cttctaatctgtctgtatata	3820
CYP4F2	18	Intron 3 + 2621	agatctgtgtagaatgctga C/A ctgtactcaaggggttgcgaa	3821
CYP4F2	19	Intron 3 + 2655	tgttggatctgttggagggc A/G tctcaaggaactctggagcc	3822
CYP4F2	20	Intron 6 + 194	gggttgaactgtgggggt C/T gtcagagctctttagggac	3823
CYP4F2	21	Intron 7 + 67	tgtgaatgtctcaga tgaag C/A atttgaacttgaatgaaggg	3824

遺伝子名	No.	存在位置	配列	配列番号
CYP4F2	22	Intron 7 + 2811	ttcagaaggaattaccatt /g aattctcttgaactcagat	3825
CYP4F2	23	Intron 7 + (3096-3097)	gggtgggggttggggggg G ttactcttcttccaga	3826
CYP4F2	23	Intron 7 + (3096-3097)	gggtgggggttggggggg ttactgcttcttccaga	3827
CYP4F2	24	Intron 8 + 145	gtctgtcttcttgggt G/A ctgaagagccagagaccc	3828
CYP4F2	25	exon 9 + 44	ctctctgggtcttgatcca G/ ctgcaagagccaccagaata	3829
CYP4F2	26	exon 11 + 48	gaaccatcacaccagct G/A tggccggagccctggggg	3830
CYP4F2	27	Intron 12 + 108	tgttcaagtccagcttc G/ ttccctcaccctcttggag	3831
CYP4F2	28	Intron 12 + 285	gatggagatccagcacag A/ tacccttcttcttctt	3832
CYP4F2	29	exon 13 + 238	agtgagagctagaattacc G/A taagaccctgttccagct	3833
CYP4F2	30	exon 13 + 342	tatgtaataattctagc G/A gccctatttcaagttagcaa	3834
CYP4F2	31	exon 13 + 563	tgttctcttcttctttaa /C gaatttccagacagacca	3835
CYP4F2	32	exon 13 + 707	aatgttctggagcttata G/C taagagagatagcacac	3836
CYP4F3	1	Intron 2 + 258	caataagacactctgagg G/ ctctggagcaggggttgg	3837
CYP4F3	2	Intron 2 + 916	ttaggacatgtcttgatc G/ acactgcttccacaaact	3838
CYP4F3	3	Intron 2 + 3417	atccagcttccacagct G/ acttctcttcttggcttag	3839
CYP4F3	4	Intron 2 + 4090	gagacataaattgggtct G/A tgtcttcttcttccagattca	3840
CYP4F3	5	Intron 3 + 89	tgtcttcttccagagct G/A ctgcccagctgscagacag	3841
CYP4F3	6	Intron 3 + 243	tcaagtctctatcgact G/ gtctgtcaccctgtattt	3842
CYP4F3	7	Intron 3 + 502	agcttggagccagggctc G/C taatgaacttcttgaagaca	3843
CYP4F3	8	Intron 3 + 755	ttttggccatgtcagg G/ tctaacacatgtcagctc	3844
CYP4F3	9	Intron 3 + 855	ggacacagagctcttcta G/A ctcttcttgaagacattc	3845
CYP4F3	10	Intron 3 + 970	ctgacatctcttctagct G/ catgttagcagctatc	3846
CYP4F3	11	Intron 6 + 122	ggagatttcttaccat G/ gttaagagctggatgaat	3847
CYP4F3	12	exon 7 + 139	ggcgacagcttcaazat G/A catctcagagagcgcc	3848
CYP4F3	13	Intron 7 + 2107	caggtgcagcttatttt /Δ ctgaagagcttcttcaag	3849
CYP4F3	14	Intron 7 + 2255	gacaaagaggtctaggag /A gcaagatggcttgggttc	3850
CYP4F3	15	Intron 8 + 132	cttcaatcagagcttctt G/C cactctgggtcttgaagca	3851
CYP4F3	16	exon 9 + 59	taccacttcaagaccc G/A gaatacagagagcctatg	3852
CYP4F3	17	Intron 9 + 13	atgaatgttgaagtcagct G/A ctgggtccctgttcttgaac	3853
CYP4F3	18	Intron 9 + 36	gggtccctgttcttgaact G/C tctatgtctgttcttccc	3854
CYP4F3	19	Intron 9 + 167	accatcttcttcttctt G/G aaageltataggcccttag	3855
CYP4F3	20	Intron 9 + 369	tccctaatcttaccctt G/A tcaagtcaggatttata	3856
CYP4F3	21	Intron 9 + 458	tcatcttcttcttctt G/C gttaagcaaatcttctata	3857
CYP4F3	22	Intron 10 + 46	ctcttggtagaagaggg A/C ccttcagagagagacattg	3858
CYP4F3	23	Intron 10 + 63	ggcccttcttcttctt G/A ttgtcttcttcttcttctt	3859
CYP4F3	24	Intron 11 + 14	ccctgagctcagggccccc G/G tctgtttttgtcttctt	3860
CYP4F3	25	Intron 11 + 84	ga tcaagagatccacat G/A ctctcttccagacacacac	3861
CYP4F3	26	Intron 11 + 113	caagcacacacacat G/C tcaaggtctgagagcttgg	3862
CYP4F3	27	Intron 11 + 164	cggcaaccttcttctt G/G cctcaggtcttcttcttctt	3863
CYP4F3	28	Intron 11 + 165	ggcaaccttcttctt G/C ctccaggtcttcttcttctt	3864
CYP4F3	29	Intron 12 + 156	gaagagccacagagtag G/A ttgggttcttcttcttctt	3865
CYP4F3	30	Intron 12 + 253	gagcttcttcttcttctt G/A atataagagccacacacac	3866
CYP4F3	31	Intron 12 + 346	lgggttcttcttcttctt G/C cgggttcttcttcttctt	3867
CYP4F8	1	5' flanking - 61	accatttcttcttctt G/ tcttcttcttcttcttctt	3868
CYP4F8	2	exon 1 + 67	gtggagcatcttcttctt G/ ctcttcttcttcttcttctt	3869

遺伝子名	No.	存在位置	配列	配列番号
CYP4F8	3	intron 1 + 707	tacgcacaggtattaccca /G/ tatcttcacattatccacgtg	3870
CYP4F8	4	intron 1 + 857	acacccctaccctcacatc G/A/ tgcacacgttggccagaag	3871
CYP4F8	5	intron 1 + 907	tgcctctccacccccc G/A/ tgcaggagcatcttcttat	3872
CYP4F8	6	intron 2 + 668	tgtgcattccacataig /C/ tcatctctcttctccag	3873
CYP4F8	7	intron 2 + 818	ggcagagacacatgctca G/A/ gccccaatactgaatgac	3874
CYP4F8	8	intron 2 + 1079	tatgttgggtatgacaa /C/ atgttggaccatgtagagc	3875
CYP4F8	9	intron 2 + 1194	cggctccctttatccccc G/A/ accctcttctctctctg	3876
CYP4F8	10	intron 5 + 45	acatggagtagagtgagg G/T/ gtgggtggagagacaaa	3877
CYP4F8	11	exon 8 + (19-20)	ggccatgacacagggcag (GCCAG) tggccctctcgggtctgt	3878
CYP4F8	11	exon 8 + (19-20)	ggccatgacacagggcag tggccctctcgggtctgt	3879
CYP4F8	12	intron 8 + 222	tttatctccacacttg G/G/ tatcagagctagtaaatc	3880
CYP4F8	13	intron 8 + 334	cttggagatattacggcaa A/T/ accgaatgactttggacc	3881
CYP4F8	14	intron 8 + 1999	tctaaagatattatctc /C/ tgcilltagatgactag	3882
CYP4F8	15	intron 8 + 4184	caggagggcgtatgctc C/T/ ctggaataattgttgggttt	3883
CYP4F8	16	exon 9 + 119	acgtggctccacagacgc C/T/ gggtcatccccaaggtgccc	3884
CYP4F8	17	intron 11 + 282	gggttgggggttccggacct G/C/ gtctctggcagtgaggccc	3885
CYP4F8	18	intron 11 + 340	tgcagtcagaccttccact C/T/ ggcctccagagactgcatgc	3886
CYP4F8	19	3' flanking + 35	atcacctaccttgcacaa /C/ tacccttgcagattccggt	3887
CYP4F8	20	3' flanking + 83	ctgtgttggccctgtacct G/C/ agtcccgagatggccagta	3888
CYP4F8	21	3' flanking + 90	ggccctgttccctacgtccc A/G/ cggatggccagtagggggc	3889
CYP27A1	1	intron 1 + 295	aggagagagctgtctggga A/G/ ggaatggcagagagcaatg	3890
CYP27A1	2	intron 1 + 17503	caatcataagcccttctga C/T/ ctctctagagagagagggac	3891
CYP27B1	1	intron 6 + 173	caacccctacccatctctg C/T/ tctctccatttggcttgg	3892
CYP27B1	2	intron 8 + 113	ataatagcccttgtagaat G/C/ atctctgaaatataatgaag	3893
CYP27B1	3	3' flanking + 1081	taccctgaaatcagtaga G/C/ aatctgccaatccctgctc	3894
AADAC	1	exon 1 + 29	attaagtaacatctcagg C/T/ atatcagtaggttacctt	3895
AADAC	2	intron 1 + 138	gcctggcccttggacaagt G/A/ ttaactagaaatgtgtttg	3896
AADAC	3	intron 1 + 142	tggcccttggacaatgttta C/T/ ttgaaatgtttgttttt	3897
AADAC	4	intron 1 + 1033	tctcagagagagacacaca A/G/ gtaaaaacacccacacaca	3898
AADAC	5	intron 1 + 1263	ttttttccctctatattgc /C/ gctctgctctacataatga	3899
AADAC	6	intron 1 + 1366	ctctgtagccttttaatta A/G/ ttaattcttcttcttctta	3900
AADAC	7	intron 1 + 1369	tggtagccttttaatttaatt A/C/ attcaatcttcttctacat	3901
AADAC	8	intron 1 + 2501	ggttacagaagaatgggtgg C/A/ ttggccaaaataatataatg	3902
AADAC	9	intron 2 + 46	tgtcactaggttagtctcca A/G/ acattttactaagctctcag	3903
AADAC	10	intron 2 + 1971	aaatagagtttagttagag A/C/ attttctttttttttttg	3904
AADAC	11	intron 2 + 1988	gagaaatttctttttttttt A/G/ tgcagagaaatataacaa	3905
AADAC	12	intron 2 + 2341	aggctctttcttatgtccc C/T/ atgcagacttgggtgacct	3906
AADAC	13	intron 2 + 2546	gtctcacaagaagatcaa /A/ ggcaraatgtccagacaaa	3907
AADAC	14	intron 2 + 2609	tagagagcttctggaaac /C/ tgaattcttcttcttcttctga	3908
AADAC	15	intron 2 + 2663	tataatacagttttaaatt /C/ gtctctgctattttaaagta	3909
AADAC	16	intron 4 + 605	tgttcagtaaaatattata /C/ taagttaggtgaatgagatca	3910
AADAC	17	intron 4 + 621	tatataggttaggtgaatga C/T/ atcatgtaattgttgagacta	3911
AADAC	18	intron 4 + 670	tttagagcttcaagcaattc A/G/ tataatcttctgactgtglat	3912
AADAC	19	intron 4 + 1680	gttaaatgtggataaatc C/T/ acaatttggcaaatatttgg	3913
AADAC	20	intron 4 + 1748	atttagagcttctacatc /C/ tttatagtatattatcacact	3914

遺伝子名	No	存在位置	配列	配列番号
AADAC	21	intron 4 + 171	taagatattacacccctc G/A aaaaacacaaatattttt	3915
AADAC	22	exon 5 + 238	caagtcattctcaaat A/G ttaattggagttccctc	3916
AADAC	23	exon 5 + 678	ttagaatggcttcttctia A/G aatggcttgaattgaccca	3917
AADAC	24	3' flanking + 208	aatctcaaaaaaa A/A Δ tcactgtagtactttggaga	3918
CEST	1	5' flanking - 983	tattcttagccagagta A/C cacagtggtttagtaatt	3919
CEST	2	5' flanking - 814	tcacattcttcaatcac A/C cctacgctctccacccta	3920
CEST	3	5' flanking - 248	agctcgcaagggtgaccc G/A Δ ttagccacaagcagttggg	3921
CEST	4	intron 1 + 22	tgaactcttgaagcaaa A/A Δ aigcgggacattttttaa	3922
CEST	5	intron 1 + 30	tcgaagtcacaaatgcgg G/A cacttttgaatcctttt	3923
CEST	6	intron 1 + 1652	aaaggaatctctagctag C/A atgacacccagtggttc	3924
CEST	7	intron 1 + 1726	ctctctgaactctcagca A/C tcttagcgggtcccgccc	3925
CEST	8	intron 1 + 2716	tgtctcaaggaagttatc A/G cagattatttgtaattagc	3926
CEST	9	intron 1 + 2747-2749	tgaattacacacacaca AA/A Δ gaaagagctaaataga	3927
CEST	10	intron 1 + 3288	ttattgtccattaaagaa A/A Δ ctgaagccttagctgca	3928
CEST	11	intron 1 + 3591	gagaataggaacccct A/G tctatctctcatccagcat	3929
CEST	12	intron 1 + 3819	tcttttctcatattttt A/G cctggatgtttttatgctc	3930
CEST	13	intron 1 + 3880	aaccagctcaatgggttag G/A agacatgacatcctc	3931
CEST	14	intron 2 + 74	gaatcaagcagtcctctga A/C agactgactcttgcctgg	3932
CEST	15	intron 2 + 552	atgaaggtgtgtccattca C/A cctggcgaagctgggaagaa	3933
CEST	16	intron 2 + 985	cagatttttagatgaaag A/C attatgattatattatgt	3934
CEST	17	intron 2 + 2001	ttggcagtcagggcggca G/A acatgtagaatacacctc	3935
CEST	18	intron 3 + 2119	cagtgagtcagatagtc A/C agacttgaaggaatggag	3936
CEST	19	intron 4 + 127	taaggaatcaagcccttc G/A taatggacacacttacc	3937
CEST	20	intron 4 + 347	cttatcatcaccttagag A/G cagccacacagtgaaagtt	3938
CEST	21	intron 4 + (1984-1985)	gtggtctgaaggtctgca C) tgaactctctctccccc	3939
CEST	21	intron 4 + (1984-1985)	gtggtctgaaggtctgca tgaactctctctccccc	3940
CEST	22	intron 5 + 766	gaatggcgaagggctgac A/C cactatggaattctcagtc	3941
CEST	23	intron 5 + 825	agatgaacttagctggaa A/G agcaggtgagtcacagccc	3942
CEST	24	intron 5 + 828	gtagatcagcctggatag C/T gagttagtcacagccccac	3943
CEST	25	intron 5 + 868	ccttgagcatgaactcc A/A cccctcactctgctcag	3944
CEST	26	intron 7 + 68	acttctatttcagctgc C/G tcttgcacagggacatttc	3945
CEST	27	intron 7 + 681	cttcaaaatcaacatcca A/G ttatcctctgctcctagtt	3946
CEST	28	intron 7 + 885	aggaciatcaagagagaa A/C aatctatatacttcgagg	3947
CEST	29	intron 7 + 2151	gtctgtaactgaatatt C/G agaggttgaatgcttcagac	3948
CEST	30	intron 7 + 2470	atatagatatcgaattcac G/A gagttagtcgggaagacct	3949
CEST	31	intron 8 + 128	ctgtttgttctgagccc A/C gagagggtagtgactcac	3950
CEST	32	intron 8 + 2618	cttagtgaacacatgaat A/C aggcctctcttaactgilea	3951
CEST	33	intron 8 + 2665	aaaatttatcatcaagat G/A aaaccttaaaatgaagacatg	3952
CEST	34	intron 8 + 3785	ccatggcagtcgcatgccc G/A gtctatggctactgtctcac	3953
CEST	35	intron 8 + 3791	cgatggcagtcgaggtcta A/C gttactggtctcacctcag	3954
CEST	36	intron 10 + 222	gtggcgtggaagctctcat C/T cctaccctgggcttggct	3955
CEST	37	intron 10 + 230	gagaactgcatctcctacc A/C agggcctggctgctctttt	3956
CEST	38	intron 11 + 1177	ctagcaggtctctctacaca C/G ctttctacagaaagggcag	3957
CEST	39	intron 11 + 1311	ggcctatgctctgctctga A/G ctatataagattcccatc	3958
CEST	40	intron 11 + 2025	tttctatttggagtgcttaag A/G ttaaaattagcataaacat	3959

遺伝子名	No.	存在位置	配列	配列番号
CES1	41	intron 11 + 2029	catltagcatctaaagatta A/G aatlagcataaacatctcca	3960
CES1	42	intron 11 + 2317	cattcaaaaagctcttctt C/T ctatgttgcctctagitt	3961
CES1	43	intron 11 + 3887	caaatatttgcctctaatlc C/T gcltccaccctacagaccla	3962
CES1	44	intron 12 + 2311	gcaccttgcgcatactact C/A tgcactcttaggcctctgc	3963
CES1	45	intron 12 + 2331	gtlcaatgtatagccgccttg C/G agctcttgttttticagaa	3964
CES1	46	3' flanking + 71	aacgggtatgaagaagacga C/T gtgaagaagaaggttgcctt	3965
CES1	47	3' flanking + 362	ttlcaaggcatcttactgccc G/A ttgcacaggcttgcacacc	3966
CES1	48	3' flanking + 581	atttctgattcttgttagta C/T gtgaagaagcttaagcatg	3967
CES1	49	3' flanking + 1348	aaatctgtcttgcgagagga C/C agcaagcagctacagatcaac	3968
CES1	50	intron 1 + (1303-1321)	caacaagcttgcctctacc A/T 17-19 gtcaagcatgttgcagaca	3969
CES2	2	exon 5 + 60	ggcccaatgtgcctgcatctac G/A ctgggtccagcagaatalcg	3970
CES2	3	exon 12 + 256	agctctgtgctccacacac A/G cccctaaagagagaaagagt	3971
CES2	4	3' flanking + (155-172)	acacatctagaccctctctc A/T 16-18 gagaagtgtagatagaa	3972
CES2	5	3' flanking + (173-178)	tcaaaaaaaataaaaaaa (CA) 4-6 gtgtgtgtatagaagctaaa	3973
CES2	6	3' flanking + 377	ggccaaggtagagacacac C/G tgaagacagaggttgcagac	3974
GZMA	1	5' flanking -424	cttcagcttgccttgcctt A/G ctatcttctataaccacaa	3975
GZMA	2	5' flanking -134	agctccctgctggcagtaga G/C ccaatcaccatctctac	3976
GZMA	3	intron 1 + 1947	gataaggttctctctatc A/T acatgtatgttttgccttgt	3977
GZMA	4	intron 2 + 958	gactgctgcacacagtagaa C/T tagcttccagcagagaaaggt	3978
GZMA	5	intron 2 + 1525	gttggtgtatttatactag C/A ttatgaatgatagctttaat	3979
GZMA	6	exon 4 + 105	ttccaaagttgcagaggttgcgg C/G aggcctacacatagtcac	3980
GZMA	7	intron 4 + 696	atagaccttaccagagaa A/G ggtctcagatctcagttgt	3981
GZMA	8	intron 4 + 1141	ctgttcaaggaggtctccgg G/A ttccaacatgttcttatt	3982
GZMB	1	5' flanking - 961	tggttagcaaatgttactg C/T gacgttgttattgtctgac	3983
GZMB	2	5' flanking - 263	ggctgataccatacttacc A/G ttacttcataggttgcct	3984
GZMB	3	exon 2 + 109	gtcgggtgctctctgatac A/G agacgacttctgctgacag	3985
GZMB	4	intron 2 + (242-243)	tgggggcatcttcttgcata A/ aatacaaacctgaagcaatt	3986
GZMB	5	intron 2 + (242-243)	tgggggcatcttcttgcata aatacaaacctgaagcaatt	3987
GZMB	6	intron 4 + 131	atttctcttgcagagagaa G/A aggggactagactgcgttgc	3988
GZMB	7	3' flanking + 182	agggcttctgcaaatlacc G/A gaggcttatgttgcgttgc	3989
GZMB	8	3' flanking + 54	attctcagaccatctg C/T gctatcagagccatgacac	3990
GZMB	9	3' flanking + 184	tccaccaggttctccagg C/T cctgccttctgccaagct	3991
GZMB	10	3' flanking + 256	ccactttgctcttgcggctt C/A aggttaacttcttactctt	3992
GZMB	11	3' flanking + 406	ctgagctcaaggtctcagct C/A tccctcagcttgcgtctc	3993
ESD	1	5' flanking - 333	gtcttgcgacagagaggttg G/A aggggttgaatlaggctct	3994
ESD	2	intron 1 + 603	gtcttcttgcagagaggttg C/T aggggaatggatlagagcgc	3995
ESD	3	intron 1 + 698	tggttgcagagagaggttg C/T taagactacgtggaattaac	3996
ESD	4	intron 1 + 1864	gccttcatcagaggttgcac G/C tagtggagatgtattagagag	3997
ESD	5	intron 1 + 2389	tttgggacaccctgctctag G/A ttgttgaagagcagctggcaat	3998
ESD	6	intron 2 + 22	tazacttgttttattgttta C/C agttactctgacatttgcga	3999
ESD	7	intron 2 + 589	taaaatagatctctctctc G/A taagtcttattttaaagata	4000
ESD	8	intron 2 + 1499	tagaaaaatgtttttccac C/T gtaagttctcagtaatttella	4001
ESD	9	intron 3 + 92	cttattcagataattatag C/A cctcatttcttcttgaact	4002
ESD	10	intron 3 + 422	gtaaagagatttaacacac C/T gcacatacacatatacctat	4003
ESD	11	intron 3 + 581	agaaaaaccctgagaatgaca C/T aatttatttgaagccatagt	4004

遺伝子名	No	存在位置	配列	配列番号
ESD	12	Intron 3 + 2270	gccagtaataacatgagcc G/A tttaacataaattagctaat	4005
ESD	13	Intron 3 + 2951	taataaataaattgttca A/G ctccclacaaaagttgaa	4006
ESD	14	Intron 3 + 3003	aaatgcagaatttttgt G/A ccgtcagatcaacacaaa	4007
ESD	15	Intron 3 + 3097	aagaagcatcacagaactt G/C ccatgagggcccttggcc	4008
ESD	16	Intron 4 + 2616	tctaatagtcacagattia A/G tgggcacatctcattgccc	4009
ESD	17	Intron 5 + 392	tcctttctctctctgttaa C/T atcacacatacagttaaaca	4010
ESD	18	Intron 7 + 107	ttagataggactaaactt T/C tctagtttgagactttgg	4011
ESD	19	Intron 8 + 1091	aaatctactaatataagg G/T ttaacttllagtaactaga	4012
ESD	20	Intron 8 + 1652	tataagttgtgttaatga A/G tatatagaataaagaattt	4013
ESD	21	Intron 8 + 2048	agaaggaataaggccattt G/C ttaagaatccctgagatag	4014
ESD	22	Intron 9 + 11523-1526	ctgcacaataactctgaaa T/C 2-3 agttttttataaaaacagc	4015
ESD	23	Intron 9 + 2458	atagaagagaagcctatct A/G cctcttaagtcctaggacc	4016
ESD	24	Intron 9 + 3352	actaagataaataatggc A/G tactcagtcacatigaaact	4017
ESD	25	Intron 9 + 5292	aggcttaatgacataattc T/C cctcacatazagatacaaca	4018
ESD	26	Intron 9 + 5298	taagacataattctcccca A/C ataaataacacalccttt	4019
ESD	27	3' flanking + 798	tatgtacttgagaataat A/G catttaagttcctaagttat	4020
CEL	1	5' flanking - 1611-6171	tgatcaagcgaataattt A/G 7-7 ggaatttttttgaagaaaa	4021
CEL	2	Intron 1 + 20098	atctctaccaagttaccaat T/G ccttaagaagaatgttaatt	4022
CEL	3	Intron 1 + 120911-20924	taatgacatttaattactagc A/G 13-15 ctgaatatgactaaactga	4023
CEL	4	Intron 1 + 22374	ttaagtaataatgaaacagc A/G ccttgcacacattatcagtg	4024
CEL	5	Intron 1 + 122460-22469	ttaatttttttttagttgtg 109-10 cttttttttttatcacatg	4025
CEL	6	Intron 1 + 24205	agaatttgacttactcttg T/G gtcctcttgactacalct	4026
CEL	7	Intron 1 + 124404-24417	gcagatttlanctgaattac A/G 11-14 ccagataaatactctat	4027
CEL	8	Intron 1 + 26983	tagattttgatagttttag T/G ttttttttttttttttccaa	4028
CEL	9	Intron 1 + 26983-26999	tagattttgatagttttag 1014-17 ccaaaagggtgggggttgt	4029
CEL	10	Intron 1 + 32166-32174	tcaacttgcctggtacccag A/G 8-9 gaaaagccacttaataatc	4030
CEL	11	Intron 1 + 37217	aaatttgaagtgaaatga T/G ataaaatctgtaacaatia	4031
CEL	12	Intron 1 + 37685	taaltcaaaatgaattatca T/A tgaataattctattttaaa	4032
CEL	13	Intron 1 + 38032	cagccctaataatgaatga T/C tcaactatgtgccacacc	4033
CEL	14	Intron 1 + 38133	attcggagtcctgtcggc A/C ttgtagaacacatccagel	4034
CEL	15	Intron 1 + 38159	cagctacatctctactctt A/T ggttgggaatttttggccc	4035
CEL	16	Intron 1 + 38544	gtttctgaactctccaga T/C ataaaacaaa tgcctctcc	4036
CEL	17	Intron 1 + 38642-38643	caatttctcaaataccie G/ attcctccagccagcaata	4037
CEL	17	Intron 1 + 38642-38643	caatttctcaaataccie attcctccagccagcaata	4038
CEL	18	Intron 1 + 48429	gaaagaaactgtgtgtccs A/C gaaactgtgtgaatgtgccc	4039
CEL	19	Intron 1 + 49038	tgaactgtcactgacacta A/G tttaatttttcaagaattt	4040
CEL	20	Intron 1 + 49040	gaaactgtcactgacacta T/G taatttttttcaagaattt	4041
CEL	21	Intron 1 + 49256	acataaaaaaataatagag C/A taatttttttcaagaattga	4042
CEL	22	Intron 1 + 49386	aatagttctagtagatatt C/A tttaactctataatttagtata	4043
CEL	23	Intron 1 + 50786	tactttgtctcaccacagc C/A taattctcccttaaacagat	4044
CEL	24	Intron 1 + 50977	ctccagccaaagagacaga T/C asctagaatttctgtttgect	4045
CEL	25	Intron 1 + 51150	agaccataagactgttttg C/G agtctcctcttattatgc	4046
CEL	26	Intron 1 + 52333	tcaatcaacttaagactc A/C ggaatctattatgaactttag	4047
CEL	27	Intron 1 + 52589	gtatcacatctgtagata C/A ggaagagatgtgaagaaa	4048
CEL	28	Intron 1 + 55538	tcttcaggttaaatagaat C/A gaatacttttaaalacaaatc	4049

遺伝子名	No.	存在位置	配列	配列番号
CEL	29	intron 1 + 56028	ataagttggaataatttgg C/C taataatataaataatttc	4050
CEL	30	intron 1 + 58738	tgttggaataatagattata C/A tctggccaacttctccat	4051
CEL	31	intron 1 + 59358	cagaattgtactttaaata A/G caactgcaagcacttcagt	4052
CEL	32	intron 1 + 59359	agaaattgtactttaaata C/T gaactgcaagcacttcagtc	4053
CEL	33	intron 1 + 59484	accgaagaaggacatctc C/G ttgtcatitgttgtaaac	4054
CEL	34	intron 1 + 61340	aaaaaacttcaaatat C/G caataccaagatttggta	4055
CEL	35	intron 1 + 62739	cagctttagacacaaag A/G caaagcttctctatct	4056
CEL	36	intron 1 + 64764-64779	ctgggtgttctcataag (1) 4-17 atgttggaatagtgatata	4057
CEL	37	intron 1 + 65243	tttcaggcttggacaaa C/C agtattatataaagctat	4058
CEL	38	intron 1 + 65269	tatgaataagctattata A/A ttgaagaatctcttact	4059
CEL	39	intron 1 + 65325	aattagaagaagcagtttg C/C ggggggggttgcaaaacaa	4060
CEL	40	intron 1 + 65326-65334	attagaagaagaagtttgg (1) 7-9 tccaaacaaaagaagaaa	4061
CEL	41	intron 1 + 65524	cacaccataaccacacat A/C gtggcttctcttgagccatg	4062
CEL	42	intron 1 + 65869	cagagtaacattgggctcc A/T acgtcttctcttataaga	4063
CEL	43	intron 1 + 65910	aaggcttctctctgctgtt C/C tggatcaaggcttgagaa	4064
CEL	44	intron 1 + 66000	actgttcttgaacactaac A/G gggcatatcacgttctctat	4065
CEL	45	intron 1 + 66226-66235	tcgttttttaaaaaaacag (1) 9-10 tcttctctcttggaaa	4066
CEL	46	intron 1 + 81816	aattgttcttacttctac A/G taltccagaagccctgaic	4067
CEL	47	intron 1 + 83480	tatgactatcagaagaaa C/C tagaattattttgttctct	4068
CEL	48	intron 1 + 83732	ggggttbaaatatctgag C/C calltctcttitttanaaa	4069
CEL	49	intron 1 + 85507	ctggaagaattttgttc A/T ctgcatattttaaagttag	4070
CEL	50	intron 1 + 87299	caatgtcattatattct C/A tgttgaagacagctcaagaa	4071
CEL	51	intron 1 + 87426	cacagataaatctcagaat C/C ctctgtctgcttggctct	4072
CEL	52	intron 1 + 87670	tatttgttctatattca C/C gacatgacacacacataa	4073
CEL	53	intron 1 - 77494-77503	ttgttctcttcttctt (1) 9-10 caactctactaacaggccc	4074
CEL	54	intron 1 - 77368	agctcaggaggagagacact C/C gggggaaggcaagaagcggg	4075
CEL	55	intron 1 - 75135-75129	tgagcgttgccctcagaagggt (1) 6-7 tggagctctctgagccctc	4076
CEL	56	intron 1 - 74785	actaccacagaagctgggg C/C ctgttgcccttctctctgt	4077
CEL	57	intron 1 - 74755	cttctctctgtgctatgaa A/G cctcagagctcctcagctacg	4078
CEL	58	intron 1 - 73099	ccccggggtctctctctggc C/T tcttctggccgcccctgt	4079
CEL	59	intron 1 - 72559	agcagcacttgagccgctcc C/A tgcaggaagtgaagtgggca	4080
CEL	60	intron 1 - 70098	acaggaagaagaagacaaa C/C ctacacacttgaatctcat	4081
CEL	61	intron 1 - 69440	atttgcatagagaagaaca C/T aggaaggtattggaagaalga	4082
CEL	62	intron 1 - 65270	attctgacttgctgggaag C/A ctggcctggccttctctggc	4083
CEL	63	intron 1 - 64434	ccacattaggagatggaaag C/T aacatctaaataattttca	4084
CEL	64	intron 1 - 63966	agatcagacatccccacc C/T atgctctagagaacagagccc	4085
CEL	65	intron 1 - 63916	actctacatctacatcag C/T ttcaggcttaccctcagctcc	4086
CEL	66	intron 1 - 60392	tcttgggctcaggatgca C/T atggaatctctggagagag	4087
CEL	67	intron 1 - 60321	aattacttgaaccccatc A/T tcccacccaccccttttcc	4088
CEL	68	intron 1 - 60318	acttgaaccccatctccat C/T caccacaccccttttctcc	4089
CEL	69	intron 1 - 56852	tgttcaagccctctccctg C/A gccagcacacccatctc	4090
CEL	70	intron 1 - 56133	actggtctctggatctcta C/T ggggttctcttggcaccctcc	4091
CEL	71	intron 1 - 55964	ccccagccctctagccg C/A cctgagacttatactgccc	4092
CEL	72	intron 1 - 52016	tcttgaactaggggtgggg C/A ggcacttccagtgccaggg	4093
CEL	73	intron 1 - 51998	gggggacttgccttgagcca C/A ggaaggagacttgcggggcac	4094

遺伝子名	No.	存在位置	配列番号
UCEL	74	intron 1 - 515-18	gtggagcagctggcattt g/c gggggaagaacatccctgggt
UCEL	75	intron 1 - 395-7	ggccagacaaagcctcca t/c gaggcctaaagcctcccaag
UCEL	76	intron 1 - 394-90	gcctttctccagtgatc a/c tggcactgatgatccacag
UCEL	77	intron 1 - (3132-31340)	tcaggaccttctatgctc t/b-b-9 ctgcctgagccctggatc
UCEL	78	intron 1 - 196-34	ttatttggcgttggccatc c/t taccgcttctcagagcctgat
UCEL	79	intron 1 - 658-9	gacgggtatgctcagagcctt t/c gctgtcccccagctgtctggg
UCEL	80	intron 1 - (3340-3345)	cttggcactgtcggctatg c/c 4-6 tccatgttggttgggttggg
UCEL	81	intron 3 + 3-5	tgccgactgtcccttggcgc g/a gggcgggttggagggcggctgc
UCEL	82	intron 6 + 1-57	atgggagagggccttggctga c/t gggatttctgggtcccttag
UCEL	83	exon 9 + 1-37	aaatagggcggccacatctt c/t gtcagcatcgacatgcttgc
UCEL	84	intron 9 + 41	tcaggggagagccttggcggg a/c gggc-gccgggaagacactg
UCEL	85	intron 9 + 1-51	gggttgatgtgacacaccc t/c tctgttgccacagccttag
UCEL	86	exon 10 + 8-2	agcactttagtctacac c/t gactctgggcccagaccc
UCEL	87	exon 12 + 5-83	ccacgggtgactccggggc g/a ccccgctgacccccacggg
UCEL	88	exon 12 + 7-59	gtttagctcactatgacc t/c tggatcaagagccacacag
UCEL	89	exon 12 + 83-2	ctttagaaggactatctc a/c aggactgagctcagcttca
UCEL	90	exon 12 + 83-2	tgcccccctttctccat c/t cactaccttctcagctc
UCEL	91	exon 12 + 83-2	ccctgagccactggacac g/a ccagtgagtgaccacagaa
UCEL	92	exon 12 + 83-2	gttgtagcttctgactaac g/a tggca tgccttctcagctt
UCEL	93	exon 12 + 83-2	ctgtagttagcttagagaa a/c ggaagcttctttagctt
UCEL	94	exon 12 + 83-2	ctgagacatctgtagagaa g/a gatttctaccctagaaat
UCEL	95	exon 12 + 83-2	tattttagctttagctt a/c tacaatagcttcttctt
UCEL	96	exon 12 + 83-2	gacttgaggcagacagaa c/t tllaagatagaaagctt
UCEL	97	exon 12 + 83-2	ccctgacttcttctct c/t cctctctcttcttcttca
UCEL	98	exon 12 + 83-2	atagtgtagagagaagaa a/c agacactgctactgctctc
UCEL	99	exon 12 + 83-2	cactcttgacacccacagaa c/c gaacacagacagcctgctc
UCEL	100	exon 12 + 83-2	cccgacacacacacacag t/c accgtctcagacagcctct
UCEL	101	exon 12 + 83-2	atggcttagagcagcagcgt t/c ggcagagctcggctggag
UCEL	102	exon 12 + 83-2	tgccgagagggcggcggcgc c/cacacacacacacacacac
UCEL	103	exon 12 + 83-2	aggctctgctcctggag t/c tggagcttcttctctctc
UCEL	104	exon 12 + 83-2	aatcttcttcttcttctt a/c tataagtagaagaattat
UCEL	105	exon 12 + 83-2	aatcttcttcttcttctt a/c tataagtagaagaattat
UCEL	106	exon 12 + 83-2	aatcttcttcttcttctt a/c tataagtagaagaattat
UCEL	107	exon 12 + 83-2	aatcttcttcttcttctt a/c tataagtagaagaattat
UCEL	108	exon 12 + 83-2	aatcttcttcttcttctt a/c tataagtagaagaattat
UCEL	109	exon 12 + 83-2	aatcttcttcttcttctt a/c tataagtagaagaattat
UCEL	110	exon 12 + 83-2	aatcttcttcttcttctt a/c tataagtagaagaattat
UCEL	111	exon 12 + 83-2	aatcttcttcttcttctt a/c tataagtagaagaattat
UCEL	112	exon 12 + 83-2	aatcttcttcttcttctt a/c tataagtagaagaattat
UCEL	113	exon 12 + 83-2	aatcttcttcttcttctt a/c tataagtagaagaattat
UCEL	114	exon 12 + 83-2	aatcttcttcttcttctt a/c tataagtagaagaattat
UCEL	115	exon 12 + 83-2	aatcttcttcttcttctt a/c tataagtagaagaattat
UCEL	116	exon 12 + 83-2	aatcttcttcttcttctt a/c tataagtagaagaattat
UCEL	117	exon 12 + 83-2	aatcttcttcttcttctt a/c tataagtagaagaattat
UCEL	118	exon 12 + 83-2	aatcttcttcttcttctt a/c tataagtagaagaattat
UCEL	119	exon 12 + 83-2	aatcttcttcttcttctt a/c tataagtagaagaattat
UCEL	120	exon 12 + 83-2	aatcttcttcttcttctt a/c tataagtagaagaattat
UCEL	121	exon 12 + 83-2	aatcttcttcttcttctt a/c tataagtagaagaattat
UCEL	122	exon 12 + 83-2	aatcttcttcttcttctt a/c tataagtagaagaattat
UCEL	123	exon 12 + 83-2	aatcttcttcttcttctt a/c tataagtagaagaattat
UCEL	124	exon 12 + 83-2	aatcttcttcttcttctt a/c tataagtagaagaattat
UCEL	125	exon 12 + 83-2	aatcttcttcttcttctt a/c tataagtagaagaattat
UCEL	126	exon 12 + 83-2	aatcttcttcttcttctt a/c tataagtagaagaattat
UCEL	127	exon 12 + 83-2	aatcttcttcttcttctt a/c tataagtagaagaattat
UCEL	128	exon 12 + 83-2	aatcttcttcttcttctt a/c tataagtagaagaattat
UCEL	129	exon 12 + 83-2	aatcttcttcttcttctt a/c tataagtagaagaattat
UCEL	130	exon 12 + 83-2	aatcttcttcttcttctt a/c tataagtagaagaattat
UCEL	131	exon 12 + 83-2	aatcttcttcttcttctt a/c tataagtagaagaattat
UCEL	132	exon 12 + 83-2	aatcttcttcttcttctt a/c tataagtagaagaattat
UCEL	133	exon 12 + 83-2	aatcttcttcttcttctt a/c tataagtagaagaattat
UCEL	134	exon 12 + 83-2	aatcttcttcttcttctt a/c tataagtagaagaattat
UCEL	135	exon 12 + 83-2	aatcttcttcttcttctt a/c tataagtagaagaattat
UCEL	136	exon 12 + 83-2	aatcttcttcttcttctt a/c tataagtagaagaattat
UCEL	137	exon 12 + 83-2	aatcttcttcttcttctt a/c tataagtagaagaatt

遺伝子名	No.	存在位置	配列	配列番号
UCL3	18	intron 3 + (944-945)	tacatagctaacgtatata	4138
UCL3	19	intron 3 + 5052	cgtaagtatactagctacg	4139
UCL3	20	intron 3 + 5282	aggcagctacgtatagacc	4140
UCL3	21	intron 6 + 2191	acctctaaatttttttga	4141
UCL3	22	intron 6 + 8264	ttcttagagtttttttga	4142
UCL3	23	intron 6 + (8741-8744)	ttcttagagtttttttga	4143
UCL3	24	intron 6 + 9411	agtgagtaaaccaatt	4144
UCL3	25	intron 6 + 9459	ttctctgttttgaatctact	4145
UCL3	26	intron 6 + 8772	ttctctgttttgaatctact	4146
UCL3	27	intron 6 + 10158	gaacaaatcagatatactg	4147
UCL3	28	intron 6 + 10839	ttattttaagaataattct	4148
UCL3	29	intron 6 + 12493	tttactaaatctacaga	4149
UCL3	30	intron 6 + (20435-20437)	agtcacatttagttacaggt	4150
UCL3	31	intron 6 + 21202	tttttaataagagctcct	4151
UCL3	32	intron 6 + 21285	tttactgtctttctctgct	4152
UCL3	33	intron 6 + 21639	caaatattattttctttt	4153
UCL3	34	intron 6 + 21778	taagaataattaaagctaa	4154
UCL3	35	intron 6 + 23299	ttcatttctcagatatac	4155
UCL3	36	intron 6 + 23498	cttttaataagagctaa	4156
UCL3	37	intron 6 + 23790	tattcagttctcagctaa	4157
UCL3	38	intron 6 + 23894	ttagccttaaaaatttggac	4158
UCL3	39	intron 6 + (24729-24732)	acattatatactctctca	4159
UCL3	40	intron 6 + (25083-25084)	agcttaatttaaaattgtt	4160
UCL3	41	intron 6 + 25084	catgtattattattattacg	4161
UCL3	42	intron 7 + 1342	catgtattattattattacg	4162
UCL3	43	intron 7 + 1387	gaagaagctatttttggc	4163
UCL3	44	intron 7 + 1760	ttttaagattgttcttctg	4164
UCL3	45	intron 7 + 2056	actcgttttttattagtag	4165
UCL3	46	intron 7 + 2873	taagtaatttacaagatgg	4166
UCL3	47	intron 7 + 7554	ttatgtattatttctctac	4167
UCL3	48	intron 8 + 207	ttctgagctctcaggttc	4168
UCL3	49	intron 8 + 252	ctctatgaacaaatgaata	4169
UCL3	50	intron 8 + (883-892)	aagactgtctattattatcc	4170
DDUST	1	intron2 629	tttactcgaanaattacac	4171
DDUST	2	intron2 3125	attctgllaagaagtttcta	4172
DDUST	3	intron2 3970	ggagaaataggaactctgc	4173
DDUST	4	intron3 189	attactatttaataataaa	4174
DDUST	5	intron6 185	actctgtctaggggttcat	4175
DDUST	6	exon8 37	ctgtctcttttttcggagg	4176
DDUST	7	intron3 37	aactatgaactactatagc	4177
DDUST	8	intron2 + 1299	ttctgccaagaatactgcc	4178
DDUST	9	intron2 + 1681	atctctgtatcagctggctt	4179
DDUST	10	intron2 + 2822	gatactgtttgtggagaaa	4180
DDUST			gtttctcaacagggttcattc	4181

遺伝子名	No.	存在位置	配列	配列番号
DDST	11	Intron2 + 3392	caaaagcctggaagccctcc C/T ggccttccctctgttgcctc	4182
DDST	12	Intron5 + 495	attcttaaccacagaacc C/A gaagttcaacttaaccgaag	4183
DDST	13	Intron6 + 226	gaacctcttggttgcacac C/T tcttttttcccatatcc	4184
DDST	14	Intron8 + 303	aaataaataagttcattagg A/T taatttgttaagcaataa	4185
DDST	15	3' flanking + 40	caacagctgaagacagggcca C/A gaagggggtttaggatt	4186
NTE	1	5' flanking - 535	cagcatctctccctcct C/T tcttaactcttaactttctg	4187
NTE	2	5' flanking - 15	gtaattcccgcccaaaaacc A/G gacggccttgcaagccac	4188
NTE	3	5' flanking - 748	agcatggcggggaagggagg C/T gtaggggggttcggggggac	4189
NTE	4	5' flanking - 690	tgaaataatgaagggggc C/T gcttcagagccggcgagaa	4190
NTE	5	Intron6 + 605	tcttgcaatacttagtag A/G ggggttctacatcaggggtt	4191
NTE	6	Intron6 + 748	agcttcagctctctctc C/T ggggttctacatcaggggtt	4192
NTE	7	Intron6 + 987	ggcttggtcttggaatccc C/T gtcgtcatatgacttacct	4193
NTE	8	Intron6 + 1882	ggcctcaagcaatctccc C/A cctggcctctcaaaagctct	4194
NTE	9	Intron6 + 2222	gaattttatagaacaga C/A agcgtatctgcggctctc	4195
NTE	10	Intron12 + 166	tatctgtaccagaagct C/G tggcctgtctctcaagggc	4196
NTE	11	Intron13 + 69	atccaggtccacggctctcc C/T gcttgaattgttttaactg	4197
NTE	12	Intron14 + 8	gcacccggccctggccctt C/T atattttcttaacccttcc	4198
NTE	13	Intron16 - 113	agacccggccggccacagac A/G tctggggagatgactccgg	4199
NTE	14	Intron21 + 34	gaataaatttgccttaag C/A gttcaaaccttaagttaga	4200
NTE	15	Intron21 + 128	ttcaaaccttaagtaggac C/G agttcaaacatctctggg	4201
NTE	16	Intron21 + 151	ccactgtactctacacagg C/T gacacagctagaacctgttt	4202
NTE	17	Intron21 + 651	tgaaatagctctgtggall C/T ttgttaggactctgggac	4203
NTE	18	Intron21 + 737	acagcttgctcctggctgta C/T tggagaacctgggaagcaac	4204
NTE	19	Intron21 + 1752	gaagcaacagctgggtcaaa A/Δ gtagcttttttttcttggc	4205
NTE	20	Intron21 + 1788	catctgaacctctccctccc A/G ggttcaagtatctctctgc	4206
NTE	21	Intron21 + 1907	cagctctgttttagtttag C/T tccccatttagacagagaa	4207
NTE	22	Intron21 + 2055	agcttgaggacacagagaca C/A gaatttcagataagagaga	4208
NTE	23	Intron21 + 2336	tgaggaggtgtgtgggtgg C/C ctggagctcaaatcttttc	4209
NTE	24	Intron23 + 41	caaatcttttagcccttag C/T ggccttcccaaccagggcct	4210
NTE	25	Intron23 + 71	cagacttgattcaagtct C/T ggccttcccaaccagggcct	4211
NTE	26	Intron23 + 81	gtggggcgcctggtagcttc A/C ggccttcccaaccagggcct	4212
NTE	27	Intron24 + 150	ggcttgagcaacacccctgac C/T cagctggggttggggggatg	4213
NTE	28	Intron29 + 37	ccctccaggtcagcagagccc C/A tggggccggctggggctccg	4214
NTE	29	Intron29 + 370	acctccgacacacacacac C/A cacacagctgggacacaca	4215
NTE	30	Intron30 + 56	aaataacaaaataaacc A/G ggcctgtgggttgggttgggt	4216
NTE	31	Intron30 + 358	ttacagagctgtgtgggtt C/C cctgttaattccagctactc	4217
NTE	32	Intron30 + 372	aaatctctgaacctggag C/T gggaggttgcagtgagctga	4218
NTE	33	Intron30 + 430	gtgtgcacacagctatata C/C gcaatgctttcttctcaggg	4219
NTE	34	Intron30 + 655	gcacacagctatata C/C gcaatgctttcttctcaggg	4220
NTE	35	Intron30 + 659	tgaaatagggcatttgcaa C/T gcatgccagctgtctccct	4221
NTE	36	Intron30 + 760	gcacacacatagaaggatg C/T ggcaccttgaccagattaa	4222
NTE	37	Intron30 + 835	tggtgcttcacataggtgtc C/T gcttaagcttttcttacttaa	4223
NTE	38	Intron31 + 40	tggtgcttcacataggtgtc C/T gcttaagcttttcttacttaa	4224
NTE	39	Intron31 + 41	gtgtgcttcacataggtgtc C/A gcttaagcttttcttacttaa	4225
NTE	40	Intron31 + 1329	gtgtgcttcacataggtgtc C/A gcttaagcttttcttacttaa	4226

遺伝子名	No.	存在位置	配列	配列番号
NIE	41	intron35 + 31	aaagcttccgtgctgtttc g/a gacggagaccacccttcig	4227
LICAM	1	intron 1 + 767	tttgacttcttactatgggt g/a actgtgtgagctacttatt	4228
LICAM	2	intron 1 + 862	gcatgggcalagatgat g/c lgaaggagcgaagatgaag	4229
LICAM	3	intron 1 + 1332	caggatataagagagagagc c/t gctgagagccacacagtg	4230
LICAM	4	intron 4 + 502	tttccctgggttttccctt t/c gcaltcaatctccctggagc	4231
LICAM	5	intron 18 + 147	aggcagctatgaattccc c/a acatttcaatttctataat	4232
LICAM	6	intron 24 + 221	cctcttaccctcccaagg c/t ccaactttaaggacatact	4233
AAAT	1	5' flanking-542	agggctcagaa tgggtgtt g/t agctggagagcagggatag	4234
AAAT	2	5' flanking-263	ccccacataaagatggg g/g ttgcaagagctcagagga	4235
AAAT	3	intron3 39	cgccagctcagagagggc t/a ctaagacagagatcagcca	4236
AAAT	4	exon4 150	cagctggcgtgcccgggc c/t ggcctcatgtccagagcgc	4237
AR01	1	intron1 + 317	cgctggcttctctggccccc c/g cctcctggggcttggcagg	4238
AR01	2	intron6 + 322	gctcttcaactctgtcac g/a caaggagccacaccttctt	4239
AR01	3	intron6 + 1095	aaggcttcaactctgacaa a/c aagtcagatgtgacctgccc	4240
AR01	4	intron6 + 1179	aggagaaactctgtatccc a/g ggaacacctctctcactcc	4241
AR01	5	intron7 + 159	cttcaggctctctagccaga c/t ggcctctctaaagccagc	4242
AR01	6	intron7 + 295	tgaccagccctggccaccca g/t gasccttgggagacacctg	4243
AR01	7	intron7 + 416	actacatggagggccccc g/a acagagccttcccctttgac	4244
NAT1	1	3' UTR 215	aataataaataaataaa a/t aaigtattttaagatggc	4245
NAT2	1	exon2 867	cgctcccaactctgtgag g/a atcccttactatttgaata	4246
NAT2	2	3' flank 521	scatcacttctggccaaa c/a agaagaacatagactttat	4247
NAT2	3	3' flank 573	gatttgaactctgtgaca c/t ggggtgaattacttttaaaa	4248
NAT2	4	3' flank 918	attttgtgttgaattcc a/g gtaacagggctatagtttaa	4249
NAT2	5	3' flank 979	actattctcctctcgact c/t gtaactataataatctt	4250
NAT2	6	3' flank 1958	tactattgaagtaagccia c/t gtataaccactatttgtt	4251
NAT2	7	3' flank 2034	ccactatctccagagctag t/g tcattaaagacagctgctt	4252
NAT2	8	3' flank 2201	cagatctagagggctact g/a ttgctcaccatagcaatg	4253
NAT2	9	3' flank 2818	aggatatttctctcttct c/g ccagtgcatatgttgaacc	4254
NAT2	10	3' flank 3237	atatacttcaatataaaa a/d caaataaatcttccaaact	4255
NAT2	11	3' flank 3386	caacaagagattttttaa g/a ctttttaaacaccagacag	4256
NAT2	12	3' flank 3660	cagcactatagcaatagca a/g agaigtgaaatcaatctaaa	4257
NAT2	13	3' flank 3973	agcgaataaataaataaig c/t gtactaggcttactcttgc	4258
NAT2	14	3' flank 4029	caaaacaacccccatgaca t/c gagtattctctatacaaaa	4259
NAT2	15	3' flank 4118	alaagataatatactaca c/a aaattcttgtttacagcttg	4260
NAT2	16	3' flank 4146	tgtttcaacttgttata c/t tgaattatgtctgtctccc	4261
NAT2	17	3' flank 4279	ttaatctgtaggatggg g/c ctttataaagaaagaaag	4262
NAT2	18	3' flank 4323	ttgctcttcccagtgccag t/g taccagaaagagccatgtg	4263
NAT2	19	3' flank 4446	tcaatggctttatctgca t/g tctggatctaggaatactc	4264
NAT2	20	3' flank 4462	ggcatctggatcaggcaa t/c actcatttctataaagaga	4265
NAT2	21	exon2 + 288	atgttaggggtattttia c/t atccctcagtttaacaaata	4266
NAT2	22	5' flank - 2053	ctggattcgaactttta t/c ccaggctcaggttttccaac	4267
NAT2	23	5' flank - 1299	gaatccagctggggaggt a/g taacagtgaaaccaagacac	4268
NAT2	24	5' flank - 1145	ctgtacaacacagatatt c/t ggaagcagtttgtacatgcc	4269
NAT2	25	5' flank - 1036	cccttccacagatcccgag t/a tcatgtgcagcagatgccaga	4270
NAT2	26	5' flank - 94	aaaagatttctaagatttc g/a caaaggcaaccttaagacct	4271

遺伝子名	No.	存在位置	配列	配列番号
NA12	2/	5' flank - 643	atgtttatattttatattaa 1/C attaatgtaataataaaattt	4272
ABC82	1	5' flank - 673	agctaaagatcaaacacc 6/C cttttccaccagctcgcg	4273
ABC82	2	5' flank - 646	ccaccagctcgcgctg 1/G cctcttcacggacactctag	4274
ABC82	3	5' flank - 563	ttgcaacgctgctgcttac 1/C ggcgacctccttgcctccc	4275
ABC82	4	5' flank - 236	gctttgagcagcgcctaac 6/1 tctgtagggacatcgcgc	4276
ABC82	5	Intron3 + 408	aaggaaactgaagccaagac 1/1 cttaatgcgaaactgcaca	4277
ABC82	6	Exon4 + 153	ccctcaaca tggcaccctg 6/G tcaacctgcctcgtcttcc	4278
ABC82	7	Intron4 + 289	gtaattttagatccaag 6/1 ggcatacgtctctcttcc	4279
ABC82	8	Intron4 + 291	attctttagcatccaagg 6/G catagctgctctcttctc	4280
ABC82	9	Intron5 - 63	ttccttagaglaaatgac 6/1 gcttctttagtccctcca	4281
ABC82	10	Intron7 - 185	gtctcctccttctcttgc 6/1 gcttctctatctctaccc	4282
ABC82	11	3' flank + 71	agccacattttagctgcgg 6/A tctctctcttttataccc	4283
ABC82	12	3' flank + 129	aactgataccttttccct 1/C aagcttttttaattcctaiga	4284
ABC82	13	3' flank + 459	cattcagggagggccagctc 6/A tctagcttcagacgtctg	4285
ABC83	1	Intron3+8	tcctctttgscaggtagtg 6/A tggscagctgggtccatttg	4286
ABC83	2	Intron4+104	cttcaccctgataccagac 6/1 tggggatgcttttctcttct	4287
ABC83	3	Intron10+219	ggacagatgagctctccccc 6/G tggscagctgggtccaggtcc	4288
ABC83	4	Intron11+(317-319)	atggtagcaggtgagatg 6/G/Δ tcatctcattctctctt	4289
ABC83	5	exon12+19	agctcaggactggaaatcc 1/C tggggatgacacagctg	4290
ABC83	6	exon12+(356-357)	aggtagggtaggtgggtg 66/1GGGGGCGA ggcgtctctgtgcaggaaa	4291
GSTM3	1	5' flank - 144	ccaacgctgctttagctgc 6/1 cctgcacagcctctgtgga	4292
GSTM3	2	Intron 7 + 165	agcctaactctataccctg 6/G aggcactgctctacaaaaa	4293
GSTM3	3	Intron 7 + 257	ctgttggacgggtgggtc 1/G ttataagattgggtatatt	4294
GSTM3	4	exon 8 + 91	cccaatgggcaacaagct 6/G tctctgagcagcagggcaga	4295
GSTM4	1	Intron 4 + 67	ttggctgagatgggtgcta 1/C gctcagagtagctctgtt	4296
GSTM4	2	Intron 7 + 77	gtagctttccagctctgga 1/G ctgcataaagaataacttgc	4297
GSTM4	3	Intron 7 + 80	gctttccagctcctggatc 6/A cataaagaataacttgcatt	4298
ALDH7	1	Intron1+464	catgaatgactcggaaag 6/G aicattcttagcaatggact	4299
ALDH7	2	Intron1+2269	aaatggatccaacagcaa 6/C agactctcctcaccggica	4300
ALDH7	3	Intron2+1349	actgaacttgcaccggcc 6/1 gcttcggccttctatgaga	4301
ALDH7	4	Intron2+1820	tcgggtggaaaggacccttc 6/G cccagctcagtggtcagga	4302
ALDH7	5	Intron2+2046	aacctcaggcctgctcag 6/G caggagaccagcttgcctccc	4303
ALDH7	6	Intron2+2939	aagcacacatgaacataga 6/A tgaatgagtagaaccgaatgaa	4304
ALDH7	7	Intron3+7	tcaccaagaaccttggtagc 6/1 ggcgggctgagcagggcag	4305
ALDH7	8	Intron4+36	ggccttcggctaccccttc 1/C ccgctcagaccctcagggcc	4306
ALDH7	9	Intron6+(116-117)	attctcctctctctctct 6/Δ ggaaccagctgggagagagtc	4307
ALDH7	10	Intron6+263	cagacctctacagtagacc 1/C gctcctcccccagctcttag	4308
HMGL1	1	3' untranslated + 864	ctttctgattttttagatg 6/C gttgaagaaggagattttaa	4309

【0033】

表1において、「遺伝子名」の欄には薬物代謝酵素をコードする遺伝子名を記載した。「配列」の欄においてアルファベット大文字で示した塩基がSNP情報である。「/」を付した2つの塩基は、その塩基のホモ又はヘテロのSNPを示す。例えば、「A/G」と表示した場合は、アレルがA/A若しくはG/Gのホモ、又はA/Gのヘテロであることを意味する。表中の配列は、SNPの前後20塩基を示している。但し、括弧を付した塩基（例えばABCB4の第27番の（T）：配列番号555）はインサートによる多型を、△（例えばNAT2の第10番目：配列番号4255）は1塩基の欠失による多型を意味する。また、括弧に数字を付した塩基は、その括弧内の塩基がその数字の数だけ繰り返されていることを意味する。例えば、配列番号689の配列（表1、ABCB11の第55番）において「(T)9-12」とあるのは、Tが9～12個の繰り返し配列であることを意味する。

【0034】

「存在位置」は、SNPのゲノム上の位置を示す。5'フランキング（flanking）領域、イントロン（intron）領域、3'フランキング（flanking）領域のSNPsの存在位置は、エキソン/イントロン結合点（exon/intron junction）の最初のイントロンの塩基配列を1番として数えた。エキソン領域のSNPsの存在位置は、エキソン/イントロン結合点の最初のエキソンの塩基配列を1番として数えた。（+）表示又は無表示は3'下流方向に、（-）は5'上流方向に向かって数えた数字を示した。「No.」の欄に記載された数字は、各遺伝子の遺伝子地図（図9～177）上のSNPの位置を示す番号と対応する。

【0035】

4. オリゴヌクレオチドプローブ又はオリゴヌクレオチドプライマーの作製

本発明の検出方法においてプライマー及び/又はプローブとして使用されるオリゴヌクレオチドは、例えばSNPを検出するときは表1に示す塩基配列（配列番号1～4309）を基本とし、これらの配列自体を合成してもよく、これらの配列の一部を含むように設計し合成してもよい。但し、その塩基配列中には必ずSNP（表1の「配列」の欄にアルファベット大文字で表示した部分）が含まれるようにする。また、本発明においてはこれらの配列の相補鎖も含まれる。

【0036】

SNPを例に説明すると、SNP部位は、プライマー又はプローブの塩基配列の3'若しくは5'端に存在するように設計し、あるいは、相補的な配列の3'若しくは5'端に存在するように設計し、又は前2者の3'若しくは5'端から4塩基内、好ましくは2塩基内に存在するように設計する。あるいは、オリゴヌクレオチドの塩基配列全長の中央にSNPが存在するように設計する。「中央」とは、SNPの塩基よりも5'端に向かう塩基の数と、3'端に向かう塩基の数とがほぼ同数となる中心部の領域をいい、オリゴヌクレオチドの塩基数が奇数の場合は、中心部の5塩基、好ましくは中心部の3塩基、さらに好ましくは最も中心部の1塩基をいう。例えば、41個の塩基数の場合は、第19番目～第23番目、好ましくは第20番目～第22番目、さらに好ましくは第21番目の塩基が「中央」となる。また、オリゴヌクレオチドの塩基数が偶数の場合は、中心部の4塩基、好ましくは中心部の2塩基をいう。例えば、40個の塩基数の場合は、第19番目～第22番目、好ましくは第20番目の塩基が「中央」となる。

【0037】

多型部位が複数の塩基で構成される場合は、プローブ又はプライマーにその配列が含まれるように設計する。特に、プローブ又はプライマーのDNAと相補する5'末端側又は3'末端側の1～4塩基のいずれか（「対応塩基」と称する。好ましくは5'末端又は3'末端の塩基。）が、当該複数の塩基の最も端の塩基に対応するように設計する。例えば、後述のインベーター法において表1のNDUFA7の第12番（配列番号3411）に示す遺伝子多型（CAGAGGCT）を検出するためにインベータープローブ及びアレルプローブを作製する場合は、図4aに示すアレルプローブについては、対応塩基（図では塩基として「T」を例示してある）の位置が「CAGAGGCT」配列の最も左の「C」となるように設計し、インベータープローブについては図4bに示す「N」の塩基が「CAGAGGCT」配列の最も左の「C」を「N」（A、T、CまたはGのいずれか）に置換して設計する。逆に、インベータープローブの対応塩基の位置を「CAGAGGCT」配列の最も右の「T」として設計する場合には、その塩基を「N」として、アレルプローブの対応塩基を「T」に設計する。なお、インベータープローブおよびアレルプローブの対応塩基を「CAGAGGCT」配列のいずれかに設定することも可能である。

【0038】

塩基配列の長さは、少なくとも13塩基、好ましくは13塩基～60塩基、さらに好ましくは15～40塩基、最も好ましくは18～30塩基となるように設計する。このオリゴヌクレオチド配列は、被検遺伝子を検出するためのプローブとして使用することができ、また、フォワード（センス）プライマー及びリバース（アンチセンス）プライマーのどちらに使用してもよい。

【0039】

また、オリゴヌクレオチドは、ゲノムDNAとハイブリダイズする領域とハイブリダイズしない領域とがタンデムに連結したものであってもよい。連結の順序はどちらが上流でも下流でもよい。このオリゴヌクレオチドのうちハイブリダイズする領域は、表1に記載のSNPを含む配列情報から設計し、ゲノムDNAとハイブリダイズする領域の最も5'側又は3'側の配列がSNPとなるように作製する。上記オリゴヌクレオチドのうちハイブリダイズしない領域は、表1に記載のSNPを含む配列とハイブリダイズしないように、ランダムに配列を設計する。このオリゴヌクレオチドは、主としてインベーター法によるSNPの検出に、プローブとして使用することができる。

【0040】

さらに、本発明において使用されるプライマーは、表1に示す塩基配列のうち、そのSNPに起因する機能変化、有効／無効の判断、副作用の有無を調べる目的で、PCRにて増幅される配列の中にSNPを含むよう設計される。この場合の、プライマーの長さは、少なくとも15塩基、好ましくは15～30塩基、さらに好ましくは18～24塩基の長さを有するように設計する。このときのプライマー配列は、増幅断片が500bp以下、好ましくは100～300bp、さらに好ましくは100～150bpとなるように鋳型DNAの領域から適宜選択する。

【0041】

以上のように設計されたオリゴヌクレオチドプライマー又はオリゴヌクレオチドプローブは、公知の手法により化学合成することができるが、通常は、市販の化学合成装置を使用して合成される。

なお、プローブには、予め蛍光標識（例えばFAM, VIC, Cy3等）を付加して作

業の自動化を図ることも可能である。

上記オリゴヌクレオチドは、ポリメラーゼ（例えばTaqポリメラーゼ）、緩衝液（例えばTris緩衝液）、dNTP、蛍光色素（VIC、FAM等）などと共に、遺伝子多型検出用キットに含めることができる。

【0042】

5. 検出

上記のようにして調製されたオリゴヌクレオチドをプライマーとし、DNAポリメラーゼを用いて薬物代謝酵素をコードする遺伝子（鋳型DNA）を増幅する。あるいは、上記のようにして調製されたプローブを鋳型DNAとハイブリダイズさせて、目的の遺伝子多型を有するDNAを検出する。鋳型となるDNAの調製は、公知の手法、例えば塩化セシウム密度勾配超遠心法、SDS溶解法又はフェノール・クロロホルム抽出法等により行うことができる。

【0043】

(1) PCRによる検出

増幅は、ポリメラーゼ連鎖反応(PCR)により行うことができる。DNAポリメラーゼとしてはLA Taq DNAポリメラーゼ(Takara)、Ex Taq ポリメラーゼ (Takara社)、Gold Taq ポリメラーゼ (Perkin Elmer)、AmpliTaq (Perkin Elmer)、Pfu DNAポリメラーゼ (Stratagene社) 等が挙げられる。

増幅の条件は、85℃～105℃で10秒～40秒、好ましくは94℃で20秒～30秒の変性工程、50℃～72℃で30秒～1分、好ましくは60℃で20秒～1分のアニーリング工程、及び65℃～75℃で1分～4分、好ましくは72℃で2分～3分の伸長工程を1サイクルとしてこれを30～40サイクル行う。但し、鋳型DNA及びプライマーを十分変性させるために、上記増幅サイクルの前に95℃で1分～5分〔但し、Gold Taq ポリメラーゼ (Perkin Elmer) を使用の際は、最低8分～15分、好ましくは10分から12分の変性工程を加えてもよく、また、増幅されたDNAを完全に伸長するために、増幅サイクルの後に72℃で1分～10分の伸長工程を加えてもよい。さらに、増幅産物の検出を直ちに行わない場合は、非特異的な増幅が起こらないようにするために、増幅産物を4℃で保存する工程を加えることが好ましい。このようにして、薬物代謝酵素をコードする遺伝子を増幅することができる。

【0044】

その後は、増幅産物についてアガロースゲル電気泳動を行い、臭化エチジウム、SYBR Green液等により染色し、そして増幅産物を1本又は2～3本のバンド（DNAフラグメント）として検出することにより、薬物代謝酵素をコードする遺伝子中の遺伝子多型を含む薬物代謝酵素の一部分をDNAフラグメントとして検出することができる。アガロースゲル電気泳動の代わりにポリアクリルアミドゲル電気泳動、あるいはキャピラリー電気泳動を実施してもよい。また、予め蛍光色素等により標識したプライマーを用いてPCRを行い、増幅産物を検出することもできる。また、マイクロプレート等の固相に増幅産物を結合させ、蛍光又は酵素反応等により検出する等、電気泳動を必要としない検出方法も採用することができる。

【0045】

(2) TaqMan PCR法による検出

TaqMan PCR法は、蛍光標識したアレル特異的オリゴとTaq DNAポリメラーゼによるPCR反応とを利用した方法である。TaqMan PCR法で用いるアレル特異的オリゴ（TaqManプローブという）は、前記SNP情報に基づいて設計することができる。TaqManプローブの5'末端はFAMやVICなどの蛍光レポーター色素Rによって標識されており、同時に3'末端がクエンチャーQ（消光物質）によって標識されている。（図1）。従って、この状態ではクエンチャーが蛍光エネルギーを吸収するため蛍光は検出できない。TaqMan プローブの3'末端はリン酸化されているため、PCR反応中にTaqManプローブからの伸長反応は起こらない（図1）。しかし、このTaqManプローブを、SNPを含む領域を増幅するように設計したプライマーとTaq DNAポリメラーゼとともにPCR反応を行うと、次の反応が起こる。

【0046】

まず、TaqManプローブが鋳型DNAの特異的な配列にハイブリダイゼーションし（図2a）、同時にPCRプライマーから伸長反応が起こる（図2b）。この際、Taq DNAポリメラーゼは5'ヌクレアーゼ活性を有しているため、PCRプライマーの伸長反応が進む際にハイブリダイゼーションしたTaqManプローブを切断する。TaqManプローブが切断されると、蛍光色素がクエンチャーの影響を受けなくなり、蛍光

を検出することができる（図2c）。

【0047】

例えば、図3に示すように、SNP部位がAのアレル（アレル1とする）と、Gのアレル（アレル2とする）が存在すると仮定する。アレル1に特異的なTaqManプローブはFAMで、アレル2に特異的なTaqManプローブはVICで標識する（図3）。2種類のアレル特異的オリゴをPCR試薬に添加し、検出の対象となる鋳型とTaqMan PCRを行う。その後、蛍光検出器にてFAM及びVICの蛍光強度を測定する。その結果、アレルのSNP部位と、TaqManプローブのSNPに対応する部位とが相補的である場合は、プローブがアレルとハイブリダイズし、Taqポリメラーゼによりプローブの蛍光色素が切断されて、クエンチャーの影響を受けなくなり、蛍光強度が検出される。

なお、鋳型がアレル1のホモ接合体である場合はFAMの強い蛍光強度を認め、VICの蛍光はほとんど認められない。鋳型がアレル1とアレル2のヘテロ接合体である場合は、FAMとVICの両者の蛍光を検出することができる。

【0048】

(3) インベーター法によるSNPの検出

インベーター法は、アレル特異的オリゴと鋳型とをハイブリダイゼーションすることによりSNPを検出する方法である。インベーター法では、2種類の非標識オリゴと1種類の蛍光標識オリゴを用いる。2種類の非標識オリゴのうちのひとつは、アレルプローブと呼ばれるものである。アレルプローブは、ゲノムDNA（鋳型DNA）とハイブリダイズして相補二本鎖を形成する領域と、鋳型DNAの配列とは無関係な配列であってゲノムDNAとハイブリダイズしない配列の領域（フラップという）とから構成されており、ハイブリダイズする領域のうち最も5'側又は3'側の位置が、SNPに対応する塩基となっている（図4a）。上記フラップ配列は、後述するフレットプローブと相補的な配列を有するオリゴヌクレオチドである。もうひとつのオリゴは、インベータープローブと呼ばれている。このオリゴは、SNP部位からゲノムDNAの3'側方向に向かって相補的にハイブリダイズするように設計されている（図4b）。但し、SNP部位に対応する配列（図4b中、「N」）は任意の塩基でよい。従って、鋳型であるゲノムDNAと上記2つのプローブをハイブリ

ダイゼーションさせると、SNP部位にインベータープローブの1塩基（N）が割り込むように侵入し（図4c）、SNP部位が3重鎖を形成する。

【0049】

一方、蛍光標識オリゴはアレルと全く無関係な配列であり、SNPの種類によらず配列は共通である。このプローブをフレット（FRET）プローブ（fluorescence resonance energy transfer probe）という（図5）。FRETプローブの5'末端の塩基（レポーター）には蛍光色素Rが標識されており、その上流にはクエンチャーQが結合している。従って、この状態ではクエンチャーが蛍光色素を吸収してしまうため蛍光を検出できない。また、FRETプローブの5'末端（レポーター塩基）から一定領域（領域1とする）は、その領域1よりも3'側の領域と向き合って相補的な配列となるように設計されている（これを領域2という）。従って、領域1は領域2と自分自身で相補鎖を形成する（図5）。また、この相補鎖形成領域よりもさらに3'方向の領域は、アレルプローブのフラップとハイブリダイズして相補鎖を形成できるように設計されている（図5）。

【0050】

インベーター法では、DNAの特殊な構造を認識して切断する特殊なエンドヌクレアーゼ活性を有する酵素（5'ヌクレオチダーゼ）の1つであるクリーバーゼ（cleavase）を用いる。クリーバーゼは、ゲノムDNA、アレルプローブ及びインベータープローブがSNP位置で3重になった時に、アレルプローブのSNP位置の3'側を切断する酵素である。従って、図4cのように3つの塩基が並び、5'末端がフラップ状になっている部分を認識して、そのフラップ部分を切断する。これによって、このSNP部位の構造がクリーバーゼにより認識され（図6a）、フラップの部位でアレルプローブが切断されフラップ部分が遊離する（図6b）。次に、アレルプローブから遊離したフラップ部分は、FRETプローブと相補的な配列をもつため相補結合する（図6c）。このとき、フラップのSNP部位がFRET自身の相補結合部位に割り込んで侵入する。クリーバーゼは再びこの構造を認識して蛍光色素部分を切断する。切断された蛍光色素は、クエンチャーの影響を受けなくなり、蛍光を発する（図6d）。SNP部位がアレルプローブのSNPに対応する配列とマッチしない場合は、図7のように、クリーバーゼが認識する特異的なDNA構造をとらないため

、プローブは切断されず、蛍光は検出されない。

【 0 0 5 1 】

例えば、あるSNPがT/Cのときに、T用のインベータープローブ、アレルプローブ、及びSNPに対応するレポーターにFAMを結合させたフレットプローブ、並びにこれとは別にC用のインベータープローブ、アレルプローブ、及びSNPに対応するレポーターにVICを結合させたフレットプローブとを準備し、全て混合してSNP検出を行う。その結果、SNPがT/Tのホモの場合にはFAMの蛍光を発し、C/Cのホモの場合にはVICの蛍光を発し、T/Cヘテロの場合にはFAMとVIC両者の蛍光を発する。FAMとVICは蛍光波長が異なるため、両者を分別できることになる。

【 0 0 5 2 】

(4) SniPer法による検出

SniPer法でSNPを検出するためには、アレルの識別をRCAによる増幅の有無で行うことができる。すなわち、鋳型になるべきゲノムDNAを直鎖状にしておいて、このゲノムDNAにプローブをハイブリダイズさせる。プローブの配列と鋳型であるゲノムDNAの配列とが相補的にマッチして相補鎖を形成すると、ゲノムDNAはライゲーション反応が起こって環状になることができる。その結果、環状DNAのRCAが進行する。これに対し、プローブの端がゲノムDNAとマッチしなければ、ライゲーションされず環状にならないため、RCAの反応は進まない。従ってSniPer法では、ゲノムDNAとアニールし、しかも環状になり得る一本鎖プローブを設計する。この一本鎖プローブをパドロックプローブという。このパドロックプローブの断端を検出目的となるSNPに対応する配列にしておいて、このパドロックプローブとゲノムDNAとを混ぜ、ライゲーション反応を行う。パドロックプローブの断端とゲノムDNAのSNP部分が相補的であれば、ライゲーション反応によってパドロックプローブは断端がつながり環状となるが、相補的でなければ環状にならない。従って、対象となるSNPに相当するパドロックプローブのみが環状となり、DNAポリメラーゼによって増幅する。SNPは、この増幅の有無を検出すればよい。検出は、両端に蛍光色素とクエンチャーをもち、ヘアピン構造を有する合成オリゴヌクレオチドを使用する。

【 0 0 5 3 】

(5) MALDI-TOF/MS法による検出

MALDI-TOF/MS (Matrix Assisted Laser Desorption-Time of Flight / Mass Spectrometry) 法は、質量分析計をSNPタイピングに応用した方法である。この方法は、以下のステップから構成される。

(i) SNPを含むDNA断片のPCR増幅及び精製

SNP部位の塩基とPCRプライマーは重複しないように設計した後DNA断片を増幅し、増幅反応産物からエキソヌクレアーゼやアルカリホスファターゼ処理によりプライマー、dNTP等を除去して増幅断片を精製する。

【 0 0 5 4 】

(ii) プライマー伸長反応（サーマルサイクル）及び精製

PCR産物である標的領域の鋳型に対して10倍以上のプライマーを加え、サーマルサイクル反応させてプライマー伸長反応を行う。ここで使用するプライマーは、その3'末端がSNP部位の塩基に隣接するように設計する。プライマーの長さは、15～30塩基、好ましくは20～25塩基である。マルチプレックス反応を行う場合には、鋳型と相補的でない配列を5'末端に付加する。また、サーマルサイクルは、85～105℃（好ましくは94℃）と35～40℃（好ましくは37℃）の2温度間で20～30サイクル（好ましくは25サイクル）行う。

得られた反応産物を、質量分析機に適した状態にするため精製キット等を用いて精製する。

【 0 0 5 5 】

(iii) 質量分析計によるDNAの質量分析

精製された伸長反応産物を質量分析機にアプライして、目的産物の質量を測定する。すなわち、精製産物をマトリックスと混合し、MALDIプレートに0.5～1.0 μ Lスポットする。プレートを乾燥後、試料にレーザー光を照射し、スペクトログラムを作成する。

【 0 0 5 6 】

(6) 塩基配列決定法による検出

本発明においては、1塩基の伸長反応を利用した多型の検出を行うことができる。つまり、異なる蛍光化合物で標識された4種類のジデオキシヌクレオチドを

、検出の対象となる遺伝子が含まれる反応系に添加し、1塩基の伸長反応を行う。この場合、伸長する塩基を多型部位としておき、また、DNA合成の停止とDNA分子の3'末端の蛍光標識という2つの反応を操作する。4種類の反応液をシーケンシング用ゲルの同一レーンやキャピラリー上で電気泳動を行ない、DNAバンドを標識した蛍光色素の違いを蛍光検出器により検出して配列決定を行う、あるいは1塩基伸長したオリゴヌクレオチドを蛍光検出装置や質量分析装置などを用いてどの塩基が伸長したかを蛍光色素の種類の違いを利用して調べる方法である。蛍光標識ジデオキシヌクレオチドの代わりにプライマーを蛍光標識し、非標識ジデオキシヌクレオチドと共に用いることもできる。

【0057】

6. 薬物の評価

本発明においては、前記のようにして得られる一塩基多型等の検出結果から、当該薬物代謝酵素によって代謝される薬物の有効性及び安全性を評価することができる。

薬物の評価は、タイピングシステムにより行うことができる。すなわち、上記いずれかの検出手法に従って、毒性（副作用）発現群と非発現群のアレル頻度を比較する。両者を比較した際、アレル頻度に差が生じるものを毒性発現認識のためのマーカーとして選出する。統計学的検定は、通常 χ^2 検定によるが、例えばFisher検定などの他の統計処理を行うこともできる。なお、この結果を、薬物の活性本体（薬物未変化体又は代謝物でもよい）の血中濃度、組織濃度に反映させることも可能である。当該全ての遺伝子多型に関して、毒性との因果関係を調べ、相関のあった遺伝子多型部位のみを選出する。その全ての遺伝子多型解析用プローブ又はプライマーと各手法に応じた試薬を、反応プレート、カード又はガラス基盤等に予め用意し、そこに予測したいヒトのゲノムDNAを添加し、反応させることで、アレルパターンを調べることができる。毒性と相関する遺伝子多型を有する場合には、そのヒトの副作用発現予測が可能となる。薬物の有効性についても同様である。また、薬物の違いにより、副作用又は有効性と相関する遺伝子多型も異なるので、それぞれに関して、当該遺伝子多型を用いてタイピング操作を行えば、有効性や副作用の予測をすることが可能となる。

【0058】

このことを利用して、その遺伝子多型頻度と有効／無効又は副作用の有／無を比較し、アレル頻度に差がある時に判定することが可能となる。

例えば、薬物Aの投与によってある毒性（副作用）を示した者のSNPを解析した結果、統計的に全体の90%がT/Tを持つ者（例えばFAMの蛍光強度を検出）であることが判明し、毒性（副作用）を示さなかった者のSNPを解析した結果、T/Tを持つ者は全体の10%にすぎず、C/Cを持つものが90%を占めたことが判明したとすると、SNP解析の結果、T/Tを持つ者は薬物Aの投与はできないと評価することができる。

【0059】

7. 薬物のスクリーニング

本発明において前記の通り得られた遺伝子多型情報は、被験者から採取した当該薬物代謝酵素をコードする遺伝子の遺伝子多型情報と比較することにより、当該薬物代謝酵素によって代謝される薬物の有効性及び安全性を解析するための指標として利用される。従って、本発明において得られた遺伝子多型情報は、どの薬物が治療に最も有効であるか、その使用すべき薬物を選択するための情報源となる。

【0060】

手法としては「5. 薬物の評価」に記載の評価方法を利用すればよい。つまり、前項で副作用又は有効性と相関が認められた遺伝子多型は、その酵素の活性、転写、翻訳に影響を与えるものであるといえる。また、副作用又は有効性の発現機構と間接的であっても何らかの因果関係があるといえる。ある薬物の代謝は、製薬会社などにおいて前臨床又は臨床試験にて調査・確認される。よって、それらの酵素遺伝子中に存在する遺伝子多型の中に重篤な副作用と相関する多型がある場合にはこれを削除すること、あるいは条件付きで使うことが可能となる。また、有効性についても同様である。この副作用と有効性の情報から薬物のスクリーニングが可能となる。

【0061】

さらに、臨床試験（第I～III相試験）において副作用発現症例のボランティア

と副作用非発現症例の遺伝子多型頻度解析を行うことで、前記した以外に副作用や有効性と相関する新たな遺伝子多型を検出することが可能となる。これを、上記と同様に調べることで薬物のスクリーニングが可能となる。

【0062】

【実施例】

以下、実施例により本発明をさらに具体的に説明する。但し、本発明はこれら実施例にその技術的範囲が限定されるものではない。

〔実施例1〕 SNP情報の取得

(1) DNA抽出

血縁関係のない48人からEDTA存在下に採血を行った。DNAの抽出は、ゲノム解析ラボマニュアル（中村祐輔編 シュプリンガー・フェアラーク東京）の方法に従って以下の通り行った。

【0063】

血液10mlを50mlのファルコンチューブに移し、室温で3000rpm、5分間遠心を行った。ピペットにて上清（血清）を採取した後、RBC溶解バッファー（10mM NH_4HCO_3 , 144mM NH_4Cl ）を30ml加えた。沈殿がほぐれるまで混和した後、室温で20分放置した。室温で3000rpm、5分間遠心を行った後、ピペットにて上清（血清）を捨て、白血球のペレットを得た。RBC溶解バッファーを30ml加え、同様の操作をさらに2回行った。白血球のペレットにProteinase Kバッファー（50mM Tris-HCl (pH7.4), 100mM NaCl, 1mM EDTA (pH8.0))を4ml、10% SDSを200 μ l、10mg/ml Proteinase Kを200 μ l加え、転倒混和した後、37℃で一晩静置した。フェノールを4ml加え、ローテーター（Rotator T-50, Taitec）にて4時間ゆっくりと転倒混和した。室温で3000rpm、10分間遠心を行い、上層を新しいチューブに回収した。4mlのフェノール-クロロホルム-イソアミルアルコール（容積比25:24:1）を加え、同様に2時間転倒混和した後、遠心した。上層を新しいチューブに回収し、4mlのクロロホルム-イソアミルアルコール（容積比24:1）を加え、同様に30分転倒混和した後、遠心した。上層を新しいチューブに回収し、8M 酢酸アンモニウム400 μ l、イソプロパノール4mlを加え、転倒混和した。糸状の白色析出物（DNA）を2ml容のチューブに回収し、70%エタノールを1ml加え、転倒混和した。新しい2ml容の

チューブにDNAを回収し風乾した後、TE溶液(10mM Tris-HCl(pH7.4), 1mM EDTA(pH7.4))を500 μ l加え、溶解後、ゲノムDNAサンプルとした。

【 0 0 6 4 】

(2) PCR

ゲノムシーケンスは、GenBank DNAデータベースから得た。RepMask コンピュータプログラムを用い、リピート配列を除いた後、PCR産物が1kb前後になるようにPCRプライマーを設計した。ゲノムDNAは、同濃度に調製した血縁関係のない48人のDNAを使用した。それぞれ3人分のDNAを1本のチューブに同量混ぜ、このうち60ngをPCRに使用した。PCRは、Ex-Taq(2.5U; TaKaRa)を使用し、GeneAmp PCR System 9700(PE Applied Biosystems)を用いて行った。94℃で2分間反応後、94℃で30秒の変性、60℃又は55℃で30秒のアニーリング、72℃で1分の伸長を行い、これを1サイクルとして35サイクル行った。

【 0 0 6 5 】

(3) シーケンス

PCR産物は、ArrayIt(Telechem)を使用し精製を行った後、BigDye Terminator RR Mix(PE Applied Biosystems)を用い、シーケンス反応を行った。GeneAmp PCR System 9700(PE Applied Biosystems)を用い、96℃で2分間反応後、96℃で20秒の変性、50℃で30秒のアニーリング、60℃で4分の伸長を行い、これを1サイクルとして25サイクル行った。シーケンス反応後、ABI PRISM 3700 DNA Analyzerにてシーケンス解析を行った。

【 0 0 6 6 】

(4) SNPの検出

SNPの検出には、PolyPhredコンピュータプログラム(Nickerson et al., 1997, Nucleic Acids Res., 25, 2745-2751)を使用し、解析を行った。

(5) 結果

表1に示すSNPの結果が得られた。また、解析を行った薬物代謝酵素名とその略号、データベース(GenBank)のACCESSION 番号、薬物代謝酵素の遺伝子の構造とSNPsの存在位置を図9~177に示した。図9~177において、エキソンは水平線で表示した遺伝子上に白抜きのボックス又は黒の線で示した。SNPsの存在位置は、

遺伝子の上側に実線で示し、番号を付した。

【0067】

〔実施例2〕

異なる2グループの被験者についてインベーター法によりタイピングを行った。結果を図178に示す。図178において、横軸(Alele 1)はTに対応するFAMの蛍光の強さを、横軸(Alele 2)はCに対応するVICの蛍光の強さを表す。斜線入りの丸はSNPのパターンがT/Tであり、黒丸(●)はC/C、白丸(○)はT/Cであることを示す。黒四角(■)はバックグラウンド値を意味し、×印は判定不能を示す。パネルA(上)のグラフに示された被検者グループはSNPのパターンがC/Cのものが多く、パネルB(下)のグラフに示された被検者グループはSNPのパターンがT/Tのものが多く分かる。

【0068】

〔実施例3〕 SNPの検出

血縁関係のない5人から実施例1に記載した方法により採取したゲノムDNAを試料とし、3種類の薬物代謝酵素遺伝子(EPHX1, ABCB2, AANAT)中のSNPの検出を、インベーター法により行った。EPHX1についてはNo.3(配列番号1965)及びNo.17(配列番号1979)、ABCB2についてはNo.4(配列番号4276)及びNo.11(配列番号4283)、AANATについてはNo.3(配列番号4236)の各配列に基づいて設計されたインベータープローブ及びアレルプローブを用いた。各SNPの存在位置は、表1に示されている。

結果を表2に示す。

【0069】

【表 2】

薬物代謝酵素 遺伝子	EPHX1		ABCB2		AANAT
	No. 3	No. 17	No. 4	No. 11	No. 3
	配列番号 1965	配列番号 1979	配列番号 4276	配列番号 4283	配列番号 4236
SNP	(T/G)	(A/G)	(G/T)	(G/A)	(T/A)
被験者 I	T/T	A/G	T/T	G/A	T/T
被験者 II	T/T	A/A	G/G	G/G	T/A
被験者 III	T/G	A/A	G/G	A/A	T/T
被験者 IV	G/G	A/G	G/T	G/G	T/T
被験者 V	T/G	A/G	G/T	G/A	T/A

表 2 の結果より、本発明の方法により各被験者の薬物代謝酵素遺伝子中の SNP の検出及びそのパターンの同定が可能であることが分かった。

【0070】

〔実施例 4〕 SNP と薬物の有効性・安全性（至適量）との関係

本実施例は、薬剤の有効性及び安全性について SNP を用いて調べたものである。

チオプリン S メチルトランスフェラーゼ（TPMT）はプリン環に付加した S 原子にメチル基を転移する酵素であり、抗癌剤である 6-メルカプトプリンや 6-チオグアニン、あるいは免疫抑制剤のアザチオプリンといったチオプリン誘導体などの主代謝酵素の 1 つである。本実施例では、TPMT（アクセッション番号：AB045146.1）のイントロン 3 の 868 番目の SNP である G/T、およびイントロン 3 の 2682 番目の SNP である C/A の組み合わせと、アザチオプリンの至適量との関係を示した（表 3、表 4）。

【0071】

【表 3】

868	2682	High	Low
TT	AA	2	0
TT	AT	3	0
TT	TT	1	0
GT	AA	0	2
GT	AT	1	7
GT	TT	4	1
GG	AA	1	0
GG	AT	0	1
GG	TT	1	0

【0 0 7 2】

至適量とは腎移植後の拒絶反応の抑制を指標として求めた量である。そして、アザチオプリン量が100mg/日で有効性が認められた患者群をhigh doseグループとし、100mg/日で副作用が発現し、50mg/日で有効性が得られた患者をlow doseグループとした。表3中、「High」、「Low」の欄の数字は、それぞれhigh doseグループ、low doseグループの患者数である。なお、副作用とは、白血球減少症、発疹、血管炎、悪心・嘔吐、食欲不振、下痢、倦怠感、筋痛、関節痛、発熱、悪寒、めまいなどで重症の場合には、血液障害、ショック様症状、感染症、肝・腎機能障害などを指す。

【0 0 7 3】

high doseグループ/low doseグループと上記2種のSNPとの関係を調べると、イントロン3の868番目にGが存在（G/GあるいはG/T）し、かつ、イントロン3の2682番目にAが存在（A/AあるいはA/T）する場合には、12人中10人が50mg/日で至適量（low doseグループ）であるのに対し、その他の組み合わせでは12人中11人が100mg/日の至適量（high doseグループ）となった（表4）。すなわち、該当する2つのSNPの組み合わせを調べることで、投与前にアザチオプリンの有効性・安全性（至適量）を予測することが可能となる。また、本結果は本報記載の薬剤代謝酵素SNPを用いて薬剤の有効性および安全性を予測できることを示すものである。

【0074】

【表4】

遺伝子型	至適量	
	100mg/日	50mg/日
868番目がG、かつ、 2682番目がA	2	10
上記以外	11	1

(Fisher exact test: p=0.0003)

【0075】

【発明の効果】

本発明により、SNPの解析方法が提供される。本発明の方法により、目的の疾患に応じた薬物の選択をすることが可能となるため、本発明の方法は極めて有用である。

【0076】

【配列表】

SEQUENCE LISTING

<110> RIKEN

Nakamura Yusuke

Sekine Akihiro

Iida Aritoshi

Saito Susumu

<120> A method of detecting gene polymorphism

<130> RJH13-147S

<150> JP2000-399443

<151> 2000-12-27

<150> JP2001-135256

<151> 2001-05-02

<150> JP2001-256862

<151> 2001-08-27

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aataataata ataataataa waaatgtatt ttaaagatgg c

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41

【 0 0 7 7 】

【配列表フリーテキスト】

- 配列番号150：nはat又は欠失を表す（存在位置21）。
- 配列番号152：nはc又は欠失を表す（存在位置21）。
- 配列番号153：nはt又は欠失を表す（存在位置21）。
- 配列番号154：nはt又は欠失を表す（存在位置21）。
- 配列番号155：nはg又は欠失を表す（存在位置21）。
- 配列番号157：nはc又は欠失を表す（存在位置21）。
- 配列番号159：nはt又は欠失を表す（存在位置21）。
- 配列番号161：nはc又は欠失を表す（存在位置21）。
- 配列番号289：nはtcaの14～16回の繰り返しを表す（存在位置21から）。
- 配列番号290：nはaの8～10回の繰り返しを表す（存在位置21から）。
- 配列番号291：nはcacagtcacat又は欠失を表す（存在位置21）。
- 配列番号292：nはtt又は欠失を表す（存在位置21）。
- 配列番号293：nはaの10～12回の繰り返しを表す（存在位置21から）。
- 配列番号294：nはc又は欠失を表す（存在位置21）。
- 配列番号295：nはaの16～18回の繰り返しを表す（存在位置21から）。
- 配列番号296：nはg又は欠失を表す（存在位置21）。
- 配列番号298：nはc又は欠失を表す（存在位置21）。
- 配列番号299：nはt又は欠失を表す（存在位置21）。
- 配列番号300：nはa又は欠失を表す（存在位置21）。
- 配列番号301：nはtg又は欠失を表す（存在位置21）。
- 配列番号303：nはtの10～13回の繰り返しを表す（存在位置21から）。
- 配列番号304：nはgtの11～13回の繰り返しを表す（存在位置21から）。
- 配列番号305：nはa又は欠失を表す（存在位置21）。

配列番号306：nはg又は欠失を表す（存在位置21）。

配列番号307：nはg又は欠失を表す（存在位置21）。

配列番号308：nはtの9～11回の繰り返しを表す（存在位置21から）。

配列番号309：nはg又は欠失を表す（存在位置21）。

配列番号311：nはtt又は欠失を表す（存在位置21）。

配列番号312：nはaの7～9回の繰り返しを表す（存在位置21から）。

配列番号313：nはtの9～11回の繰り返しを表す（存在位置21から）。

配列番号314：nはaの9～10回の繰り返しを表す（存在位置21から）。

配列番号315：nはgt又は欠失を表す（存在位置21）。

配列番号316：nはa又は欠失を表す（存在位置21）。

配列番号317：nはt又は欠失を表す（存在位置21）。

配列番号319：nはa又は欠失を表す（存在位置21）。

配列番号320：nはct又は欠失を表す（存在位置21）。

配列番号321：nはg又は欠失を表す（存在位置21）。

配列番号322：nはa又は欠失を表す（存在位置21）。

配列番号323：nはa又は欠失を表す（存在位置21）。

配列番号324：nはa又は欠失を表す（存在位置21）。

配列番号325：nはc又は欠失を表す（存在位置21）。

配列番号326：nは又aaagは欠失を表す（存在位置21）。

配列番号391：nはtの22～26回の繰り返しを表す（存在位置21から）。

配列番号392：nはgの8～10回の繰り返しを表す（存在位置21から）。

配列番号393：nはcの6～7回の繰り返しを表す（存在位置21から）。

配列番号394：nはaの12～14回の繰り返しを表す（存在位置21から）。

配列番号473：nはtt又は欠失を表す（存在位置21）。

配列番号474：nはaの9～11回の繰り返しを表す（存在位置21から）。

配列番号475：nはaの8～12回の繰り返しを表す（存在位置21から）。

配列番号476：nはt又は欠失を表す（存在位置21）。

配列番号477：nはt又は欠失を表す（存在位置21）。

配列番号478：nはt又は欠失を表す（存在位置21）。

配列番号479 : nはa又は欠失を表す (存在位置21)。
配列番号480 : nはt又は欠失を表す (存在位置21)。
配列番号481 : nはt又は欠失を表す (存在位置21)。
配列番号482 : nはtの11~15回の繰り返しを表す (存在位置21から)。
配列番号483 : nはcat又は欠失を表す (存在位置21)。
配列番号484 : nはt又は欠失を表す (存在位置21)。
配列番号485 : nはa又は欠失を表す (存在位置21)。
配列番号486 : nはa又は欠失を表す (存在位置21)。
配列番号487 : nはt又は欠失を表す (存在位置21)。
配列番号488 : nはa又は欠失を表す (存在位置21)。
配列番号497 : nはg又は欠失を表す (存在位置21)。
配列番号519 : nはa又は欠失を表す (存在位置21)。
配列番号525 : nはaaag又は欠失を表す (存在位置21)。
配列番号555 : nはt又は欠失を表す (存在位置21)。
配列番号558 : nはa又は欠失を表す (存在位置21)。
配列番号566 : nはat又は欠失を表す (存在位置21)。
配列番号573 : nはa又は欠失を表す (存在位置21)。
配列番号590 : nはc又は欠失を表す (存在位置21)。
配列番号593 : nはgg又は欠失を表す (存在位置21)。
配列番号602 : nはgtc又は欠失を表す (存在位置21)。
配列番号624 : nはt又は欠失を表す (存在位置21)。
配列番号631 : nはtt又は欠失を表す (存在位置21)。
配列番号634 : nはtの9~12回の繰り返しを表す (存在位置21から)。
配列番号636 : nはa又は欠失を表す (存在位置21)。
配列番号638 : nはaの10~13回の繰り返しを表す (存在位置21から)。
配列番号641 : nはct又は欠失を表す (存在位置21)。
配列番号644 : nはcagatcttcttcagctaatttagaaatgt又は欠失を表す (存在位置21)。
配列番号670 : nはa又は欠失を表す (存在位置21)。

配列番号677 : nはc又は欠失を表す (存在位置21) 。
配列番号682 : nはt又は欠失を表す (存在位置21) 。
配列番号689 : nはtの9～12回の繰り返しを表す (存在位置21から) 。
配列番号692 : nはt又は欠失を表す (存在位置21) 。
配列番号694 : nはg(a)4, a(a)4又はaを表す (存在位置21) 。
配列番号698 : nはt又は欠失を表す (存在位置21) 。
配列番号707 : nはc又は欠失を表す (存在位置21) 。
配列番号709 : nはa又は欠失を表す (存在位置21) 。
配列番号710 : nはc又は欠失を表す (存在位置21) 。
配列番号717 : nはg又は欠失を表す (存在位置21) 。
配列番号719 : nはtの18～20回の繰り返しを表す (存在位置21から) 。
配列番号724 : nはaの11～13回の繰り返しを表す (存在位置21から) 。
配列番号725 : nはgaaa又は欠失を表す (存在位置21) 。
配列番号729 : nはaの10～12回の繰り返しを表す (存在位置21から) 。
配列番号732 : nはc又は欠失を表す (存在位置21) 。
配列番号742 : nはca又は欠失を表す (存在位置21) 。
配列番号749 : nはat又は欠失を表す (存在位置21) 。
配列番号753 : nはctt又は欠失を表す (存在位置21) 。
配列番号755 : nはg又は欠失を表す (存在位置21) 。
配列番号757 : nはggggct又は欠失を表す (存在位置21) 。
配列番号761 : nはtの19～22回の繰り返しを表す (存在位置21から) 。
配列番号766 : nはtの6～7回の繰り返しを表す (存在位置21から) 。
配列番号769 : nはtの11～13回の繰り返しを表す (存在位置21から) 。
配列番号813 : nはcの7～8回の繰り返しを表す (存在位置21から) 。
配列番号815 : nはaの10～12回の繰り返しを表す (存在位置21から) 。
配列番号823 : nはc又は欠失を表す (存在位置21) 。
配列番号828 : nはaaga又は欠失を表す (存在位置21) 。
配列番号830 : nはaの9～11回の繰り返しを表す (存在位置21から) 。
配列番号833 : nはct又は欠失を表す (存在位置21) 。

配列番号838：nはtの8～9回の繰り返しを表す（存在位置21から）。

配列番号858：nはg又は欠失を表す（存在位置21）。

配列番号864：nはcttt又は欠失を表す（存在位置21）。

配列番号869：nはt又は欠失を表す（存在位置21）。

配列番号874：nはc又は欠失を表す（存在位置21）。

配列番号875：nはa又は欠失を表す（存在位置21）。

配列番号878：nはgtt又は欠失を表す（存在位置21）。

配列番号879：nはt又は欠失を表す（存在位置21）。

配列番号899：nはat又は欠失を表す（存在位置21）。

配列番号913：nはg又は欠失を表す（存在位置21）。

配列番号920：nはaの15～17回の繰り返しを表す（存在位置21から）。

配列番号934：nはt又は欠失を表す（存在位置21）。

配列番号938：nはt又は欠失を表す（存在位置21）。

配列番号950：nはt又は欠失を表す（存在位置21）。

配列番号954：nはa又は欠失を表す（存在位置21）。

配列番号955：nはtの13～15回の繰り返しを表す（存在位置21から）。

配列番号956：nはaの12～13回の繰り返しを表す（存在位置21から）。

配列番号957：nはt又は欠失を表す（存在位置21）。

配列番号959：nはt又は欠失を表す（存在位置21）。

配列番号960：nはaの13～15回の繰り返しを表す（存在位置21から）。

配列番号965：nはa又は欠失を表す（存在位置21）。

配列番号971：nはtの5～11回の繰り返しを表す（存在位置21から）。

配列番号973：nはtの8～9回の繰り返しを表す（存在位置21から）。

配列番号974：nはt又は欠失を表す（存在位置21）。

配列番号985：nはtの9～10回の繰り返しを表す（存在位置21から）。

配列番号988：nはaの10～11回の繰り返しを表す（存在位置21から）。

配列番号994：nはa又は欠失を表す（存在位置21）。

配列番号1001：nはa又は欠失を表す（存在位置21）。

配列番号1012：nはct又は欠失を表す（存在位置21）。

配列番号1031 : nはt又は欠失を表す (存在位置21)。
配列番号1037 : nはa又は欠失を表す (存在位置21)。
配列番号1038 : nはat又は欠失を表す (存在位置21)。
配列番号1048 : nはtgtccaaaggaaggacacg又は欠失を表す (存在位置21)。
配列番号1054 : nはtcの6～8回の繰り返しを表す (存在位置21から)。
配列番号1056 : nはc又は欠失を表す (存在位置21)。
配列番号1059 : nはt又は欠失を表す (存在位置21)。
配列番号1064 : nはt又は欠失を表す (存在位置21)。
配列番号1065 : nはc又は欠失を表す (存在位置21)。
配列番号1073 : nはa又は欠失を表す (存在位置21)。
配列番号1075 : nはt又は欠失を表す (存在位置21)。
配列番号1082 : nはgattの6～7回の繰り返しを表す (存在位置21から)。
配列番号1083 : nはt又は欠失を表す (存在位置21)。
配列番号1088 : nはt又は欠失を表す (存在位置21)。
配列番号1089 : nはgt又は欠失を表す (存在位置21)。
配列番号1092 : nはa又は欠失を表す (存在位置21)。
配列番号1093 : nはa又は欠失を表す (存在位置21)。
配列番号1097 : nはt又は欠失を表す (存在位置21)。
配列番号1100 : nはat又は欠失を表す (存在位置21)。
配列番号1106 : nはa又は欠失を表す (存在位置21)。
配列番号1109 : nはt又は欠失を表す (存在位置21)。
配列番号1112 : nはat又は欠失を表す (存在位置21)。
配列番号1113 : nはa又は欠失を表す (存在位置21)。
配列番号1114 : nはtの12～14回の繰り返しを表す (存在位置21から)。
配列番号1117 : nはt又は欠失を表す (存在位置21)。
配列番号1119 : nはcac又は欠失を表す (存在位置21)。
配列番号1126 : nはcca又は欠失を表す (存在位置21)。
配列番号1154 : nはt又は欠失を表す (存在位置21)。
配列番号1184 : nはc又は欠失を表す (存在位置21)。

配列番号1192：nはaaaa又は欠失を表す（存在位置21）。

配列番号1205：nはc又は欠失を表す（存在位置21）。

配列番号1215：nはtの8～9回の繰り返しを表す（存在位置21から）。

配列番号1216：nはa又は欠失を表す（存在位置21）。

配列番号1228：nはtaac又は欠失を表す（存在位置21）。

配列番号1229：nはctcttt又は欠失を表す（存在位置21）。

配列番号1230：nはct又は欠失を表す（存在位置21）。

配列番号1237：nはa又は欠失を表す（存在位置21）。

配列番号1240：nはt又は欠失を表す（存在位置21）。

配列番号1243：nはg又は欠失を表す（存在位置21）。

配列番号1246：nはaattagaa又は欠失を表す（存在位置21）。

配列番号1247：nはttttaaaa又はtttttaaを表す（存在位置21）。

配列番号1250：nはt又は欠失を表す（存在位置21）。

配列番号1255：nはt又は欠失を表す（存在位置21）。

配列番号1267：nはc又は欠失を表す（存在位置21）。

配列番号1292：nはtの11～14回の繰り返しを表す（存在位置21から）。

配列番号1293：nはt又は欠失を表す（存在位置21）。

配列番号1294：nはtの10～13回の繰り返しを表す（存在位置21から）。

配列番号1295：nはt又は欠失を表す（存在位置21）。

配列番号1297：nはt又は欠失を表す（存在位置21）。

配列番号1298：nはta又は欠失を表す（存在位置21）。

配列番号1300：nはtの13～15回の繰り返しを表す（存在位置21から）。

配列番号1301：nはc又は欠失を表す（存在位置21）。

配列番号1302：nはaの17～20回の繰り返しを表す（存在位置21から）。

配列番号1303：nはtの11～13回の繰り返しを表す（存在位置21から）。

配列番号1304：nはtの8～9回の繰り返しを表す（存在位置21から）。

配列番号1305：nはaの10～11回の繰り返しを表す（存在位置21から）。

配列番号1306：nはaの16～19回の繰り返しを表す（存在位置21から）。

配列番号1398：nはg又は欠失を表す（存在位置21）。

- 配列番号1400 : nはaの6～7回の繰り返しを表す (存在位置21から)。
- 配列番号1401 : nはc又は欠失を表す (存在位置21)。
- 配列番号1403 : nはtcctcaggg又は欠失を表す (存在位置21)。
- 配列番号1404 : nはcgcの8～10回の繰り返しを表す (存在位置21から)。
- 配列番号1405 : nはaの10～12回の繰り返しを表す (存在位置21から)。
- 配列番号1406 : nはcaccaggcagcagactctgatgaggaggggaggggg又は欠失を表す (存在位置21)。
- 配列番号1408 : nはg又は欠失を表す (存在位置21)。
- 配列番号1448 : nはtcac又は欠失を表す (存在位置21)。
- 配列番号1449 : nはt又は欠失を表す (存在位置21)。
- 配列番号1450 : nはtの9～11回の繰り返しを表す (存在位置21から)。
- 配列番号1451 : nはaの7～8回の繰り返しを表す (存在位置21から)。
- 配列番号1487 : nはagg又は欠失を表す (存在位置21)。
- 配列番号1488 : nはtaacatt又は欠失を表す (存在位置21)。
- 配列番号1489 : nはaの10～12回の繰り返しを表す (存在位置21から)。
- 配列番号1490 : nはtの15～17回の繰り返しを表す (存在位置21から)。
- 配列番号1491 : nはaの11～13回の繰り返しを表す (存在位置21から)。
- 配列番号1517 : nはtの11～13回の繰り返しを表す (存在位置21から)。
- 配列番号1518 : nはt又は欠失を表す (存在位置21)。
- 配列番号1519 : nはt又は欠失を表す (存在位置21)。
- 配列番号1520 : nはaの10～12回の繰り返しを表す (存在位置21から)。
- 配列番号1521 : nはt又は欠失を表す (存在位置21)。
- 配列番号1523 : nはcの7～9回の繰り返しを表す (存在位置21から)。
- 配列番号1524 : nはa又は欠失を表す (存在位置21)。
- 配列番号1531 : nはtの13～16回の繰り返しを表す (存在位置21から)。
- 配列番号1532 : nはtの9～10回の繰り返しを表す (存在位置21から)。
- 配列番号1533 : nはtの14～16回の繰り返しを表す (存在位置21から)。
- 配列番号1534 : nはtの13～17回の繰り返しを表す (存在位置21から)。
- 配列番号1535 : nはt又は欠失を表す (存在位置21)。

配列番号1537 : nはaの8～9回の繰り返しを表す (存在位置21から)。
配列番号1538 : nはtの8～9回の繰り返しを表す (存在位置21から)。
配列番号1539 : nはgcagtattactgtagt又は欠失を表す (存在位置21)。
配列番号1540 : nはtの13～14回の繰り返しを表す (存在位置21から)。
配列番号1541 : nはtの9～10回の繰り返しを表す (存在位置21から)。
配列番号1542 : nはtの10～11回の繰り返しを表す (存在位置21から)。
配列番号1547 : nはaの10～14回の繰り返しを表す (存在位置21から)。
配列番号1548 : nはaの13～15回の繰り返しを表す (存在位置21から)。
配列番号1549 : nはa又は欠失を表す (存在位置21)。
配列番号1550 : nはt又は欠失を表す (存在位置21)。
配列番号1558 : nはaの13～15回の繰り返しを表す (存在位置21から)。
配列番号1559 : nはaの12～15回の繰り返しを表す (存在位置21から)。
配列番号1576 : nはg又は欠失を表す (存在位置21)。
配列番号1578 : nはaa又は欠失を表す (存在位置21)。
配列番号1623 : nはa又は欠失を表す (存在位置21)。
配列番号1625 : nはaa又は欠失を表す (存在位置21)。
配列番号1626 : nはca又は欠失を表す (存在位置21)。
配列番号1627 : nはt又は欠失を表す (存在位置21)。
配列番号1628 : nはtgtgtg又は欠失を表す (存在位置21)。
配列番号1716 : nはa又は欠失を表す (存在位置21)。
配列番号1718 : nはg又は欠失を表す (存在位置21)。
配列番号1720 : nはactt又は欠失を表す (存在位置21)。
配列番号1721 : nはttta又は欠失を表す (存在位置21)。
配列番号1722 : nはaの11～13回の繰り返しを表す (存在位置21から)。
配列番号1723 : nはtの8～10回の繰り返しを表す (存在位置21から)。
配列番号1724 : nはaの12～14回の繰り返しを表す (存在位置21から)。
配列番号1725 : nはcttgta又は欠失を表す (存在位置21)。
配列番号1726 : nはaの9～10回の繰り返しを表す (存在位置21から)。
配列番号1727 : nはctt又は欠失を表す (存在位置21)。

配列番号1728：nはctt又は欠失を表す（存在位置21）。

配列番号1730：nはa又は欠失を表す（存在位置21）。

配列番号1731：nはaの9～11回の繰り返しを表す（存在位置21から）。

配列番号1732：nはtgt又は欠失を表す（存在位置21）。

配列番号1733：nはaの24～27回の繰り返しを表す（存在位置21から）。

配列番号1734：nはtaの10～21回の繰り返しを表す（存在位置21から）。

配列番号1735：nはaの8～10回の繰り返しを表す（存在位置21から）。

配列番号1736：nはaの11～13回の繰り返しを表す（存在位置21から）。

配列番号1737：nはaの8～10回の繰り返しを表す（存在位置21から）。

配列番号1795：nはctat又は欠失を表す（存在位置21）。

配列番号1796：nはatattcacttggtatctg又は欠失を表す（存在位置21）。

配列番号1797：nはttta又は欠失を表す（存在位置21）。

配列番号1798：nはt又は欠失を表す（存在位置21）。

配列番号1800：nはg又は欠失を表す（存在位置21）。

配列番号1801：nはa又は欠失を表す（存在位置21）。

配列番号1802：nはaの9～11回の繰り返しを表す（存在位置21から）。

配列番号1803：nはg又は欠失を表す（存在位置21）。

配列番号1804：nはatの4～5回の繰り返しを表す（存在位置21から）。

配列番号1805：nはtの7～8回の繰り返しを表す（存在位置21から）。

配列番号1806：nはtの19～23回の繰り返しを表す（存在位置21から）。

配列番号1807：nはt又は欠失を表す（存在位置21）。

配列番号1808：nはtgat又は欠失を表す（存在位置21）。

配列番号1809：nはtの8～10回の繰り返しを表す（存在位置21から）。

配列番号1810：nはa又は欠失を表す（存在位置21）。

配列番号1827：nはgtg又は欠失を表す（存在位置21）。

配列番号1829：nはgg又はtggtgggtggaを表す（存在位置21）。

配列番号1849：nはacaaca又は欠失を表す（存在位置21）。

配列番号1850：nはtの11～13回の繰り返しを表す（存在位置21から）。

配列番号1852：nはacの15～18回の繰り返しを表す（存在位置21から）。

配列番号1858：nはtの18～26回の繰り返しを表す（存在位置21から）。

配列番号1867：nはtc又は欠失を表す（存在位置21）。

配列番号1871：nはtの16～18回の繰り返しを表す（存在位置21から）。

配列番号1886：nはtの18～20回の繰り返しを表す（存在位置21から）。

配列番号1887：nはtggttaagt又は欠失を表す（存在位置21）。

配列番号1889：nはt又は欠失を表す（存在位置21）。

配列番号1895：nはg又は欠失を表す（存在位置21）。

配列番号1896：nはg又は欠失を表す（存在位置21）。

配列番号1897：nはc又は欠失を表す（存在位置21）。

配列番号1898：nはctct又は欠失を表す（存在位置21）。

配列番号1901：nはa又は欠失を表す（存在位置21）。

配列番号1904：nはt又は欠失を表す（存在位置21）。

配列番号1911：nはtの14～17回の繰り返しを表す（存在位置21から）。

配列番号1916：nはtの12～15回の繰り返しを表す（存在位置21から）。

配列番号1917：nはaの10～13回の繰り返しを表す（存在位置21から）。

配列番号1918：nはaの25～27回の繰り返しを表す（存在位置21から）。

配列番号1939：nはc又は欠失を表す（存在位置21）。

配列番号1948：nはtの20～24回の繰り返しを表す（存在位置21から）。

配列番号1951：nはt又は欠失を表す（存在位置21）。

配列番号1952：nはt又は欠失を表す（存在位置21）。

配列番号1954：nはg又は欠失を表す（存在位置21）。

配列番号1960：nはtの18～23回の繰り返しを表す（存在位置21から）。

配列番号1980：nはc又は欠失を表す（存在位置21）。

配列番号2040：nはa又は欠失を表す（存在位置21）。

配列番号2044：nはa又は欠失を表す（存在位置21）。

配列番号2047：nはtt又は欠失を表す（存在位置21）。

配列番号2050：nはat又は欠失を表す（存在位置21）。

配列番号2076：nはtgt又は欠失を表す（存在位置21）。

配列番号2085：nはt又は欠失を表す（存在位置21）。

配列番号2190：nはt又は欠失を表す（存在位置21）。

配列番号2196：nはg又は欠失を表す（存在位置21）。

配列番号2197：nはtの11～13回の繰り返しを表す（存在位置21から）。

配列番号2199：nはa又は欠失を表す（存在位置21）。

配列番号2201：nはtの9～11回の繰り返しを表す（存在位置21から）。

配列番号2204：nはt又は欠失を表す（存在位置21）。

配列番号2206：nはt又は欠失を表す（存在位置21）。

配列番号2210：nはt又は欠失を表す（存在位置21）。

配列番号2215：nはaaga又は欠失を表す（存在位置21）。

配列番号2219：nはaaaa又は欠失を表す（存在位置21）。

配列番号2223：nはtの9～11回の繰り返しを表す（存在位置21から）。

配列番号2231：nはa又は欠失を表す（存在位置21）。

配列番号2254：nはtの11～13回の繰り返しを表す（存在位置21から）。

配列番号2270：nはacta又は欠失を表す（存在位置21）。

配列番号2276：nはgtg又は欠失を表す（存在位置21）。

配列番号2281：nはtの11～12回の繰り返しを表す（存在位置21から）。

配列番号2291：nはtta又は欠失を表す（存在位置21）。

配列番号2305：nはg又は欠失を表す（存在位置21）。

配列番号2307：nはa又は欠失を表す（存在位置21）。

配列番号2309：nはcct又は欠失を表す（存在位置21）。

配列番号2320：nはgga又は欠失を表す（存在位置21）。

配列番号2330：nはtの12～14回の繰り返しを表す（存在位置21から）。

配列番号2335：nはtの16～17回の繰り返しを表す（存在位置21から）。

配列番号2347：nはg又は欠失を表す（存在位置21）。

配列番号2380：nはc又は欠失を表す（存在位置21）。

配列番号2440：nはag又は欠失を表す（存在位置21）。

配列番号2446：nはg又は欠失を表す（存在位置21）。

配列番号2447：nはa又は欠失を表す（存在位置21）。

配列番号2475：nはg又は欠失を表す（存在位置21）。

配列番号2479 : nはc又は欠失を表す (存在位置21)。
配列番号2484 : nはct又は欠失を表す (存在位置21)。
配列番号2486 : nはgc又は欠失を表す (存在位置21)。
配列番号2489 : nはc又は欠失を表す (存在位置21)。
配列番号2524 : nはc又は欠失を表す (存在位置21)。
配列番号2530 : nはtc又は欠失を表す (存在位置21)。
配列番号2542 : nはc又は欠失を表す (存在位置21)。
配列番号2544 : nはg又は欠失を表す (存在位置21)。
配列番号2557 : nはa又は欠失を表す (存在位置21)。
配列番号2561 : nはca又は欠失を表す (存在位置21)。
配列番号2562 : nはt又は欠失を表す (存在位置21)。
配列番号2574 : nはct又は欠失を表す (存在位置21)。
配列番号2605 : nはa又は欠失を表す (存在位置21)。
配列番号2620 : nはt又は欠失を表す (存在位置21)。
配列番号2621 : nはt又は欠失を表す (存在位置21)。
配列番号2626 : nはtの11～13回の繰り返しを表す (存在位置21から)。
配列番号2627 : nはt又は欠失を表す (存在位置21)。
配列番号2629 : nはtの16～18回の繰り返しを表す (存在位置21から)。
配列番号2631 : nはctta又は欠失を表す (存在位置21)。
配列番号2632 : nはc又は欠失を表す (存在位置21)。
配列番号2634 : nはaの10～12回の繰り返しを表す (存在位置21から)。
配列番号2635 : nはgt又は欠失を表す (存在位置21)。
配列番号2636 : nはa又は欠失を表す (存在位置21)。
配列番号2641 : nはaatt又は欠失を表す (存在位置21)。
配列番号2643 : nはt又は欠失を表す (存在位置21)。
配列番号2649 : nはg又は欠失を表す (存在位置21)。
配列番号2661 : nはat又は欠失を表す (存在位置21)。
配列番号2667 : nはcaaaaの4～5回の繰り返しを表す (存在位置21から)。
配列番号2676 : nはaの9～10回の繰り返しを表す (存在位置21から)。

配列番号2681：nはa又は欠失を表す（存在位置21）。

配列番号2687：nはt又は欠失を表す（存在位置21）。

配列番号2691：nはt又は欠失を表す（存在位置21）。

配列番号2692：nはg又は欠失を表す（存在位置21）。

配列番号2700：nはt又は欠失を表す（存在位置21）。

配列番号2701：nはt又は欠失を表す（存在位置21）。

配列番号2702：nはa又は欠失を表す（存在位置21）。

配列番号2712：nはgaa又は欠失を表す（存在位置21）。

配列番号2713：nはag又は欠失を表す（存在位置21）。

配列番号2729：nはtの9～11回の繰り返しを表す（存在位置21から）。

配列番号2730：nはa又は欠失を表す（存在位置21）。

配列番号2731：nはt又は欠失を表す（存在位置21）。

配列番号2813：nはtat又は欠失を表す（存在位置21）。

配列番号2814：nはacの14～17回の繰り返しを表す（存在位置21から）。

配列番号2815：nはaの16～27回の繰り返しを表す（存在位置21から）。

配列番号2816：nはt又は欠失を表す（存在位置21）。

配列番号2817：nはaの8～10回の繰り返しを表す（存在位置21から）。

配列番号2818：nはgtの9～11回の繰り返しを表す（存在位置21から）。

配列番号2819：nはaa又は欠失を表す（存在位置21）。

配列番号2820：nはt又は欠失を表す（存在位置21）。

配列番号2821：nはacの8～12回の繰り返しを表す（存在位置21から）。

配列番号2822：nはa又は欠失を表す（存在位置21）。

配列番号2842：nはagg又は欠失を表す（存在位置21）。

配列番号2844：nはaの11～15回の繰り返しを表す（存在位置21から）。

配列番号2845：nはaの11～14回の繰り返しを表す（存在位置21から）。

配列番号2848：nはgt又は欠失を表す（存在位置21）。

配列番号2864：nはta又は欠失を表す（存在位置21）。

配列番号2947：nはaの16～19回の繰り返しを表す（存在位置21から）。

配列番号2948：nはaa又は欠失を表す（存在位置21）。

- 配列番号2950：nはt又は欠失を表す（存在位置21）。
- 配列番号2951：nはtの10～12回の繰り返しを表す（存在位置21から）。
- 配列番号2952：nはaa又は欠失を表す（存在位置21）。
- 配列番号2953：nはttgacagtccaatat, ttgaca, gtccaatat又は欠失を表す（存在位置21）。
- 配列番号2954：nはcta又は欠失を表す（存在位置21）。
- 配列番号2955：nはa又は欠失を表す（存在位置21）。
- 配列番号2957：nはtの9～11回の繰り返しを表す（存在位置21から）。
- 配列番号2958：nはc又は欠失を表す（存在位置21）。
- 配列番号2960：nはgagatgttgtggctcacat又は欠失を表す（存在位置21）。
- 配列番号2962：nはcc又は欠失を表す（存在位置21）。
- 配列番号2963：nはact又は欠失を表す（存在位置21）。
- 配列番号3045：nはa又は欠失を表す（存在位置21）。
- 配列番号3055：nはtの8～11回の繰り返しを表す（存在位置21から）。
- 配列番号3056：nはtの10～13回の繰り返しを表す（存在位置21から）。
- 配列番号3112：nはg又は欠失を表す（存在位置21）。
- 配列番号3113：nはc又は欠失を表す（存在位置21）。
- 配列番号3194：nはt又は欠失を表す（存在位置21）。
- 配列番号3195：nはtの12～15回の繰り返しを表す（存在位置21から）。
- 配列番号3249：nはa又は欠失を表す（存在位置21）。
- 配列番号3250：nはat又は欠失を表す（存在位置21）。
- 配列番号3365：nはcctgcの16回の繰り返し又はcctgtの16回の繰り返しを表す（存在位置21から）。
- 配列番号3366：nはt又は欠失を表す（存在位置21）。
- 配列番号3368：nはc又は欠失を表す（存在位置21）。
- 配列番号3379：nはacac又は欠失を表す（存在位置21）。
- 配列番号3388：nはgatttgtggtatccag又は欠失を表す（存在位置21）。
- 配列番号3390：nはag又は欠失を表す（存在位置21）。
- 配列番号3391：nはta又は欠失を表す（存在位置21）。

配列番号3397 : nはt又は欠失を表す (存在位置21) 。

配列番号3399 : nはgtの12～14回の繰り返しを表す (存在位置21から) 。

配列番号3411 : nはcagaggct又は欠失を表す (存在位置21) 。

配列番号3412 : nはct又は欠失を表す (存在位置21) 。

配列番号3413 : nはag又は欠失を表す (存在位置21) 。

配列番号3425 : nはgtaaa又は欠失を表す (存在位置21) 。

配列番号3426 : nはaaaaa又は欠失を表す (存在位置21) 。

配列番号3427 : nはa又は欠失を表す (存在位置21) 。

配列番号3468 : nはtc又は欠失を表す (存在位置21) 。

配列番号3470 : nはt又は欠失を表す (存在位置21) 。

配列番号3471 : nはt又は欠失を表す (存在位置21) 。

配列番号3472 : nはgaagaaactgttgacagttt又は欠失を表す (存在位置21) 。

配列番号3473 : nはcct又は欠失を表す (存在位置21) 。

配列番号3474 : nはtttc又は欠失を表す (存在位置21) 。

配列番号3475 : nはttctttttaaattg又は欠失を表す (存在位置21) 。

配列番号3477 : nはttcaggccttt又は欠失を表す (存在位置21) 。

配列番号3479 : nはggcctg又は欠失を表す (存在位置21) 。

配列番号3481 : nはa又は欠失を表す (存在位置21) 。

配列番号3510 : nはcの9～11回の繰り返しを表す (存在位置21から) 。

配列番号3511 : nはaの15～21回の繰り返しを表す (存在位置21から) 。

配列番号3512 : nはggggtggcggggtggg又は欠失を表す (存在位置21) 。

配列番号3513 : nはt又は欠失を表す (存在位置21) 。

配列番号3514 : nはa又は欠失を表す (存在位置21) 。

配列番号3516 : nはa又は欠失を表す (存在位置21) 。

配列番号3517 : nはtの10～12回の繰り返しを表す (存在位置21から) 。

配列番号3518 : nはtt又は欠失を表す (存在位置21) 。

配列番号3520 : nはtccctccttgaagctgacgt又は欠失を表す (存在位置21) 。

配列番号3521 : nはcaの12～18回の繰り返しを表す (存在位置21から) 。

配列番号3534 : nはgtt又は欠失を表す (存在位置21) 。

配列番号3537 : nはga又は欠失を表す (存在位置21)。
配列番号3561 : nはt又は欠失を表す (存在位置21)。
配列番号3580 : nはt又は欠失を表す (存在位置21)。
配列番号3581 : nはt又は欠失を表す (存在位置21)。
配列番号3582 : nはt又は欠失を表す (存在位置21)。
配列番号3605 : nはat又は欠失を表す (存在位置21)。
配列番号3606 : nはa又は欠失を表す (存在位置21)。
配列番号3607 : nはc又は欠失を表す (存在位置21)。
配列番号3637 : nはc又は欠失を表す (存在位置21)。
配列番号3645 : nはt又は欠失を表す (存在位置21)。
配列番号3646 : nはttc又は欠失を表す (存在位置21)。
配列番号3657 : nはctt又は欠失を表す (存在位置21)。
配列番号3689 : nはaの8～9回の繰り返しを表す (存在位置21から)。
配列番号3693 : nはtの10～12回の繰り返しを表す (存在位置21から)。
配列番号3699 : nはtの22～25回の繰り返しを表す (存在位置21から)。
配列番号3710 : nはt又は欠失を表す (存在位置21)。
配列番号3713 : nはa又は欠失を表す (存在位置21)。
配列番号3714 : nはa又は欠失を表す (存在位置21)。
配列番号3716 : nはc又は欠失を表す (存在位置21)。
配列番号3717 : nはtの10～12回の繰り返しを表す (存在位置21から)。
配列番号3718 : nはa又は欠失を表す (存在位置21)。
配列番号3719 : nはtの9～11回の繰り返しを表す (存在位置21から)。
配列番号3722 : nはa又は欠失を表す (存在位置21)。
配列番号3725 : nはt又は欠失を表す (存在位置21)。
配列番号3729 : nはa又は欠失を表す (存在位置21)。
配列番号3741 : nはa又は欠失を表す (存在位置21)。
配列番号3745 : nはa又は欠失を表す (存在位置21)。
配列番号3754 : nはtの9～10回の繰り返しを表す (存在位置21から)。
配列番号3755 : nはaag又は欠失を表す (存在位置21)。

配列番号3757：nはt又は欠失を表す（存在位置21）。

配列番号3758：nはt又は欠失を表す（存在位置21）。

配列番号3760：nはt又は欠失を表す（存在位置21）。

配列番号3761：nはt又は欠失を表す（存在位置21）。

配列番号3763：nはt又は欠失を表す（存在位置21）。

配列番号3765：nはa又は欠失を表す（存在位置21）。

配列番号3767：nはa又は欠失を表す（存在位置21）。

配列番号3774：nはgtの7～8回の繰り返しを表す（存在位置21から）。

配列番号3786：nはcct又は欠失を表す（存在位置21）。

配列番号3788：nはtc又は欠失を表す（存在位置21）。

配列番号3804：nはca又は欠失を表す（存在位置21）。

配列番号3826：nはg又は欠失を表す（存在位置21）。

配列番号3849：nはt又は欠失を表す（存在位置21）。

配列番号3878：nはgccag又は欠失を表す（存在位置21）。

配列番号3918：nはa又は欠失を表す（存在位置21）。

配列番号3921：nはg又は欠失を表す（存在位置21）。

配列番号3922：nはt又は欠失を表す（存在位置21）。

配列番号3927：nはaaa又は欠失を表す（存在位置21）。

配列番号3928：nはa又は欠失を表す（存在位置21）。

配列番号3939：nはc又は欠失を表す（存在位置21）。

配列番号3969：nはaの17～19回の繰り返しを表す（存在位置21から）。

配列番号3972：nはaの16～18回の繰り返しを表す（存在位置21から）。

配列番号3973：nはgaの4～6回の繰り返しを表す（存在位置21から）。

配列番号3986：nはa又は欠失を表す（存在位置21）。

配列番号4015：nはtcの2～3回の繰り返しを表す（存在位置21から）。

配列番号4021：nはaの6～7回の繰り返しを表す（存在位置21から）。

配列番号4023：nはaの13～15回の繰り返しを表す（存在位置21から）。

配列番号4025：nはtの9～10回の繰り返しを表す（存在位置21から）。

配列番号4027：nはaの11～14回の繰り返しを表す（存在位置21から）。

配列番号4029：nはtの14～17回の繰り返しを表す（存在位置21から）。

配列番号4030：nはaの8～9回の繰り返しを表す（存在位置21から）。

配列番号4037：nはg又は欠失を表す（存在位置21）。

配列番号4057：nはtの14～17回の繰り返しを表す（存在位置21から）。

配列番号4061：nはgの7～9回の繰り返しを表す（存在位置21から）。

配列番号4066：nはaの9～10回の繰り返しを表す（存在位置21から）。

配列番号4074：nはaの9～10回の繰り返しを表す（存在位置21から）。

配列番号4076：nはgの6～7回の繰り返しを表す（存在位置21から）。

配列番号4083：nはg又は欠失を表す（存在位置21）。

配列番号4098：nはaの8～9回の繰り返しを表す（存在位置21から）。

配列番号4101：nはcの4～6回の繰り返しを表す（存在位置21から）。

配列番号4123：nはggcgaaggcggcggc又は欠失を表す（存在位置21）。

配列番号4125：nはata又は欠失を表す（存在位置21）。

配列番号4128：nはtの11～12回の繰り返しを表す（存在位置21から）。

配列番号4129：nはtの12～14回の繰り返しを表す（存在位置21から）。

配列番号4133：nはtの9～10回の繰り返しを表す（存在位置21から）。

配列番号4135：nはtaの6～7回の繰り返しを表す（存在位置21から）。

配列番号4137：nはtgtatacgtatacatatacgtatacatatatacatatacgtatatata又は
欠失を表す（存在位置21）。

配列番号4143：nはatatt又は欠失を表す（存在位置21）。

配列番号4150：nはcct又は欠失を表す（存在位置21）。

配列番号4159：nはtggtt又は欠失を表す（存在位置21）。

配列番号4160：nはa又は欠失を表す（存在位置21）。

配列番号4171：nはtの9～10回の繰り返しを表す（存在位置21から）。

配列番号4178：nはa又は欠失を表す（存在位置21）。

配列番号4206：nはa又は欠失を表す（存在位置21）。

配列番号4255：nはa又は欠失を表す（存在位置21）。

配列番号4289：nはgtg又は欠失を表す（存在位置21）。

配列番号4291：nはgg又はtggtgggtggaを表す（存在位置21）。

配列番号4307：nはct又は欠失を表す（存在位置21）。

【図面の簡単な説明】

【図 1】

TaqMan プローブを示す図である。

【図 2】

TaqMan PCR法の概要を示す図である。

【図 3】

蛍光色素を付したプローブを示す図である。

【図 4】

インベーター法の概要を示す図である。

【図 5】

フレットプローブを示す図である。

【図 6】

インベーター法の概要を示す図である。

【図 7】

アレルとマッチしないプローブを示す図である。

【図 8】

ライゲーション反応によるアレルの識別の概要を示す図である。

【図 9 A】

ATP結合カセットサブファミリーAメンバー1（ABCA1）遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号（Accession No.）：AF275948.1 及びAL359846.11

【図 9 B】

ATP結合カセットサブファミリーAメンバー1（ABCA1）遺伝子の構造とSNPの存在位置を示す図である。（図 9 A の続き）

アクセッション番号：AF275948.1 及びAL359846.11

【図 1 0】

ATP結合カセットサブファミリーAメンバー4（ABCA4）遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号：NT_019258.1

【図 1 1】

ATP結合カセットサブファミリーAメンバー7 (ABCA7) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号：NT_025194.1

【図 1 2】

ATP結合カセットサブファミリーAメンバー8 (ABCA8) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号：AC005922.1 及びAC015844.5

【図 1 3】

ATP結合カセットサブファミリーBメンバー1 (ABCB1) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号：AC002457.1及びAC005068.1

【図 1 4】

ATP結合カセットサブファミリーBメンバー4 (ABCB4) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号：AC079591.1, AC079303.3 及び AC005045.2

【図 1 5】

ATP結合カセットサブファミリーBメンバー7 (ABCB7) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号：AL360179.3及びAC002417.1

【図 1 6】

ATP結合カセットサブファミリーBメンバー8 (ABCB8) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号：AC010973.4

【図 1 7】

ATP結合カセットサブファミリーBメンバー9 (ABCB9) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号：AC026362.9 及び AC073857.10

【図 1 8】

ATP結合カセットサブファミリーBメンバー10 (ABCB10) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号 : AL121990.9

【図 1 9】

ATP結合カセットサブファミリーBメンバー11 (ABCB11) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号 : AC008177.3 及び AC069137.3

【図 2 0】

ATP結合カセットサブファミリーCメンバー1 (ABCC1) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号 : AC026452.5 及び AC025778.4

【図 2 1】

ATP結合カセットサブファミリーCメンバー2 (ABCC2) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号 : AL392107.4

【図 2 2】

ATP結合カセットサブファミリーCメンバー3 (ABCC3) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号 : AC004590.1 及び AC005921.3

【図 2 3 A】

ATP結合カセットサブファミリーCメンバー4 (ABCC4) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号 : AL356257.11, AL157818.12 及び AL139381.12

【図 2 3 B】

ATP結合カセットサブファミリーCメンバー4 (ABCC4) 遺伝子の構造とSNPの存在位置を示す図である。(図 2 3 Aの続き)

アクセッション番号 : AL356257.11, AL157818.12 及び AL139381.12

【図 2 4】

ATP結合カセットサブファミリーCメンバー5 (ABCC5) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号: AC068644.5

【図 2 5】

ATP結合カセットサブファミリーCメンバー7 (ABCC7) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号: AC000111.1 及び AC000061.1

【図 2 6】

ATP結合カセットサブファミリーCメンバー8 (ABCC8) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号: AC000406.1

【図 2 7】

ATP結合カセットサブファミリーCメンバー9 (ABCC9) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号: AC084806.9 及び AC008250.23

【図 2 8】

ATP結合カセットサブファミリーDメンバー1 (ABCD1) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号: U52111.2

【図 2 9】

ATP結合カセットサブファミリーDメンバー3 (ABCD3) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号: NT_019284.3

【図 3 0】

ATP結合カセットサブファミリーDメンバー4 (ABCD4) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号: AC005519.3

【図 3 1】

ATP結合カセットサブファミリーGメンバー1 (ABCG1) 遺伝子の構造とSNPの存

在位置を示す図である。

アクセッション番号：AP001746.1

【図 3 2】

ATP結合カセットサブファミリーGメンバー2 (ABCG2) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号：NT_022959.2

【図 3 3】

ATP結合カセットサブファミリーGメンバー4 (ABCG4) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号：AP001315.3

【図 3 4】

ATP結合カセットサブファミリーGメンバー5 (ABCG5) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号：AC084265.2 及び AC011242.8

【図 3 5】

ATP結合カセットサブファミリーGメンバー8 (ABCG8) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号：AC084265.2

【図 3 6】

ATP結合カセットサブファミリーEメンバー1 (ABCE1) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号：NT_006296.2

【図 3 7】

ATP結合カセットサブファミリーFメンバー1 (ABCF1) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号：NT_007592.3

【図 3 8】

オーガニック アニオン トランスポーター 1 (OAT1) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号：AP001858.3, AJ249369.1, 及び AP000438.4

【図 3 9】

オーガニック アニオン トランスポーター2(OAT2) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号：AC26532.3

【図 4 0】

オーガニック アニオン トランスポーター3(OAT3) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号：AP001858.3

【図 4 1】

オーガニック アニオン トランスポーター ポリペプチド1(OATP1) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号：AC022224.22

【図 4 2】

オーガニック アニオン トランスポーター ポリペプチド2(OATP2) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号：NT_024399.2

【図 4 3】

オーガニック アニオン トランスポーター ポリペプチド8(OATP8) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号：NT_024399.2

【図 4 4】

トランスポーター1 ATP結合カセット サブファミリーB(TAP1)遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号：X66401.1

【図 4 5】

トランスポーター2 ATP結合カセット サブファミリーB(TAP2)遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号：X66401.1

【図 4 6】

SLC22A4 ソリユート キャリア ファミリー-22 (オーガニック カチオン トランスporter) メンバー4(OCTN1)遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号 : AC008599.6

【図 4 7】

SLC22A5 ソリユート キャリア ファミリー-22 (オーガニック カチオン トランスporter) メンバー5(OCTN2)遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号 : AC023861.3

【図 4 8】

SLC22A1 ソリユート キャリア ファミリー-22 (オーガニック カチオン トランスporter) メンバー1(OCT1)遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号 : AL35625.5

【図 4 9】

SLC22A2 ソリユート キャリア ファミリー-22 (オーガニック カチオン トランスporter) メンバー2(OCT2)遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号 : AL162582.18

【図 5 0】

SLC10A2 ソリユート キャリア ファミリー-10 (ナトリウム/胆汁酸 コトランスporter ファミリー) メンバー2(NTCP)遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号 : AL157789.6

【図 5 1】

SLC15A1 ソリユート キャリア ファミリー-15 (オリゴペプチド トランスporter) メンバー1(PEPT1)遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号 : AL353574.8 及び AL391670.6

【図 5 2】

ミクロソームエポキシドヒドロラーゼ1 (EPHX1) 遺伝子の構造と SNP の存在位置を示す図である。

アクセッション番号 : AC058782.8

【図 5 3】

細胞質エポキシドヒドロラーゼ (EPHX2) 遺伝子の構造と SNP の存在位置を示す図である。

アクセッション番号 : AC010856.3

【図 5 4】

カテコール-O-メチルトランスフェラーゼ (COMT) 遺伝子の構造と SNP の存在位置を示す図である。

アクセッション番号 : AC000080.2

【図 5 5】

グアニジノアセテートN-メチルトランスフェラーゼ (GAMT) 遺伝子の構造と SNP の存在位置を示す図である。

アクセッション番号 : NT_000879.1

【図 5 6】

フェニルエタノールアミンN-メチルトランスフェラーゼ (PNMT) 遺伝子の構造と SNP の存在位置を示す図である。

アクセッション番号 : AC040933.3

【図 5 7】

ヒスタミン N-メチルトランスフェラーゼ (HNMT) 遺伝子の構造と SNP の存在位置を示す図である。

アクセッション番号 : AC019304.3

【図 5 8】

ニコチンアミドN-メチルトランスフェラーゼ (NNMT) 遺伝子の構造と SNP の存在位置を示す図である。

アクセッション番号 : AC019290.3

【図 5 9】

ホスファチジルエタノールアミンN-メチルトランスフェラーゼ (PEMT) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号 : AC020558.3

【図 6 0】

アルデヒド デヒドロゲナーゼ 1 ファミリー メンバーA1 (ALDH1A1) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号 : AC009284.2 及び AL162416.3

【図 6 1】

アルデヒド デヒドロゲナーゼ 1 ファミリー メンバーA2 (ALDH1A2) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号 : AC025431.7 及び AC012653.8

【図 6 2】

アルデヒド デヒドロゲナーゼ 1 ファミリー メンバーA3 (ALDH1A3) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号 : AC015712.7

【図 6 3】

アルデヒド デヒドロゲナーゼ 1 ファミリー メンバーB1 (ALDH1B1) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号 : AL135785.9

【図 6 4 A】

フォルミルテトラヒドロフォレート デヒドロゲナーゼ (ALDH1L1) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号 : AC079848.6

【図 6 4 B】

フォルミルテトラヒドロフォレート デヒドロゲナーゼ (ALDH1L1) 遺伝子の構造とSNPの存在位置を示す図である。(図 6 4 Aの続き)

アクセッション番号 : AC079848.6

【図 6 5】

アルデヒドデヒドロゲナーゼ 2 (ALDH2) 遺伝子の構造とSNPの存在位置を示す図

である。

アクセッション番号：AC002996.1 及び AC003029.2

【図 6 6】

アルデヒド デヒドロゲナーゼ 3 ファミリー メンバー A1 (ALDH3A1) 遺伝子の構造と SNP の存在位置を示す図である。

アクセッション番号：AC005722.1

【図 6 7】

アルデヒド デヒドロゲナーゼ 3 ファミリー メンバー A2 (ALDH3A2) 遺伝子の構造と SNP の存在位置を示す図である。

アクセッション番号：AC005722.1

【図 6 8】

アルデヒド デヒドロゲナーゼ 3 ファミリー メンバー B1 (ALDH3B1) 遺伝子の構造と SNP の存在位置を示す図である。

アクセッション番号：AC004923.2

【図 6 9】

アルデヒド デヒドロゲナーゼ 3 ファミリー メンバー B2 (ALDH3B2) 遺伝子の構造と SNP の存在位置を示す図である。

アクセッション番号：AC021987.3

【図 7 0】

アルデヒド デヒドロゲナーゼ 5 ファミリー メンバー A1 (ALDH5A1) 遺伝子の構造と SNP の存在位置を示す図である。

アクセッション番号：AL031230.1

【図 7 1】

アルデヒド デヒドロゲナーゼ 6 ファミリー メンバー A1 (ALDH6A1) 遺伝子の構造と SNP の存在位置を示す図である。

アクセッション番号：AC005484.2

【図 7 2】

アルデヒド デヒドロゲナーゼ 8 ファミリー メンバー A1 (ALDH8A1) 遺伝子の構造と SNP の存在位置を示す図である。

アクセッション番号 : AL445190.9 及び AL021939.1

【図 7 3】

アルデヒド デヒドロゲナーゼ 9 ファミリー メンバー A1 (ALDH9A1) 遺伝子の構造と SNP の存在位置を示す図である。

アクセッション番号 : AL451074.4

【図 7 4】

アルコールデヒドロゲナーゼ 1 (ADH1) 遺伝子の構造と SNP の存在位置を示す図である。

アクセッション番号 : AP002027.1

【図 7 5】

アルコールデヒドロゲナーゼ 2 (ADH2) 遺伝子の構造と SNP の存在位置を示す図である。

アクセッション番号 : AP002027.1

【図 7 6】

アルコールデヒドロゲナーゼ 3 (ADH3) 遺伝子の構造と SNP の存在位置を示す図である。

アクセッション番号 : AP002027.1

【図 7 7】

アルコールデヒドロゲナーゼ 4 (ADH4) 遺伝子の構造と SNP の存在位置を示す図である。

アクセッション番号 : AP002026.1

【図 7 8】

アルコールデヒドロゲナーゼ 5 (ADH5) 遺伝子の構造と SNP の存在位置を示す図である。

アクセッション番号 : AC019131.4

【図 7 9】

アルコールデヒドロゲナーゼ 6 (ADH6) 遺伝子の構造と SNP の存在位置を示す図である。

アクセッション番号 : AP002026.1

【図 8 0】

アルコールデヒドロゲナーゼ7 (ADH7) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号 : AC027065.3

【図 8 1】

短鎖アルコールデヒドロゲナーゼファミリー遺伝子 (HEP27) の構造とSNPの存在位置を示す図である。

アクセッション番号 : AL135999.3

【図 8 2】

UDP グリコシルトランスフェラーゼ1ファミリー ポリペプチドA1 (UGT1A1) の構造とSNPの存在位置を示す図である。

アクセッション番号 : AC006985.2

【図 8 3】

UDP グリコシルトランスフェラーゼ2ファミリー ポリペプチドA1 (UGT2A1) の構造とSNPの存在位置を示す図である。

アクセッション番号 : AC011254.3

【図 8 4】

UDP グリコシルトランスフェラーゼ2ファミリー ポリペプチドB15 (UGT2B15) の構造とSNPの存在位置を示す図である。

アクセッション番号 : AC019173.4

【図 8 5】

UDP グリコシルトランスフェラーゼ8 (UGT8) の構造とSNPの存在位置を示す図である。

アクセッション番号 : U31353.1

【図 8 6】

グルタチオン S トランスフェラーゼ A 1 (GSTA1) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号 : AC021133.4

【図 8 7】

グルタチオン S トランスフェラーゼ A 4 (GSTA4) 遺伝子の構造と SNP の存在位置を示す図である。

アクセッション番号 : AC025085.4

【図 8 8】

グルタチオン S トランスフェラーゼ M 1 (GSTM1) 遺伝子の構造と SNP の存在位置を示す図である。

アクセッション番号 : AC000032.7

【図 8 9】

グルタチオン S トランスフェラーゼ M 2 (GSTM2) 遺伝子の構造と SNP の存在位置を示す図である。

アクセッション番号 : AC000031.5

【図 9 0】

グルタチオン S トランスフェラーゼ Z 1 (GSTZ1) 遺伝子の構造と SNP の存在位置を示す図である。

アクセッション番号 : AC007954.7

【図 9 1】

グルタチオン S トランスフェラーゼ P i (GSTPi) 遺伝子の構造と SNP の存在位置を示す図である。

アクセッション番号 : X08058.1 及び M24485.1

【図 9 2】

グルタチオン S トランスフェラーゼ T 1 (GSTT1) 遺伝子の構造と SNP の存在位置を示す図である。

アクセッション番号 : AF240786.1 及び AP000351.3

【図 9 3】

ミクロソームのグルタチオン S トランスフェラーゼ 1 (MGST1) 遺伝子の構造と SNP の存在位置を示す図である。

アクセッション番号 : AC007528.5

【図 9 4】

ミクロソームのグルタチオン S トランスフェラーゼ 1 like 1 (MGST1L1) 遺伝子

の構造とSNPの存在位置を示す図である。

アクセッション番号：AC007936.2

【図 9 5】

ミクロソームのグルタチオン S トランスフェラーゼ T 2 (MGST2) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号：AC019049.4

【図 9 6】

ミクロソームのグルタチオン S トランスフェラーゼ T 3 (MGST3) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号：AC064827.2

【図 9 7】

スルホトランスフェラーゼ1A1 (SULT1A1/STP1) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号：U52852.2

【図 9 8】

スルホトランスフェラーゼ1A2 (SULT1A2/STP2) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号：U33886.1, U34804.1 及び AC020765.5

【図 9 9】

スルホトランスフェラーゼ1A3 (SULT1A3/STM/HAST) 遺伝子の構造とSNPの存在位置を示す図である

アクセッション番号：L34160.1 及び AC012645.4

【図 1 0 0】

スルホトランスフェラーゼ1C1 (SULT1C1) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号：AC019100.4

【図 1 0 1】

スルホトランスフェラーゼ1C2 (SULT1C2) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号：AF186263.1

【図 1 0 2】

スルホトランスフェラーゼ2A1 (SULT2A1) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号：AC024582.4, AC008745.5, NT_011190.1及び AC024582.4

【図 1 0 3】

スルホトランスフェラーゼ2B1 (SULT2B1) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号：AC040922.2 及び AC008403.6

【図 1 0 4】

スルホトランスフェラーゼ-関連タンパク質3 (SULTX3) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号：Z97055.1

【図 1 0 5】

チロシルタンパク質スルホトランスフェラーゼ1 (TPST1) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号：AC026281.5

【図 1 0 6】

チロシルタンパク質スルホトランスフェラーゼ2 (TPST2) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号：Z95115.1

【図 1 0 7】

セレブロシドスルホトランスフェラーゼ (CST) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号：AC005006.2

【図 1 0 8】

甲状腺ホルモンスルホトランスフェラーゼ (ST1B2) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号：AC027059.2

【図 1 0 9】

カルボハイドレート スルホトランスフェラーゼ 1 (CHST1) 遺伝子の構造と SN
P の存在位置を示す図である。

アクセッション番号 : NT_008982.1

【図 1 1 0】

カルボハイドレート スルホトランスフェラーゼ 2 (CHST2) 遺伝子の構造と SNP
の存在位置を示す図である。

アクセッション番号 : AC055737.10

【図 1 1 1】

カルボハイドレート スルホトランスフェラーゼ 3 (CHST3) 遺伝子の構造と SN
P の存在位置を示す図である。

アクセッション番号 : AC073370.3

【図 1 1 2】

カルボハイドレート スルホトランスフェラーゼ 4 (CHST4) 遺伝子の構造と SNP
の存在位置を示す図である。

アクセッション番号 : AC010547.5

【図 1 1 3】

カルボハイドレート スルホトランスフェラーゼ 5 (CHST5) 遺伝子の構造と SNP
の存在位置を示す図である。

アクセッション番号 : AC025287.3

【図 1 1 4】

HNK-スルホトランスフェラーゼ (HNK-1ST) 遺伝子の構造と SNP の存在位置を示
す図である。

アクセッション番号 : AC012493.4

【図 1 1 5】

エストロゲンスルホトランスフェラーゼ (STE) 遺伝子の構造と SNP の存在位置
を示す図である。

アクセッション番号 : AC074273.1

【図 1 1 6】

NAD(P)H: キノンオキシドレダクターゼ1(NQ01) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号 : M81596.1

【図 1 1 7】

NRH: キノンオキシドレダクターゼ2(NQ02) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号 : AB050248.1

【図 1 1 8】

キノンオキシドレダクターゼ相同体のp53誘導遺伝子3 (PIG3) の構造とSNPの存在位置を示す図である。

アクセッション番号 : AC008073.3

【図 1 1 9】

NADH-デハイドロゲナーゼ (ユビキノ) 1 α サブコンプレックス 1 (NDUFA1) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号 : AC002477.1

【図 1 2 0】

NADH-デハイドロゲナーゼ (ユビキノ) 1 α サブコンプレックス 2 (NDUFA2) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号 : AB054976.1

【図 1 2 1】

NADH-デハイドロゲナーゼ (ユビキノ) 1 α サブコンプレックス 3 (NDUFA3) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号 : AC009968.6

【図 1 2 2】

NADH-デハイドロゲナーゼ (ユビキノ) 1 α サブコンプレックス 5 (NDUFA5) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号 : AC073323.5

【図 1 2 3】

NADH-デハイドロゲナーゼ (ユビキノ) 1 α サブコンプレックス 6 (NDU

FA6) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号 : AL021878.1

【図 1 2 4】

NADH-デハイドロゲナーゼ (ユビキノン) 1 α サブコンプレックス 7 (NDU

FA7) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号 : AC010323.6

【図 1 2 5】

NADH-デハイドロゲナーゼ (ユビキノン) 1 α サブコンプレックス 8 (NDU

FA8) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号 : AL162423.10

【図 1 2 6】

NADH-デハイドロゲナーゼ (ユビキノン) 1 α サブコンプレックス 9 (NDU

FA9) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号 : AC005832.1

【図 1 2 7】

NADH-デハイドロゲナーゼ (ユビキノン) 1 α サブコンプレックス 10 (N

DUFA10) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号 : AC013469.8

【図 1 2 8】

NADH-デハイドロゲナーゼ (ユビキノン) 1 α/β サブコンプレックス 1 (N

NDUFAB1) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号 : AC008870.6

【図 1 2 9】

NADH-デハイドロゲナーゼ (ユビキノン) 1 β サブコンプレックス 3 (NDU

FB3) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号 : AC007272.3

【図 1 3 0】

NADH-デハイドロゲナーゼ (ユビキノン) 1 β サブコンプレックス 5 (NDU

FB5) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号 : AC068361.2

【図 1 3 1】

N A D H - デハイドロゲナーゼ (ユビキノン) 1 β サブコンプレックス 7 (NDUFB7) 遺伝子の構造と SNP の存在位置を示す図である。

アクセッション番号 : AC010527.4

【図 1 3 2】

N A D H - デハイドロゲナーゼ (ユビキノン) F e - S タンパク質 1 (NDUFS1) 遺伝子の構造と SNP の存在位置を示す図である。

アクセッション番号 : AC007383.4

【図 1 3 3】

N A D H - デハイドロゲナーゼ (ユビキノン) F e - S タンパク質 3 (NDUFS3) 遺伝子の構造と SNP の存在位置を示す図である。

アクセッション番号 : AC067943.4

【図 1 3 4】

N A D H - デハイドロゲナーゼ (ユビキノン) F e - S タンパク質 4 (NDUFS4) 遺伝子の構造と SNP の存在位置を示す図である。

アクセッション番号 : AC024569.3

【図 1 3 5】

N A D H - デハイドロゲナーゼ (ユビキノン) F e - S タンパク質 5 (NDUFS5) 遺伝子の構造と SNP の存在位置を示す図である。

アクセッション番号 : AL139015.5

【図 1 3 6】

N A D H - デハイドロゲナーゼ (ユビキノン) F e - S タンパク質 6 (NDUFS6) 遺伝子の構造と SNP の存在位置を示す図である。

アクセッション番号 : AC026443.2

【図 1 3 7】

N A D H - デハイドロゲナーゼ (ユビキノン) F e - S タンパク質 8 (NDUFS8) 遺伝子の構造と SNP の存在位置を示す図である。

アクセッション番号 : AC034259.2

【図 138】

NADH-デハイドロゲナーゼ (ユビキノン) フラボプロテイン 1 (NDUFV1)
遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号: NT_009304.2

【図 139】

NADH-デハイドロゲナーゼ (ユビキノン) フラボプロテイン 2 (NDUFV2)
遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号: NT_011024.2

【図 140】

NADH-デハイドロゲナーゼ (ユビキノン) フラボプロテイン 3 (NDUFV3)
遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号: AP001748.1

【図 141】

ガンマ-グルタミルトランスフェラーゼ1 (GGT1) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号: D87002.1

【図 142】

トランスグルタミナーゼ1 (TGM1) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号: M98447.1

【図 143】

チトクローム P450 サブファミリー 1 (アロマティック化合物誘発性) ポリペプチド 1 (CYP1A1) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号: X04300.1 及び AC020705.4

【図 144】

チトクローム P450 サブファミリー 1 (アロマティック化合物誘発性) ポリペプチド 2 (CYP1A2) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号: AC020705.4

【図 145】

チトクローム P 4 5 0 サブファミリー 1 (ジオキシン誘発性) ポリペプチド 1 (CYP1B1) 遺伝子の構造と SNP の存在位置を示す図である。

アクセッション番号：AC009229.4

【図 1 4 6】

チトクローム P 4 5 0 サブファミリー 3 A (アロマティック化合物誘発性) ポリペプチド 4 (CYP3A4) 遺伝子の構造と SNP の存在位置を示す図である。

アクセッション番号：AF280107.1

【図 1 4 7】

チトクローム P 4 5 0 サブファミリー 3 A (アロマティック化合物誘発性) ポリペプチド 5 (CYP3A5) 遺伝子の構造と SNP の存在位置を示す図である。

アクセッション番号：AC005020.5

【図 1 4 8】

チトクローム P 4 5 0 サブファミリー 3 A ポリペプチド 7 (CYP3A7) 遺伝子の構造と SNP の存在位置を示す図である。

アクセッション番号：AF280107.1

【図 1 4 9】

チトクローム P 4 5 0 ポリペプチド 4 3 (CYP3A43) 遺伝子の構造と SNP の存在位置を示す図である。

アクセッション番号：AC011904.3

【図 1 5 0】

チトクローム P 4 5 0 サブファミリー IVB ポリペプチド 1 (CYP4B1) 遺伝子の構造と SNP の存在位置を示す図である。

アクセッション番号：AL356793.10

【図 1 5 1】

チトクローム P 4 5 0 サブファミリー IVF ポリペプチド 2 (CYP4F2) 遺伝子の構造と SNP の存在位置を示す図である。

アクセッション番号：AC005336.1

【図 1 5 2】

チトクローム P 4 5 0 サブファミリー IVF ポリペプチド 3 (CYP4F3) 遺伝子

の構造とSNPの存在位置を示す図である。

アクセッション番号 : AD000685.1

【図 1 5 3】

チトクローム P 4 5 0 サブファミリー IVF ポリペプチド 8 (CYP4F8) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号 : AC068845.3

【図 1 5 4】

チトクローム P 4 5 0 サブファミリー XXVIIA ポリペプチド 1 (CYP27A1) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号 : AC009974.7

【図 1 5 5】

チトクローム P 4 5 0 サブファミリー XXVII B ポリペプチド 1 (CYP27B1) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号 : AC025165.27

【図 1 5 6】

アリルアセタミド デアセチラーゼ (AADAC) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号 : AC068647.4

【図 1 5 7】

カルボキシルエステラーゼ 1 (CES1) 遺伝子の構造とSNPの存在位置を示す図である

アクセッション番号 : AC007602.4

【図 1 5 8】

カルボキシルエステラーゼ 2 (CES2) 遺伝子の構造とSNPの存在位置を示す図である

アクセッション番号 : AC027131.4

【図 1 5 9】

グランザイム A (GZMA) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号 : AC091977.1

【図 160】

グランザイムB(GZMB)遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号: AL136018.3

【図 161】

エステラーゼD/ホルミルグルタチオンヒドロラーゼ(ESD) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号: AL136958.9

【図 162A】

カルボキシル エステル リパーゼ (胆汁酢酸誘発リパーゼ) (CEL) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号: AL138750.8, AL162417.20 及び AF072711.1

【図 162B】

カルボキシル エステル リパーゼ (胆汁酢酸誘発リパーゼ) (CEL) 遺伝子の構造とSNPの存在位置を示す図である。(図 162Aの続き)

アクセッション番号: AL138750. , AL162417.20 及び AF072711.1

【図 163】

インターロイキン17 (サイトトキシック Tリンパ球 アソシエイト セリンエステラーゼ8) (IL17) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号: AL355513.11

【図 164】

ユビキチン カルボキシル ターミナル エステラーゼL3(ユビキチン チオールエステラーゼ) (UCHL3) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号: AL137244.28

【図 165】

ドリシル-ジホスホオリゴサッカライド-タンパク質グリコシルトランスフェラーゼ (DDOST) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号: D89060

【図 166】

ニューロパチーターゲットエステラーゼ(NTE)遺伝子の構造とSNPの存在位置を

示す図である。

アクセッション番号：AC021153

【図 1 6 7】

L1細胞接着分子（L1CAM）遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号：U52112

【図 1 6 8】

アリアルアルキルアミン N-アセチルトランスフェラーゼ（AANAT）遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号：U40391

【図 1 6 9】

サッカロミセス・セレビシエ（*Saccharomyces cerevisiae*）のN-アセチルトランスフェラーゼ相同体（ARD1）遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号：U52112

【図 1 7 0】

N-アセチルトランスフェラーゼ（NAT1）遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号：X17059

【図 1 7 1】

N-アセチルトランスフェラーゼ2（NAT2）遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号：D10870

【図 1 7 2】

ATP結合カセットサブファミリーBメンバー2（ABCB2）遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号：X66401

【図 1 7 3】

ATP結合カセットサブファミリーBメンバー3（ABCB3）遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号：X66401

【図 1 7 4】

グルタチオンSトランスフェラーゼM3 (GSTM3) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号 : AF043105.1

【図 1 7 5】

グルタチオンSトランスフェラーゼM4 (GSTM4) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号 : M96233.1

【図 1 7 6】

アルデヒドデヒドロゲナーゼ 7 (ALDH7) 遺伝子の構造とSNPの存在位置を示す図である。

アクセッション番号 : AC004923

【図 1 7 7】

high-mobility group protein 17-like 1 (HMG17L1) 遺伝子の構造とSNPの存在位置を示す図である。

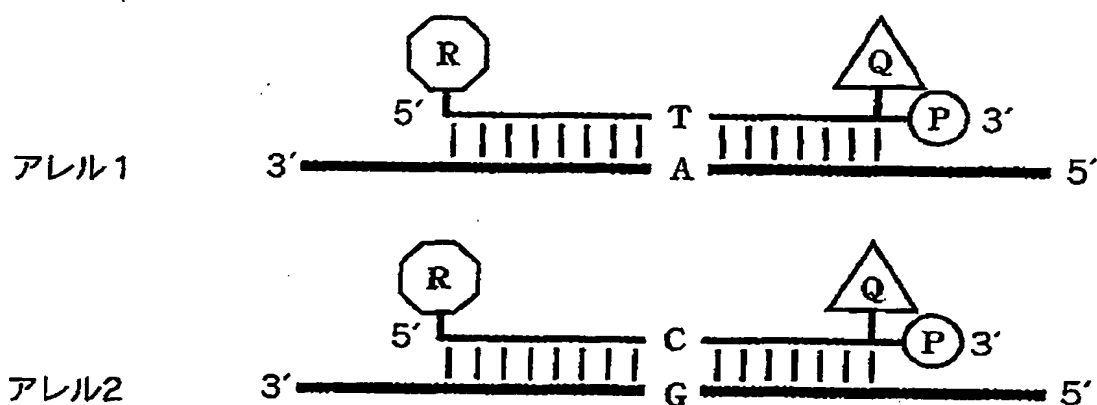
アクセッション番号 : Z97055.1

【図 1 7 8】

異なる 2 グループの被験者についてインベーター法によりタイピングを行った結果を示す図である。

【書類名】 図面

【図1】



【図2】

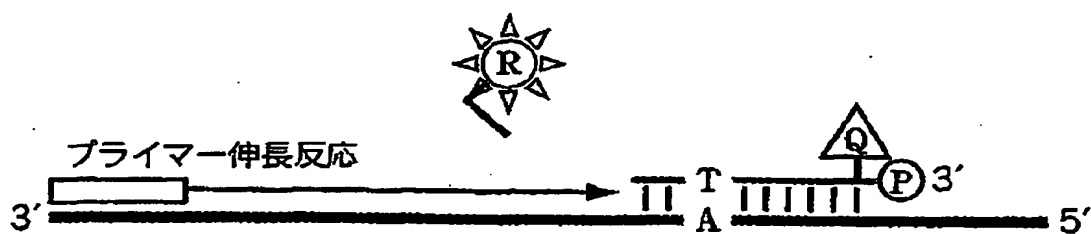
a. ハイブリダイゼーション



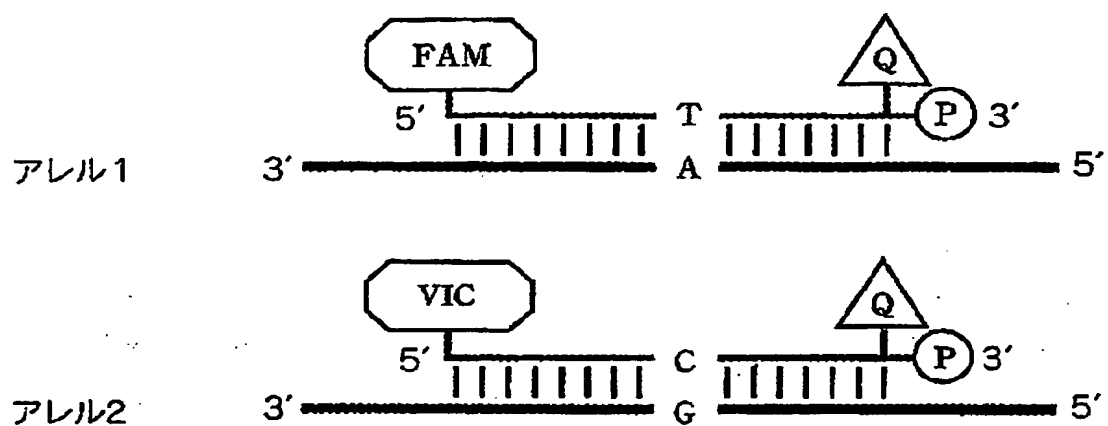
b. PCR反応



c. 5'ヌクレアーゼ活性



【図3】



【図4】

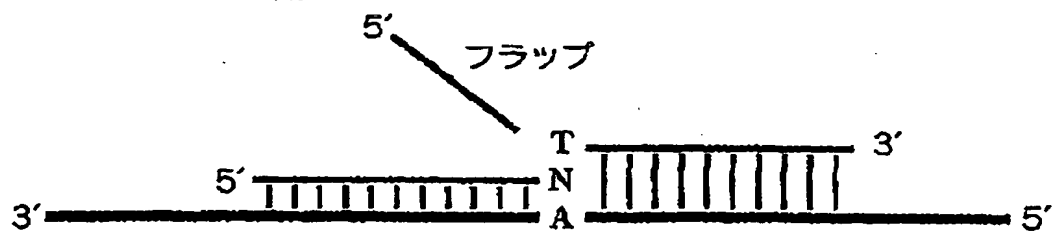
a. アレルプローブ



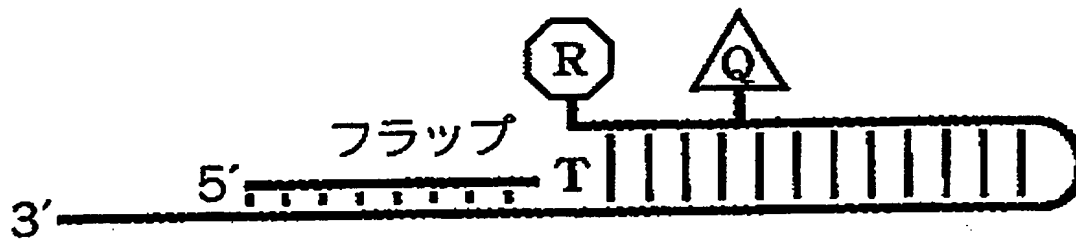
b. インベータープローブ



c. 5'ヌクレアーゼ活性

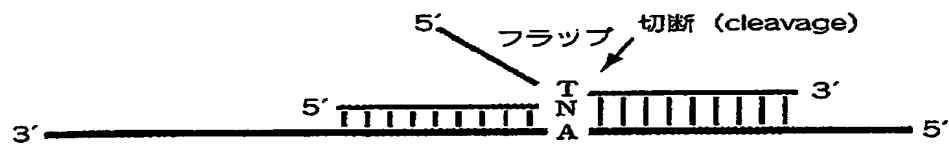


【図5】

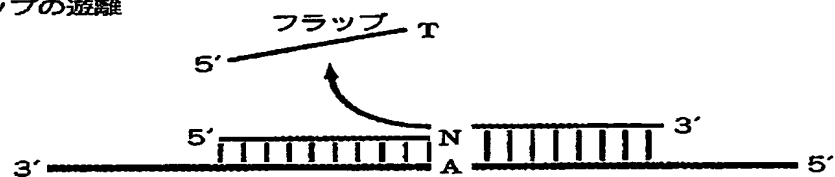


【図6】

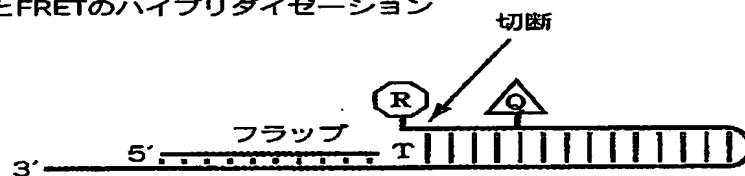
a. cleavageによるアレルプロローブの切断



b. フラップの遊離



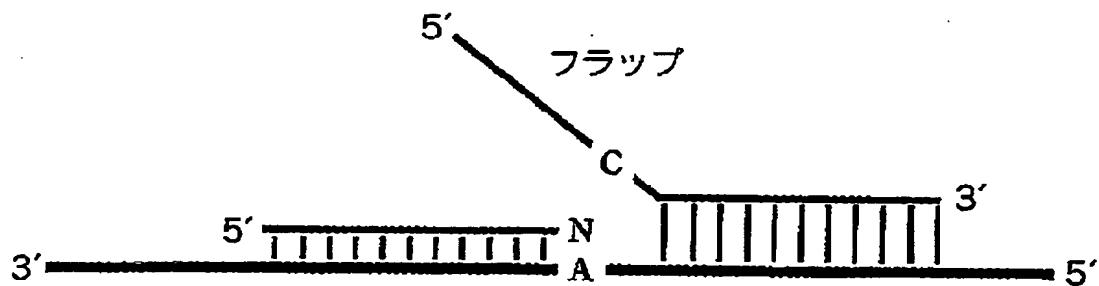
c. フラップとFRETのハイブリダイゼーション



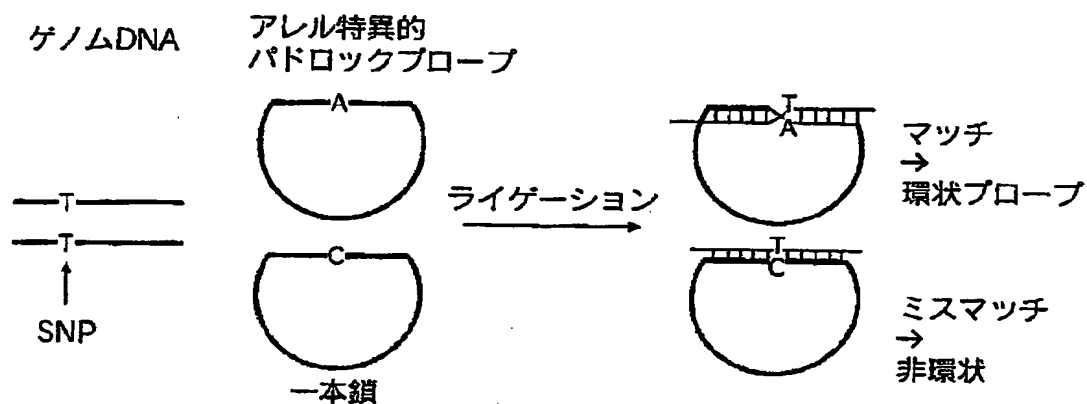
d. 蛍光色素の遊離



【図 7】

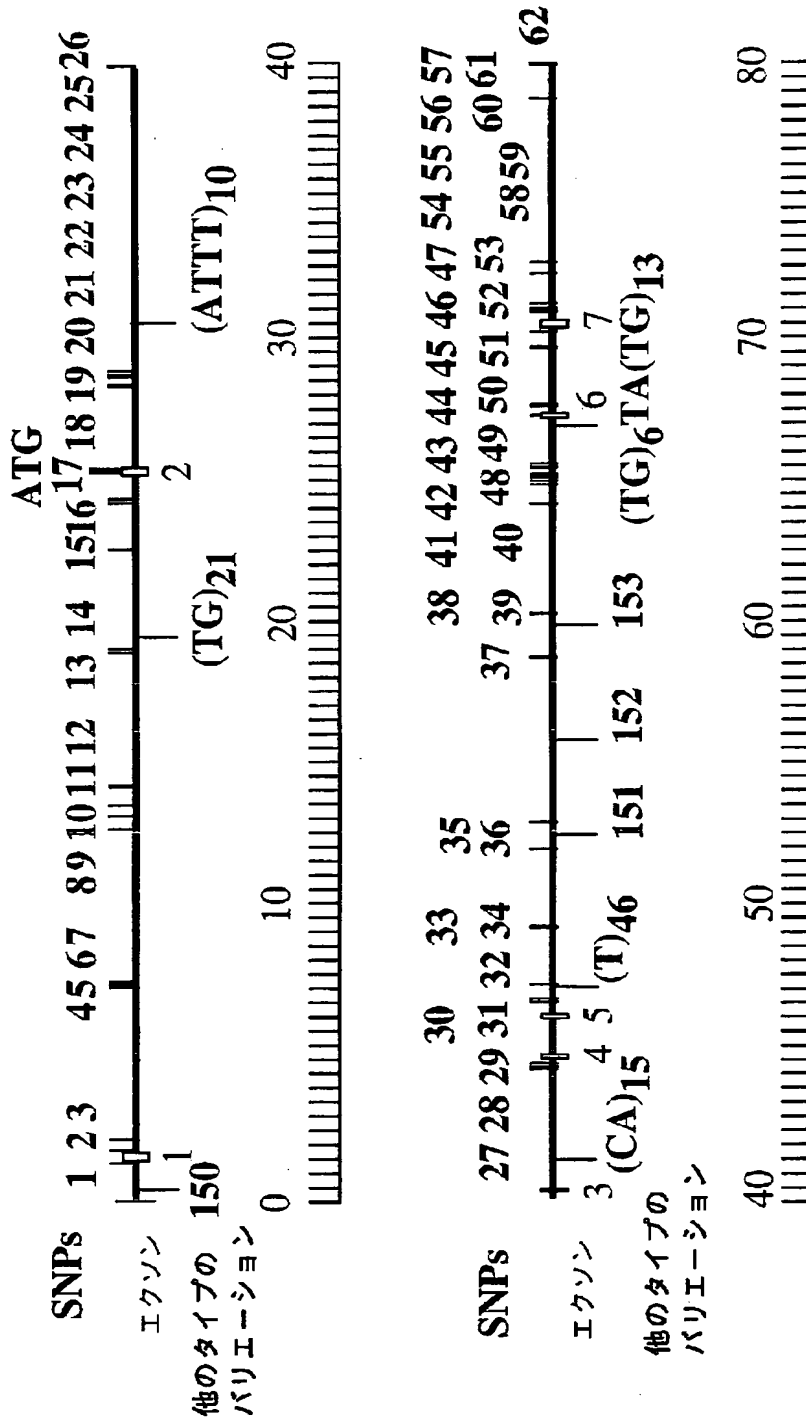


【図 8】

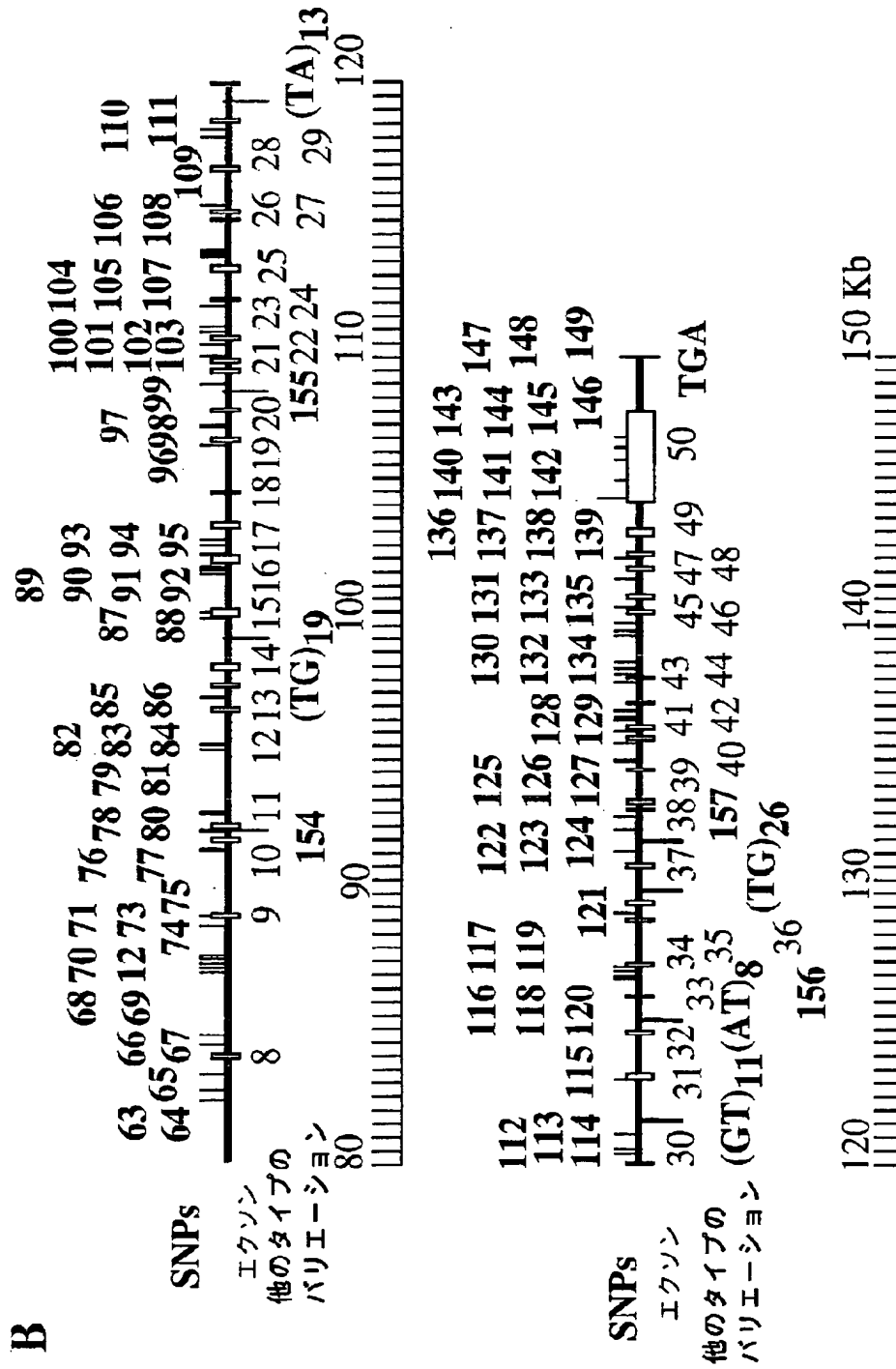


【図 9 A】

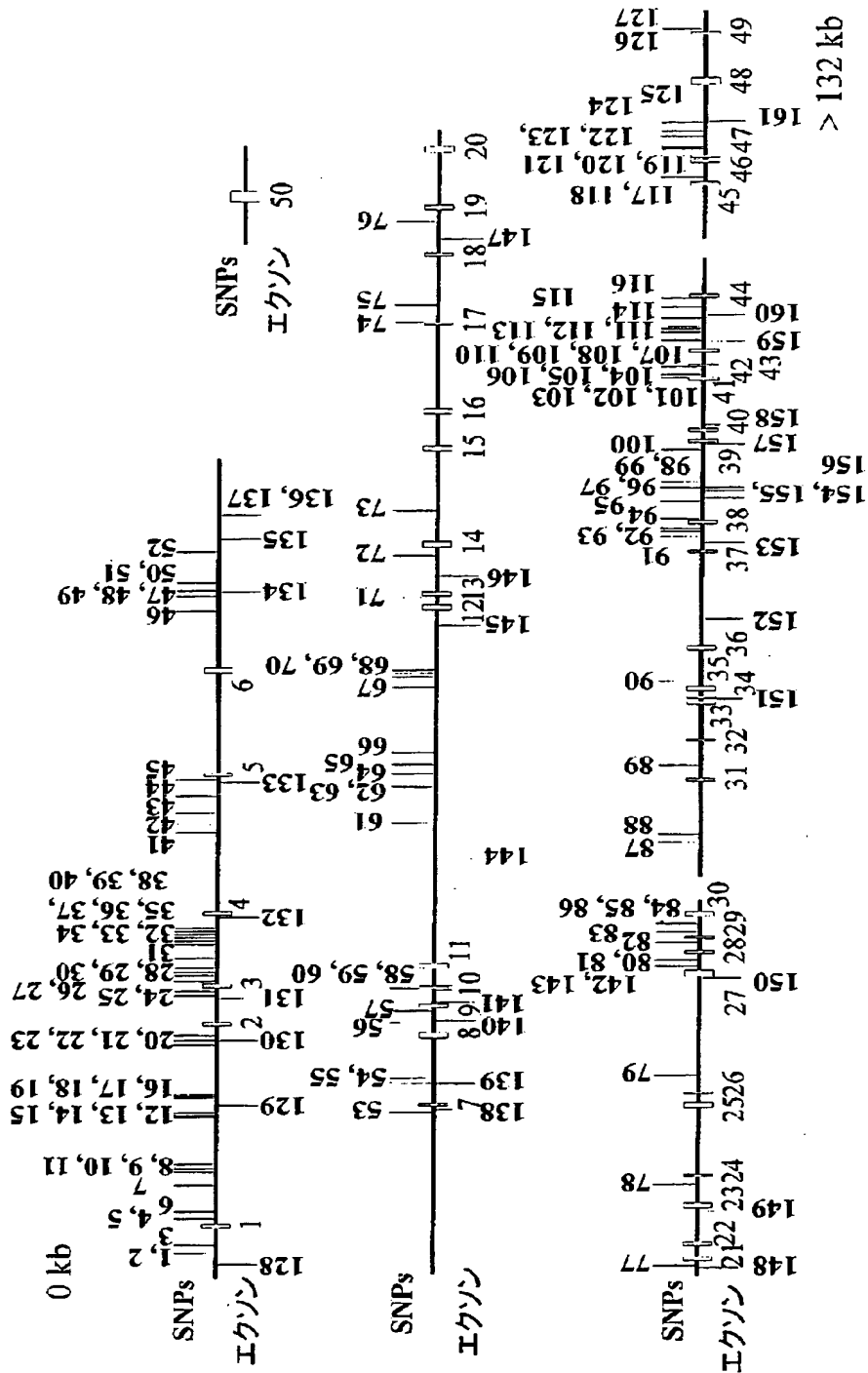
A



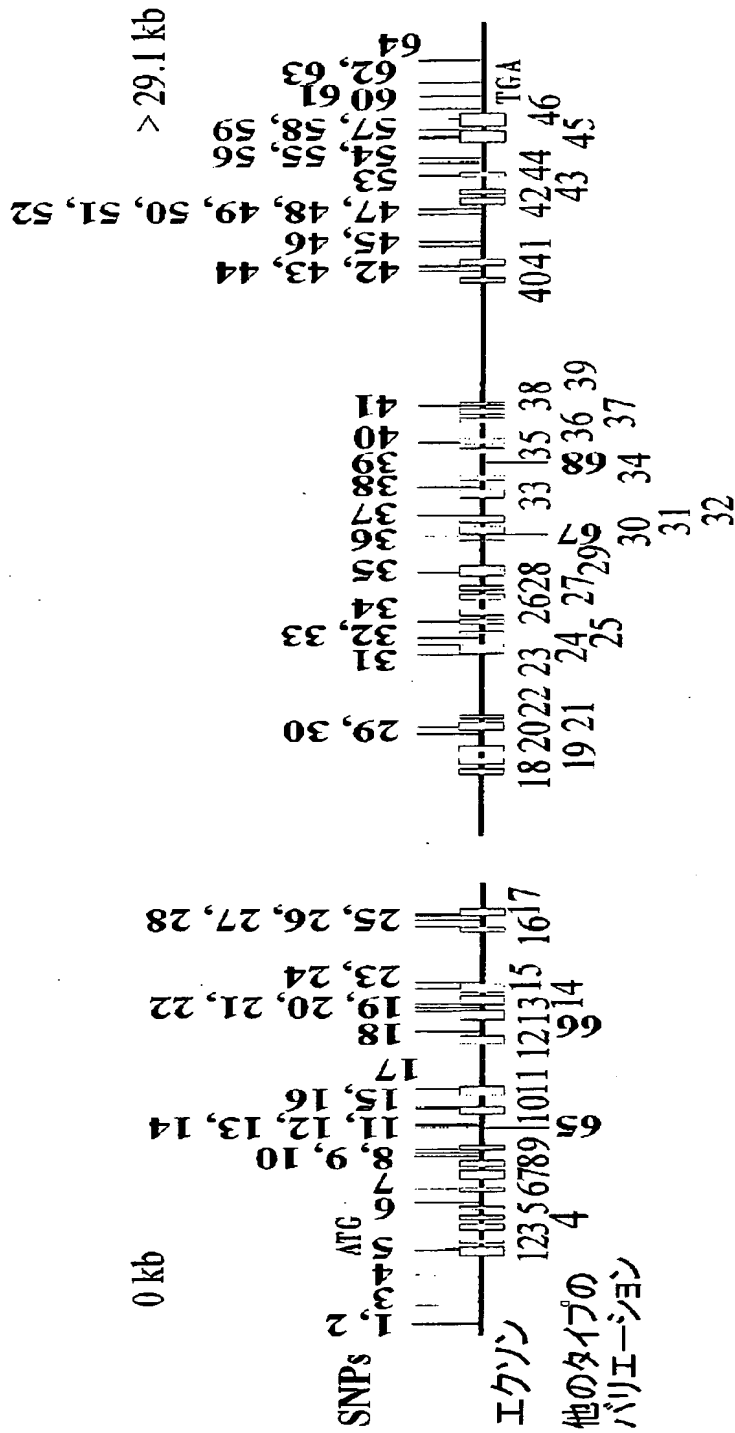
【図 9 B】



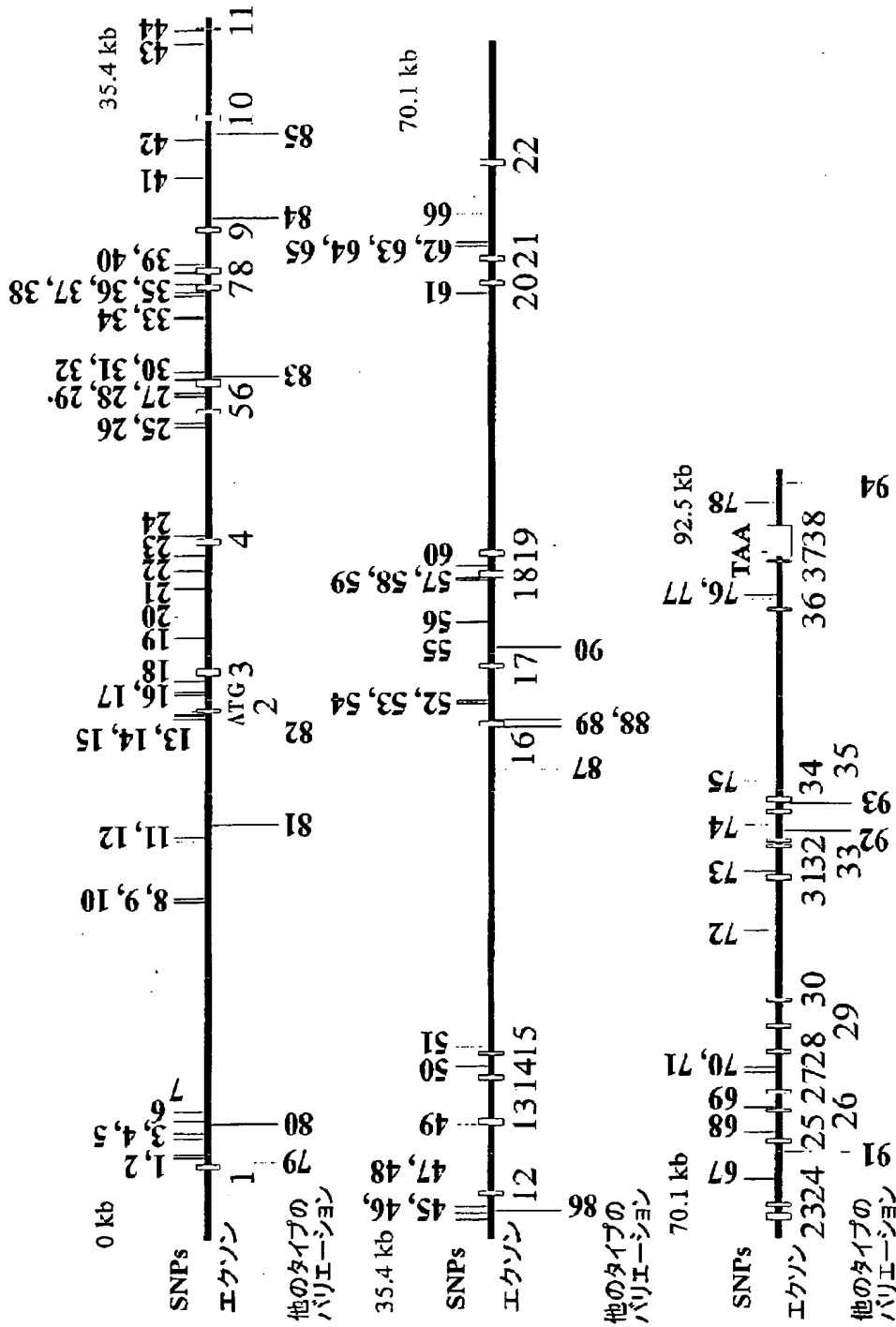
【図 10】



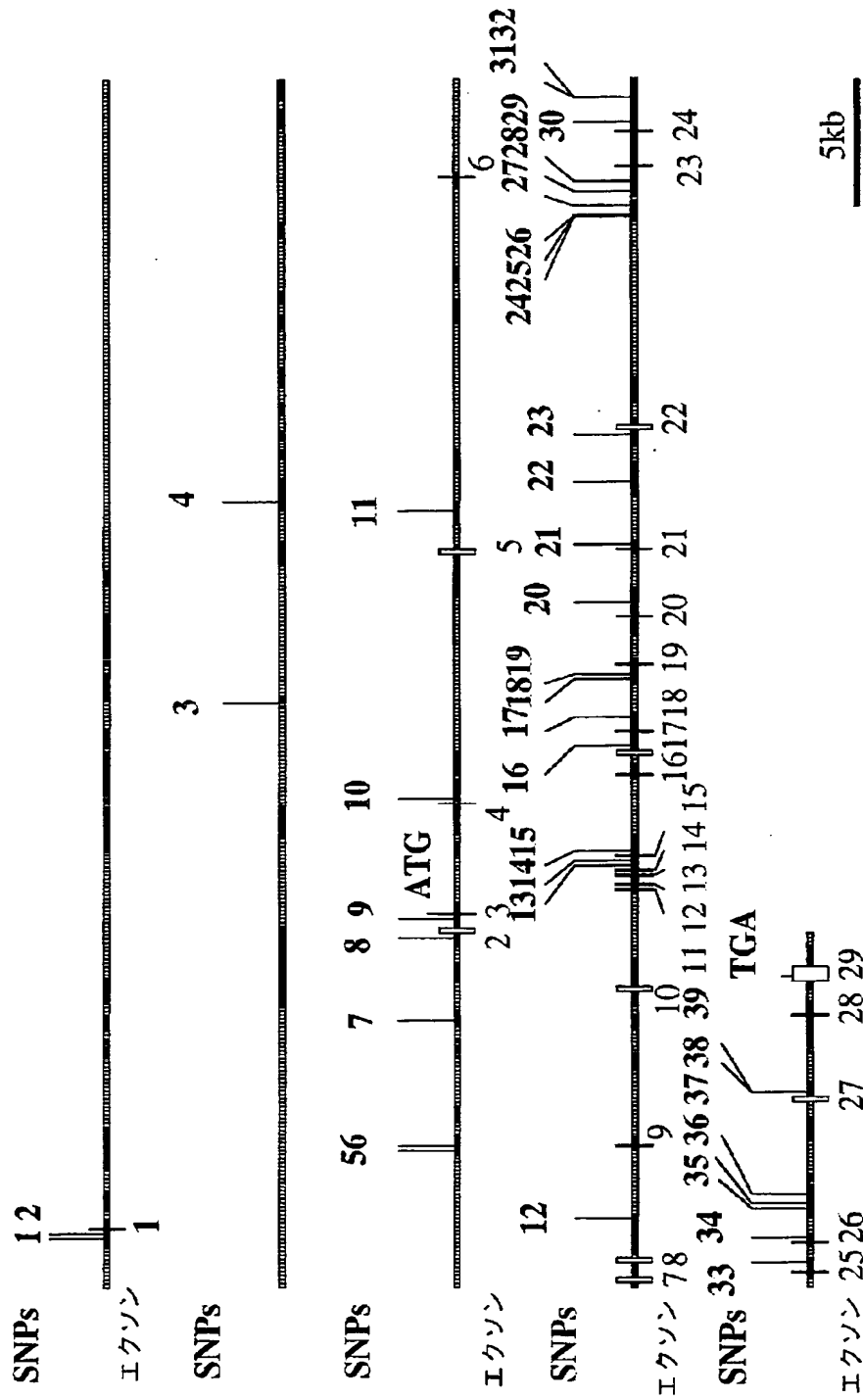
【図11】



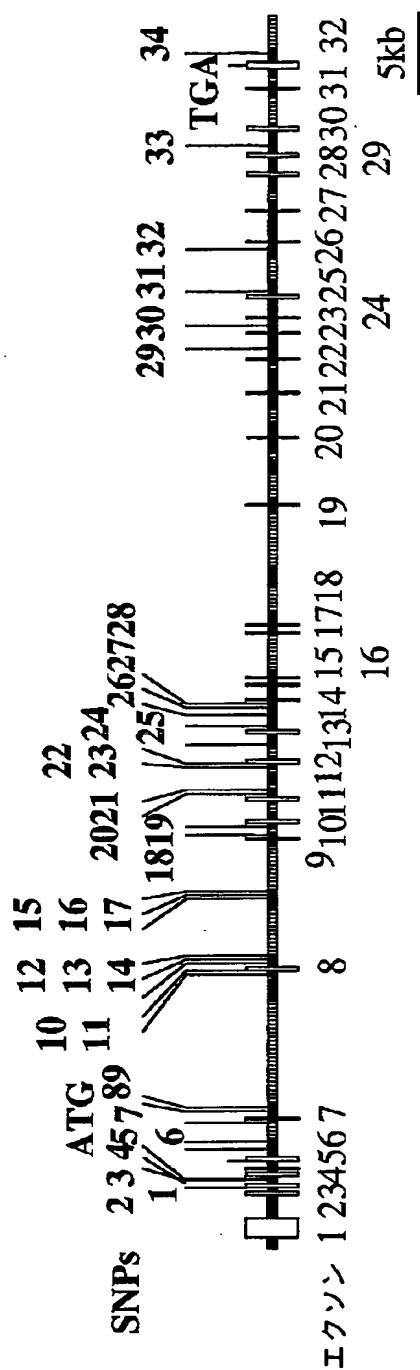
【図12】



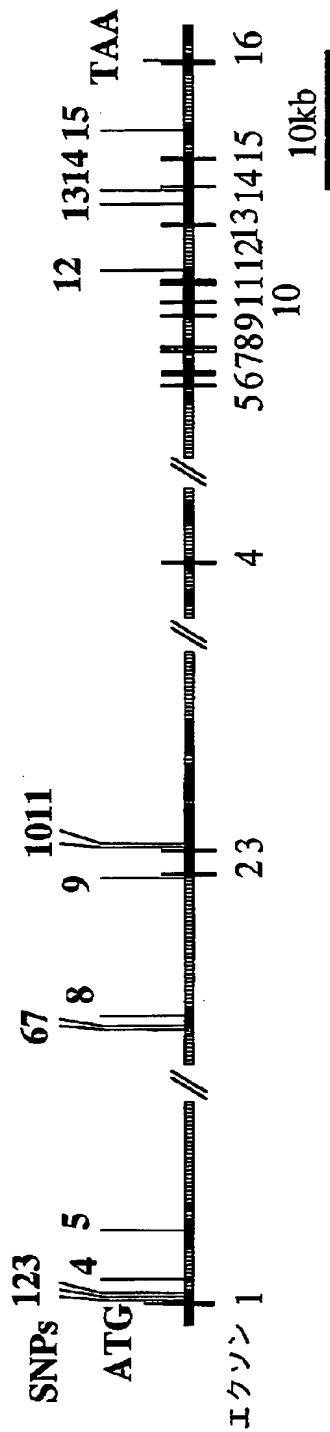
【図 13】



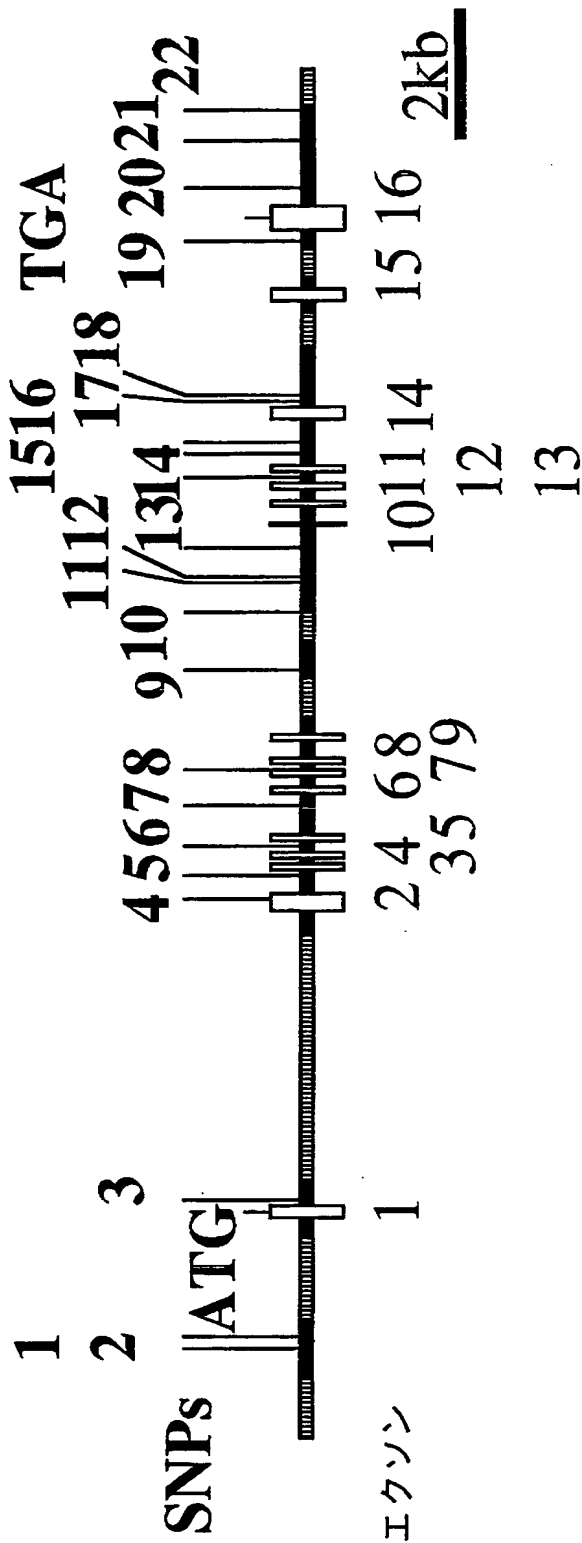
【図 14】



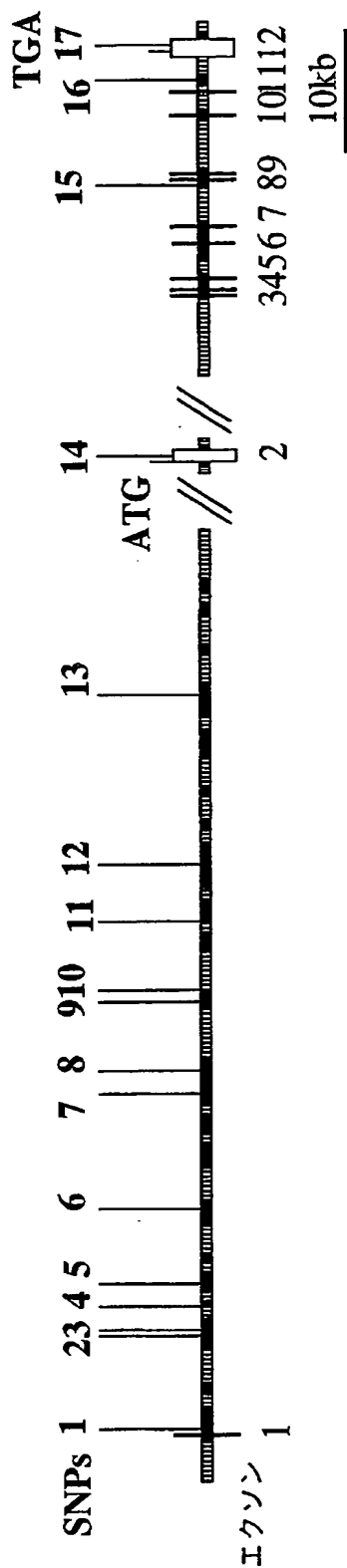
【図 15】



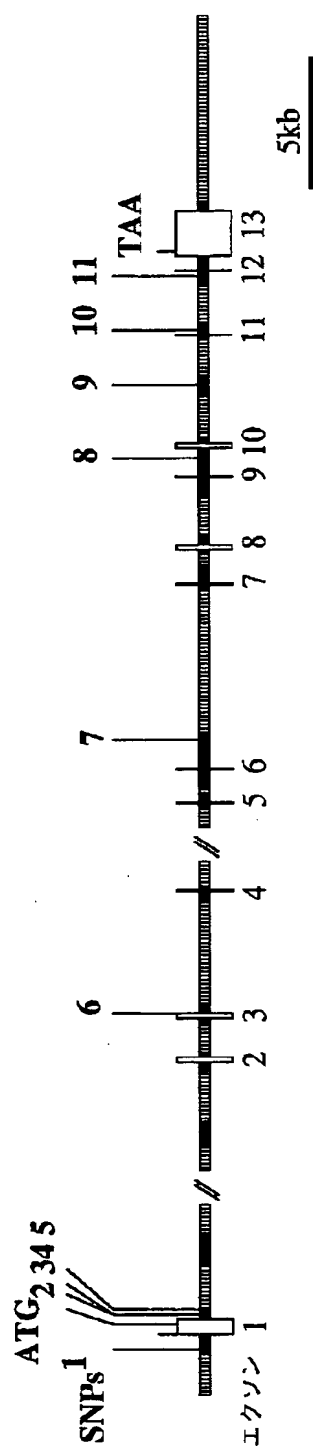
【図 16】



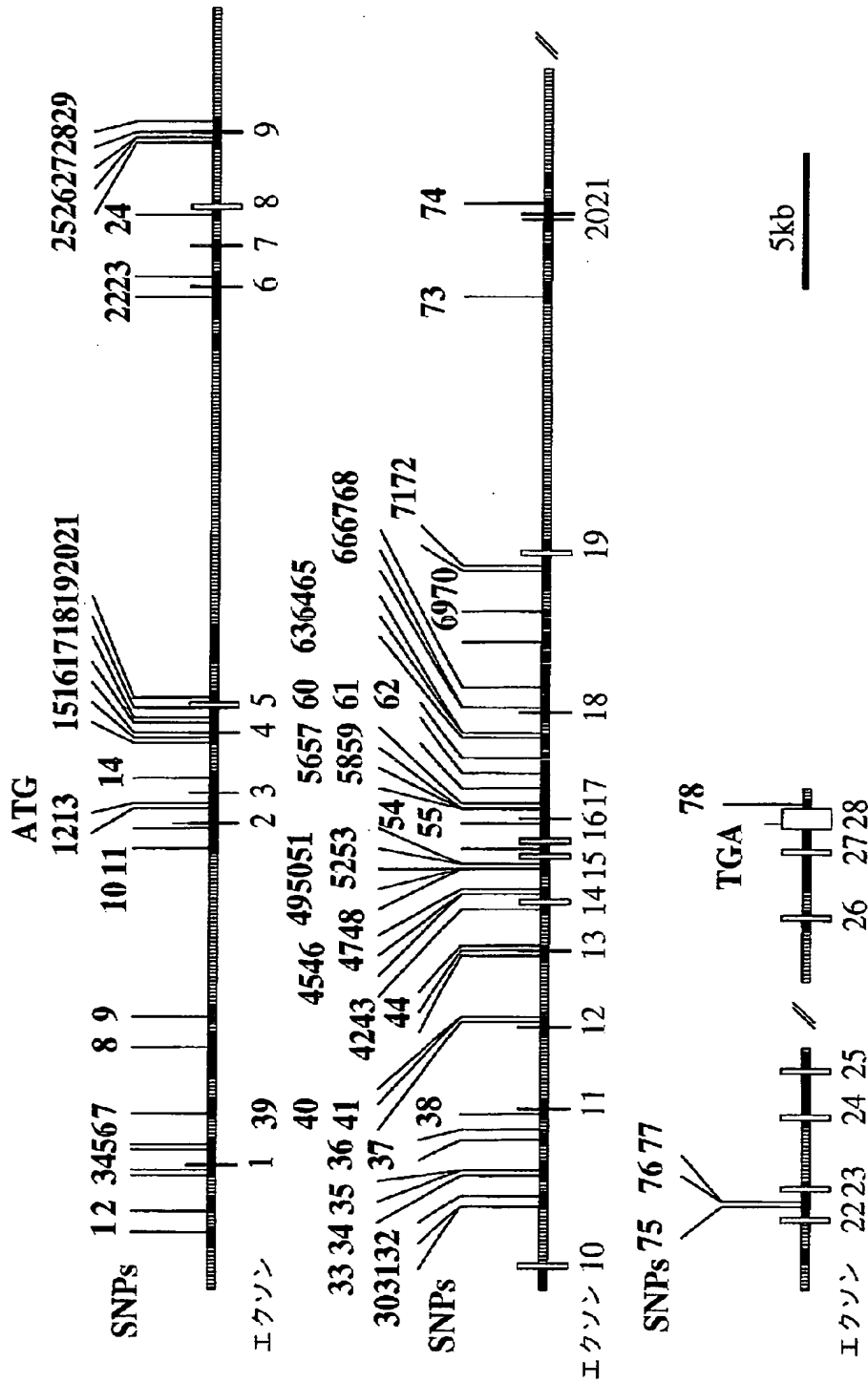
【図 17】



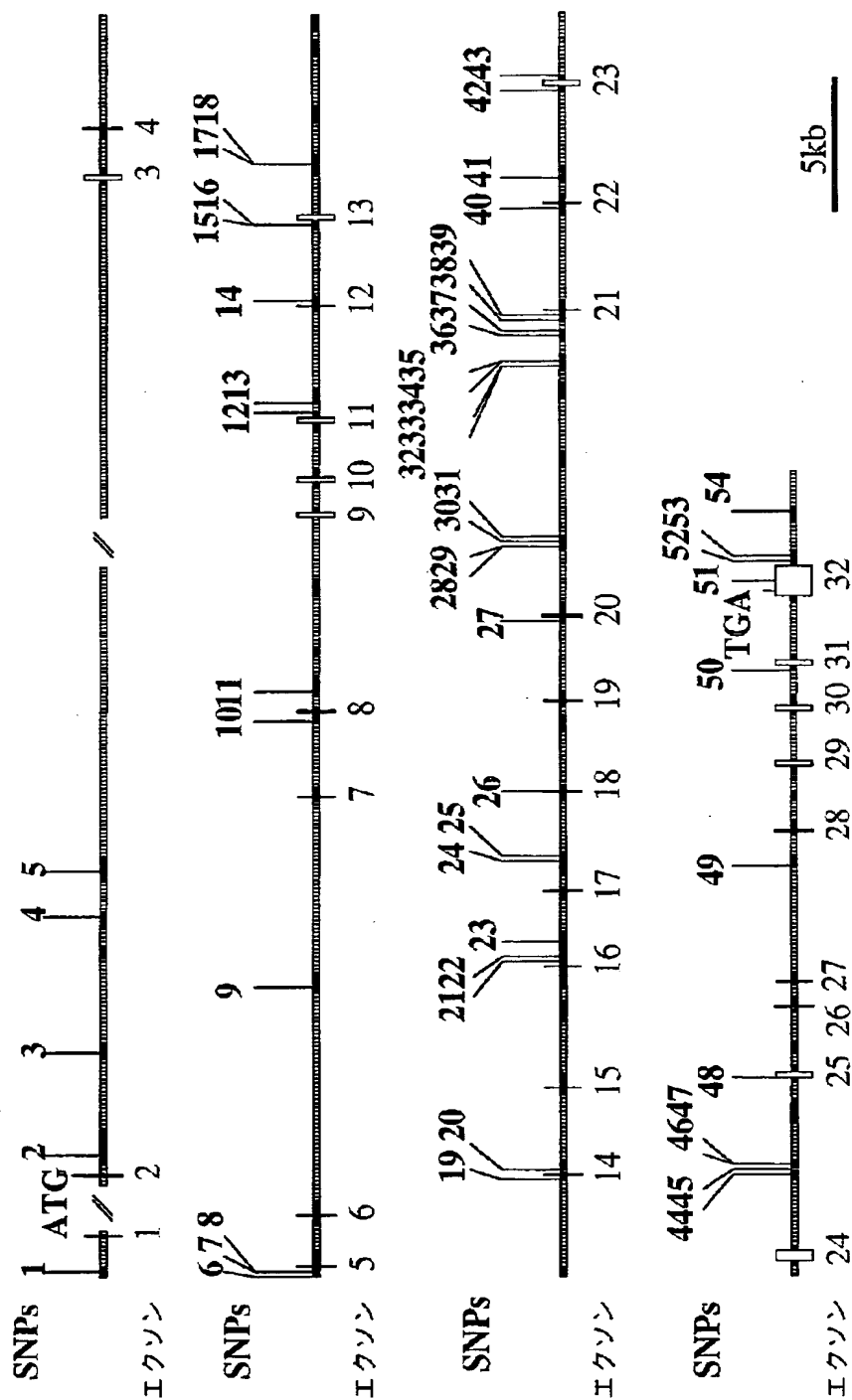
【図 18】



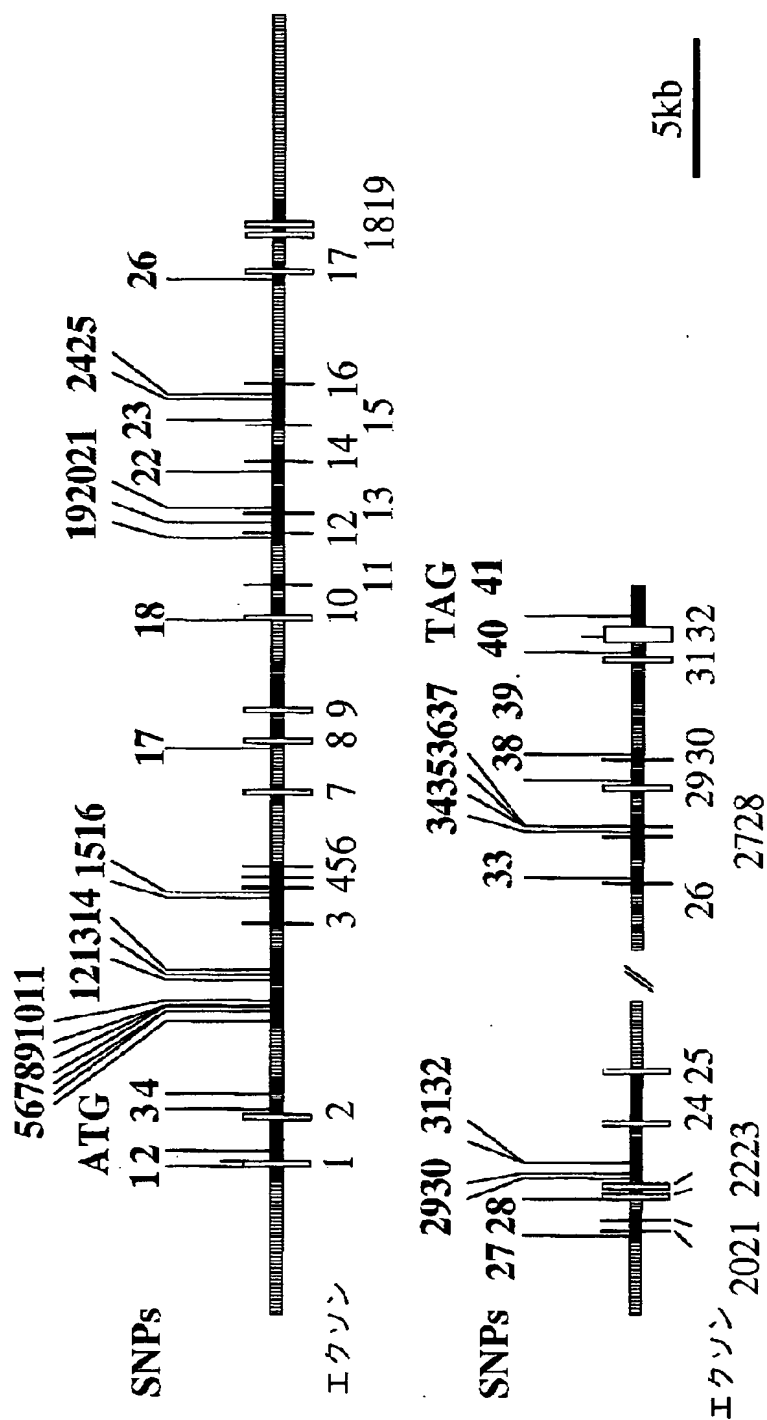
【図 19】



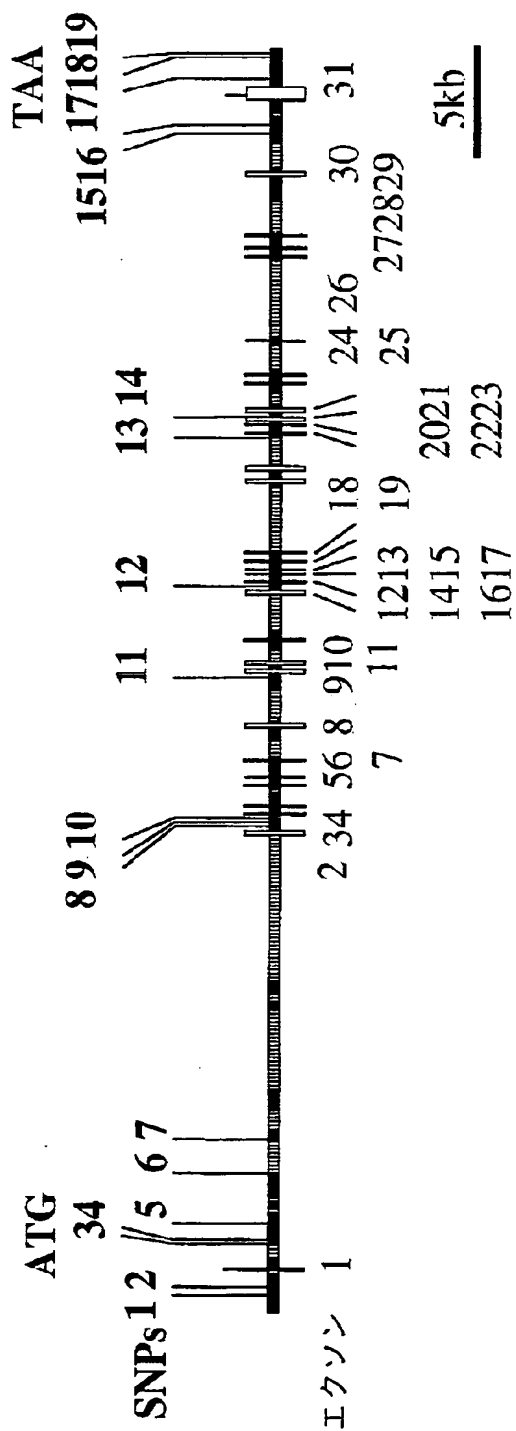
【図 20】



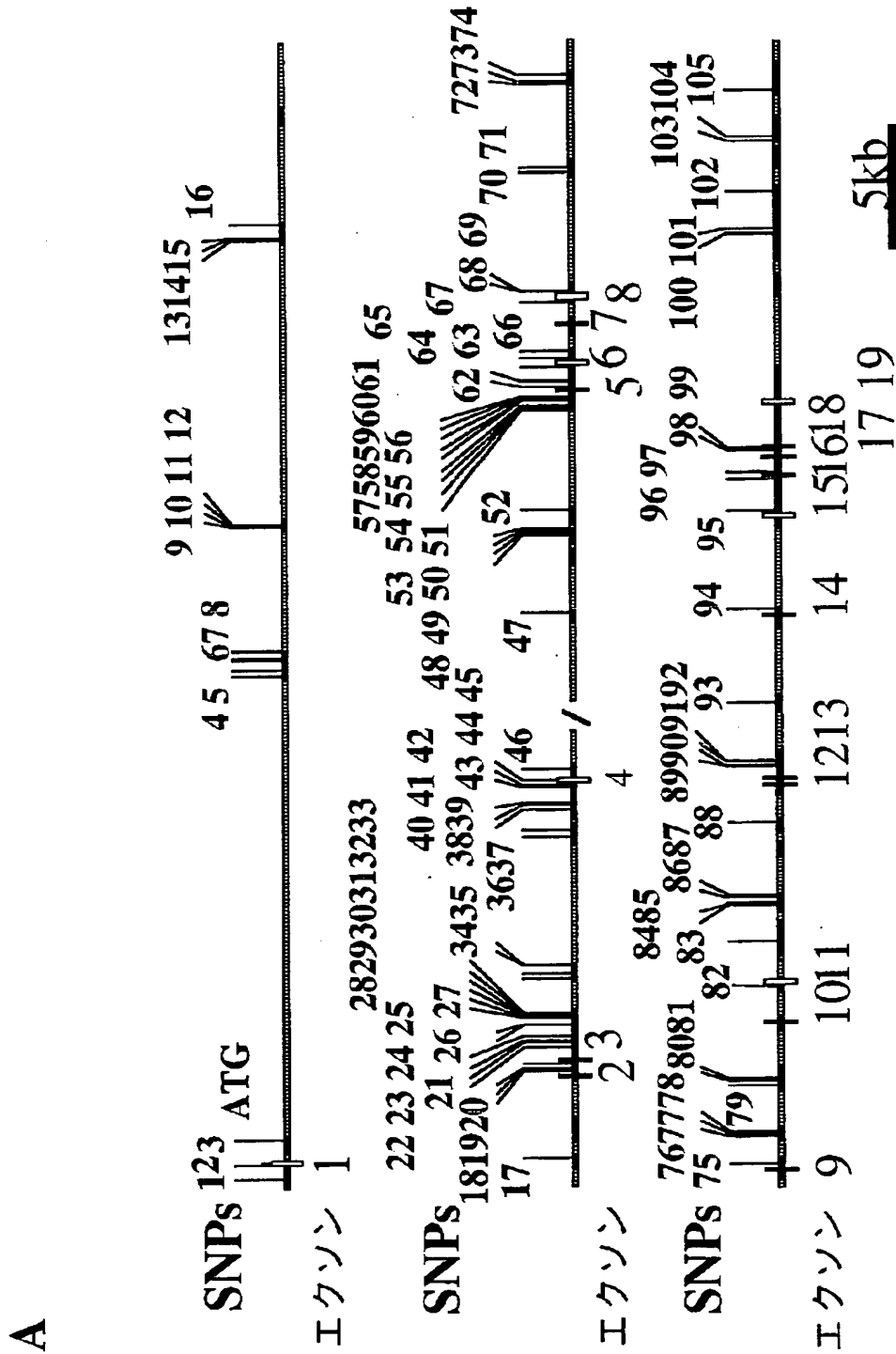
【図 21】



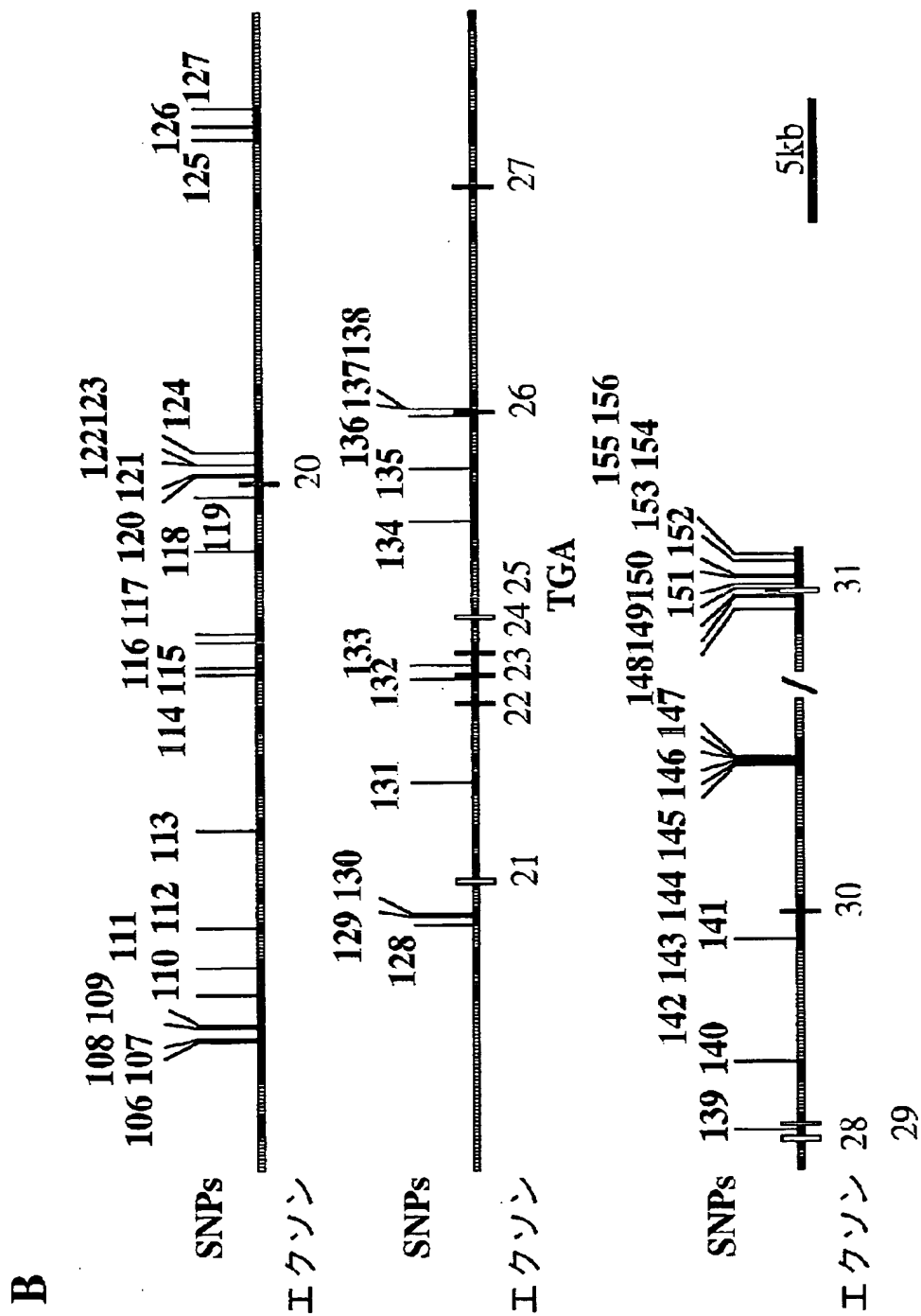
【図 22】



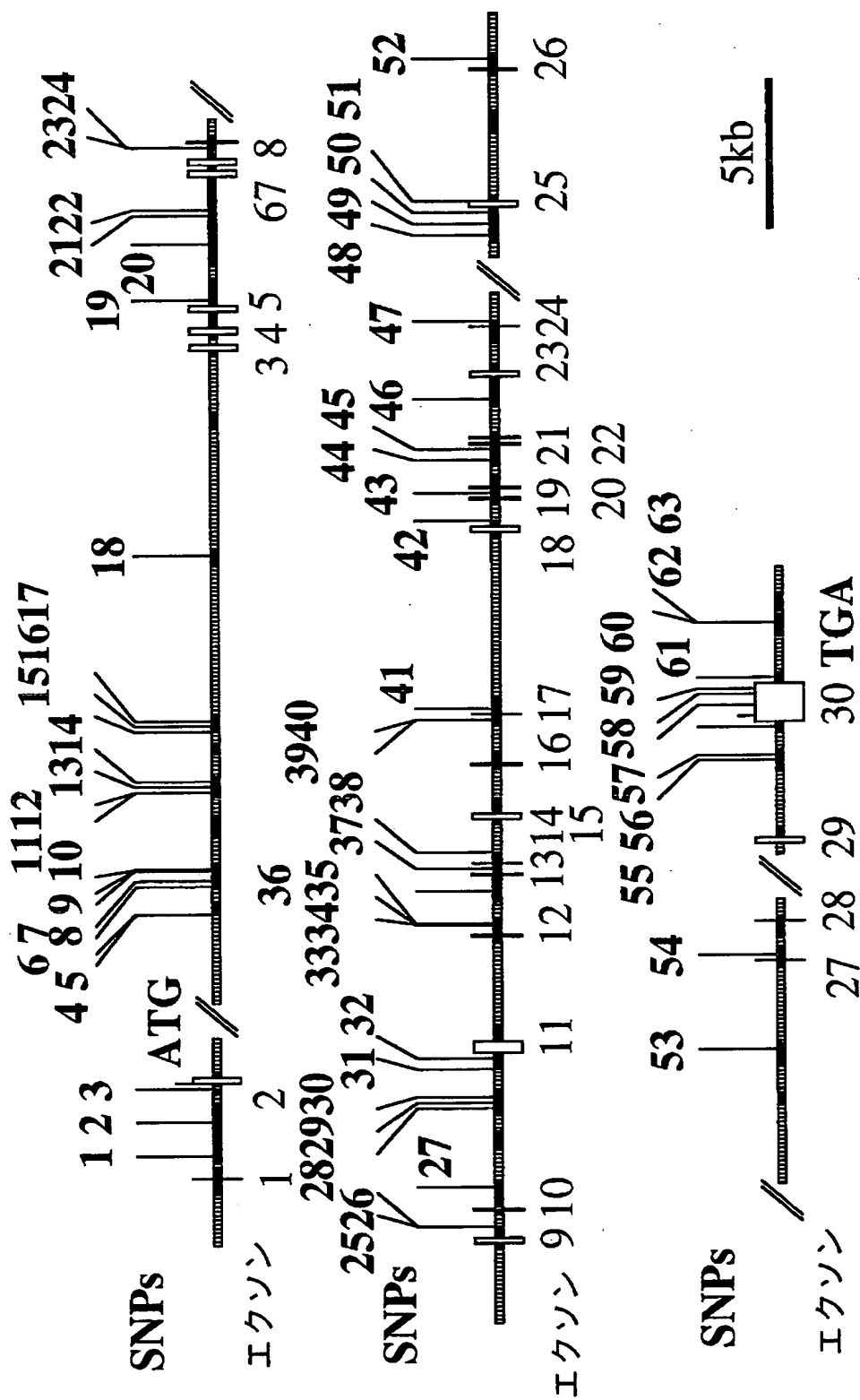
【図 23A】



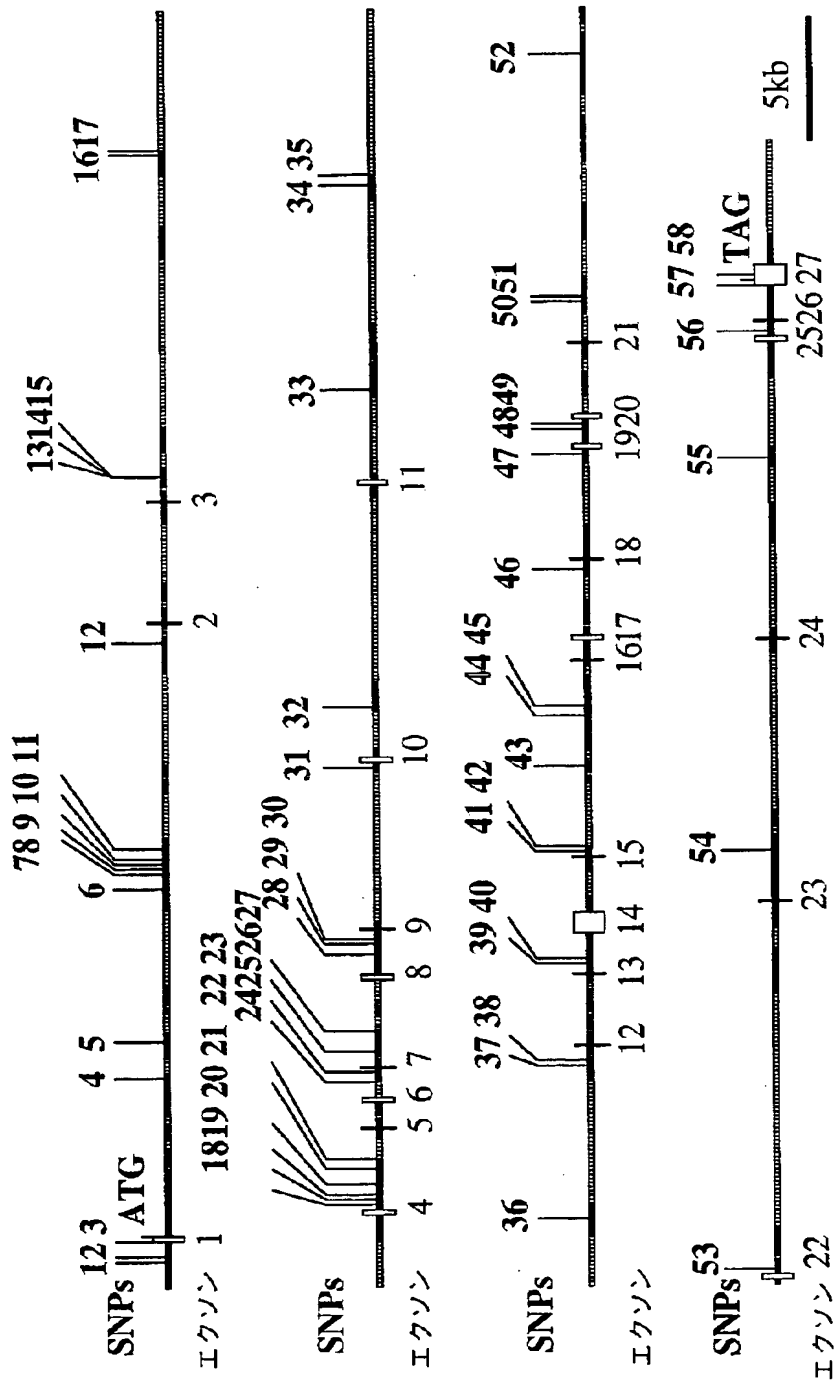
【図 23 B】



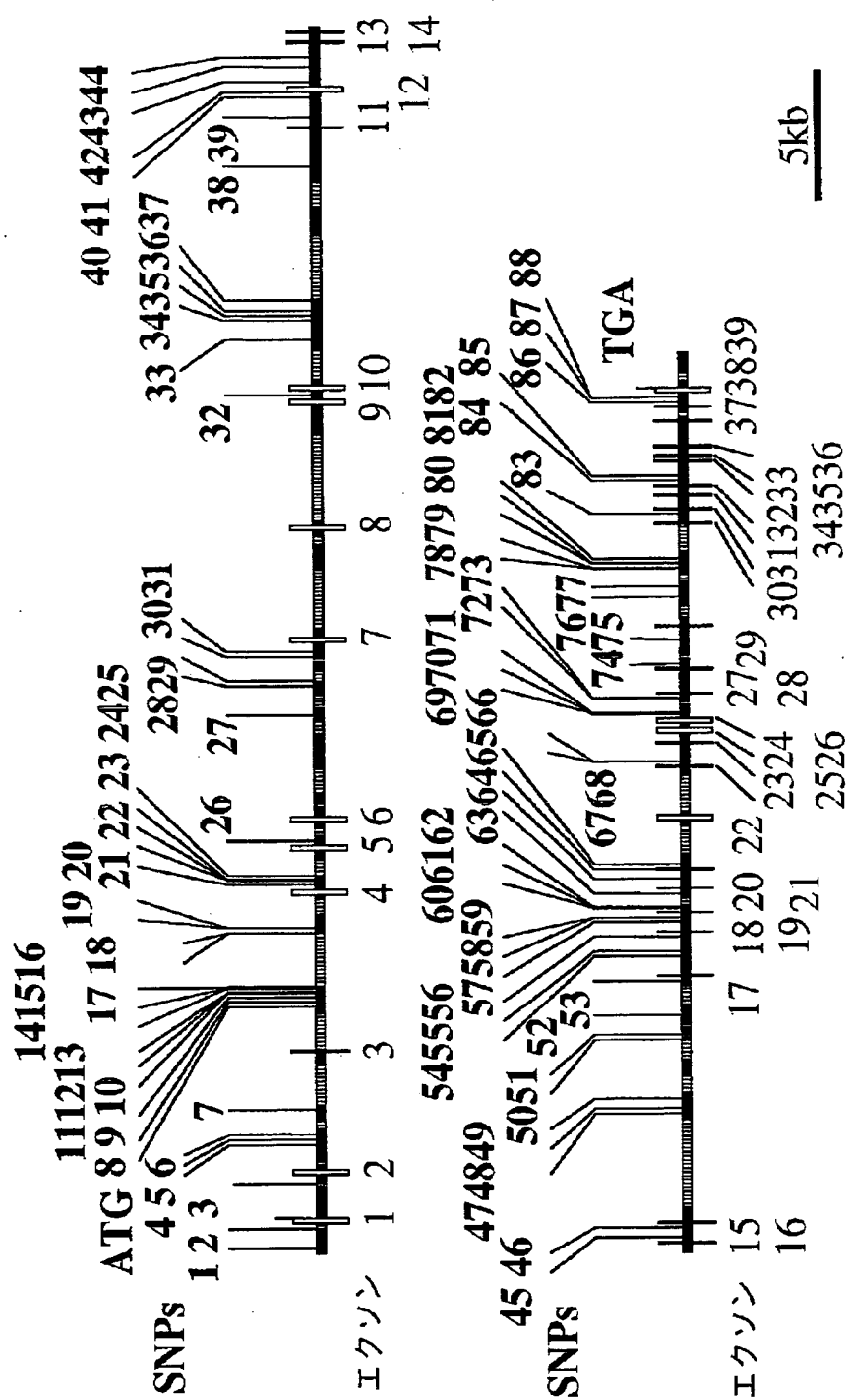
【図 24】



【図 25】

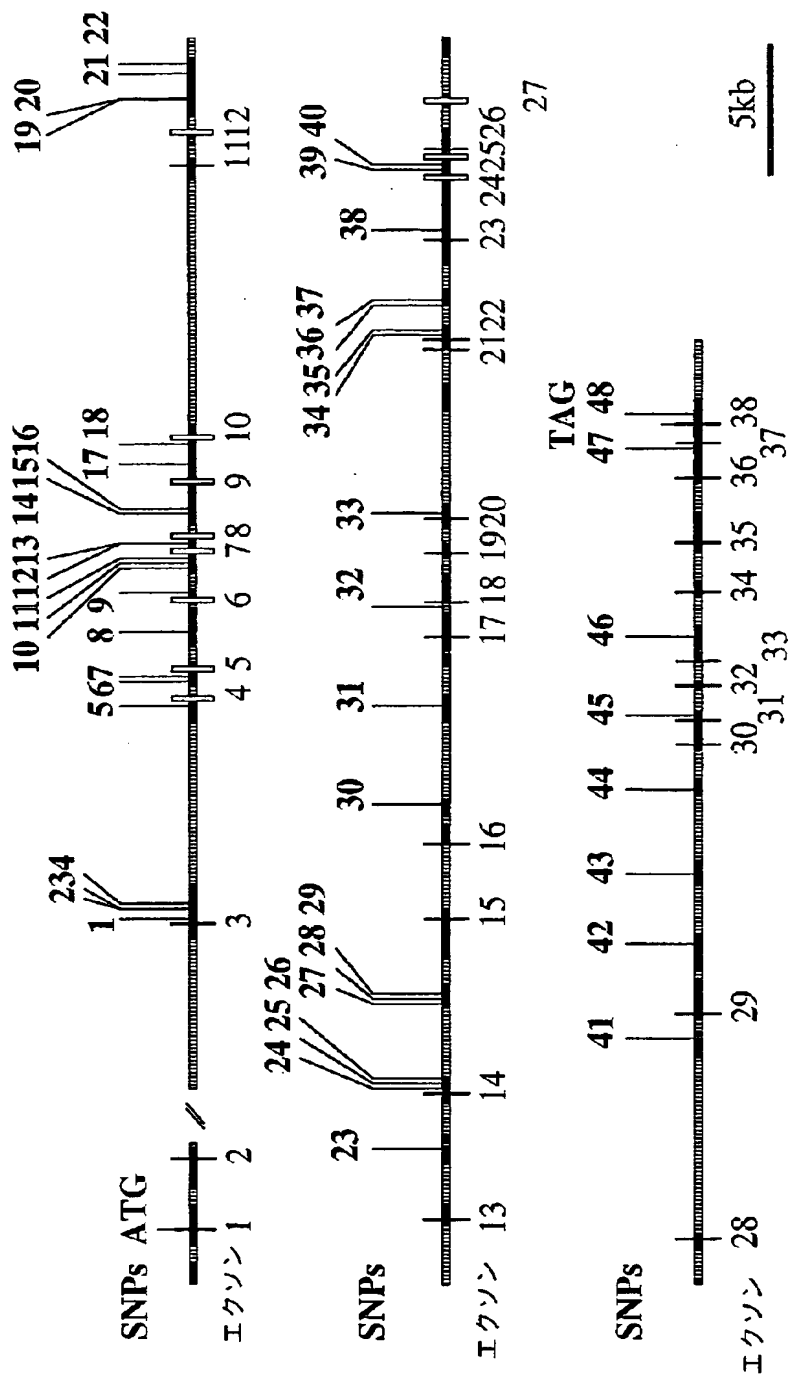


【図 26】

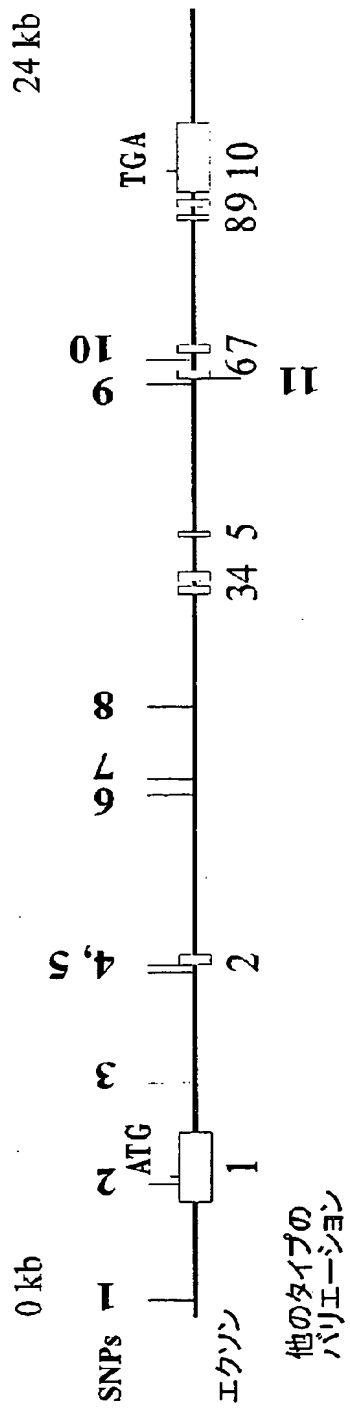


5kb

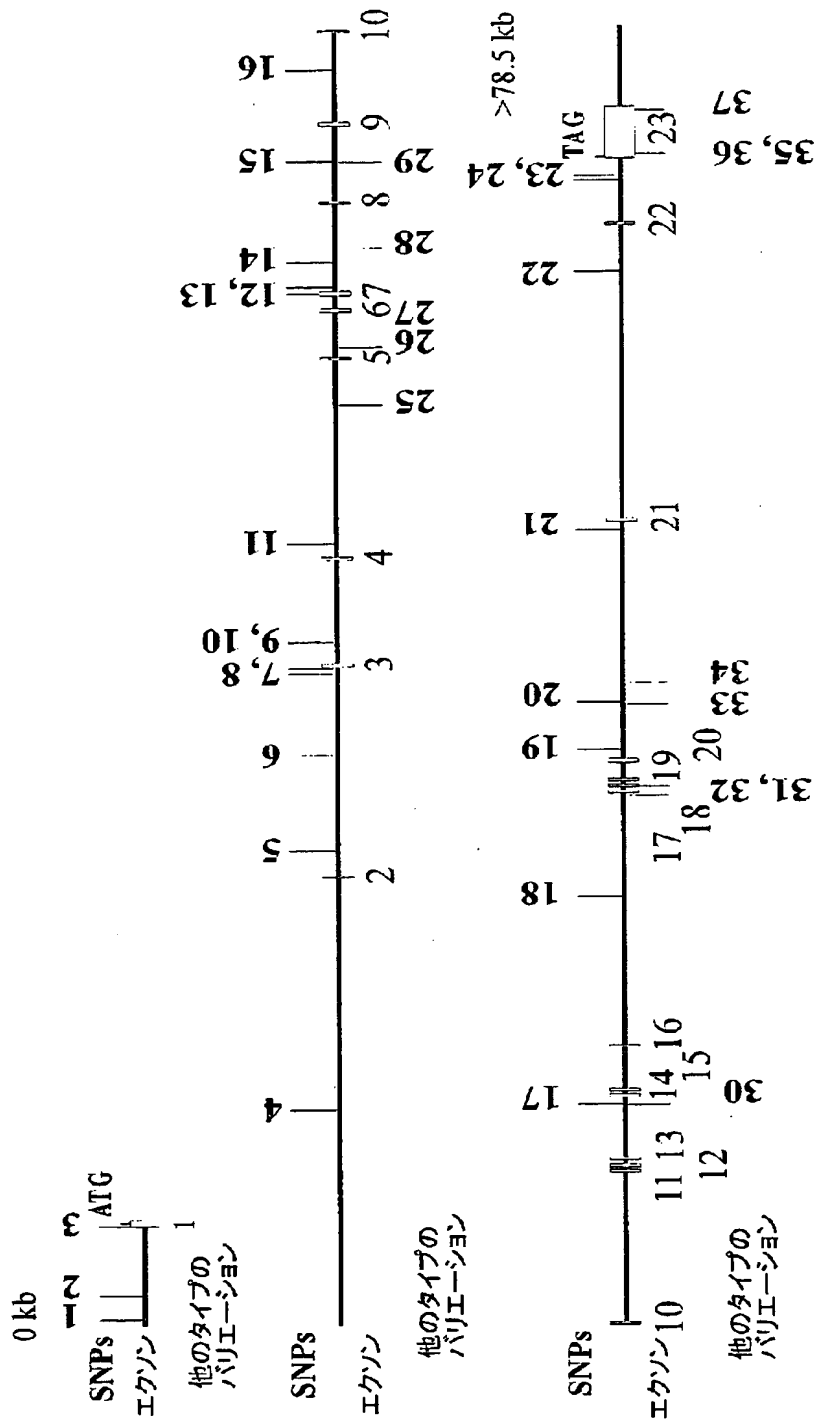
【図 27】



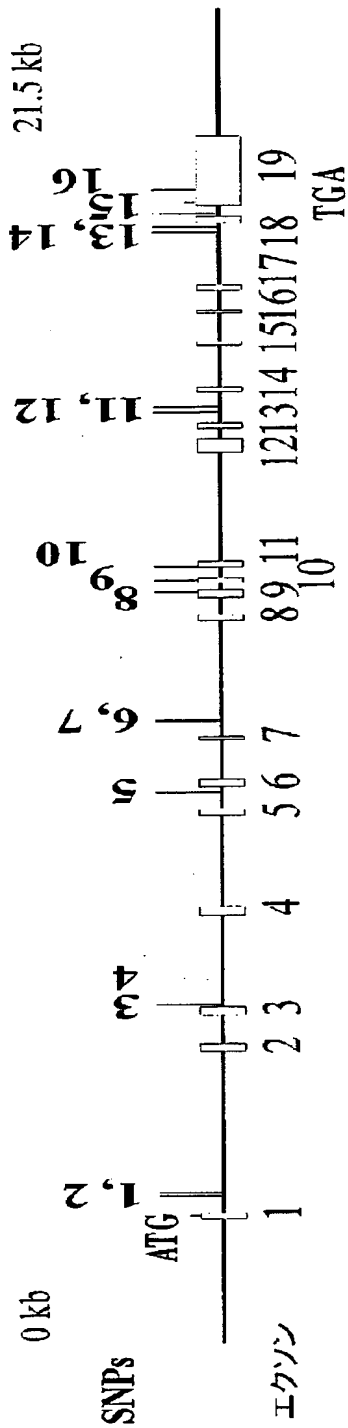
【図 28】



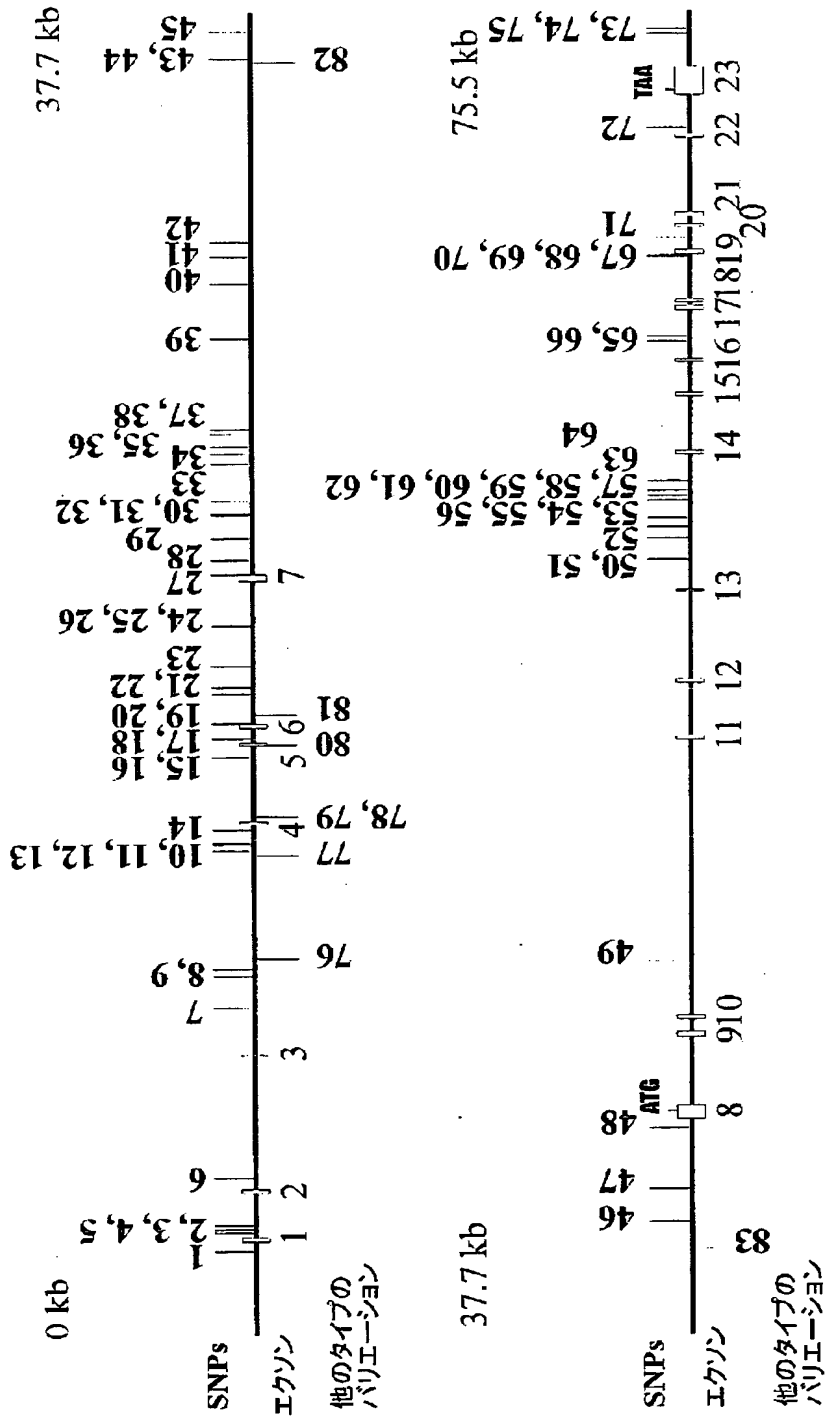
【図 29】



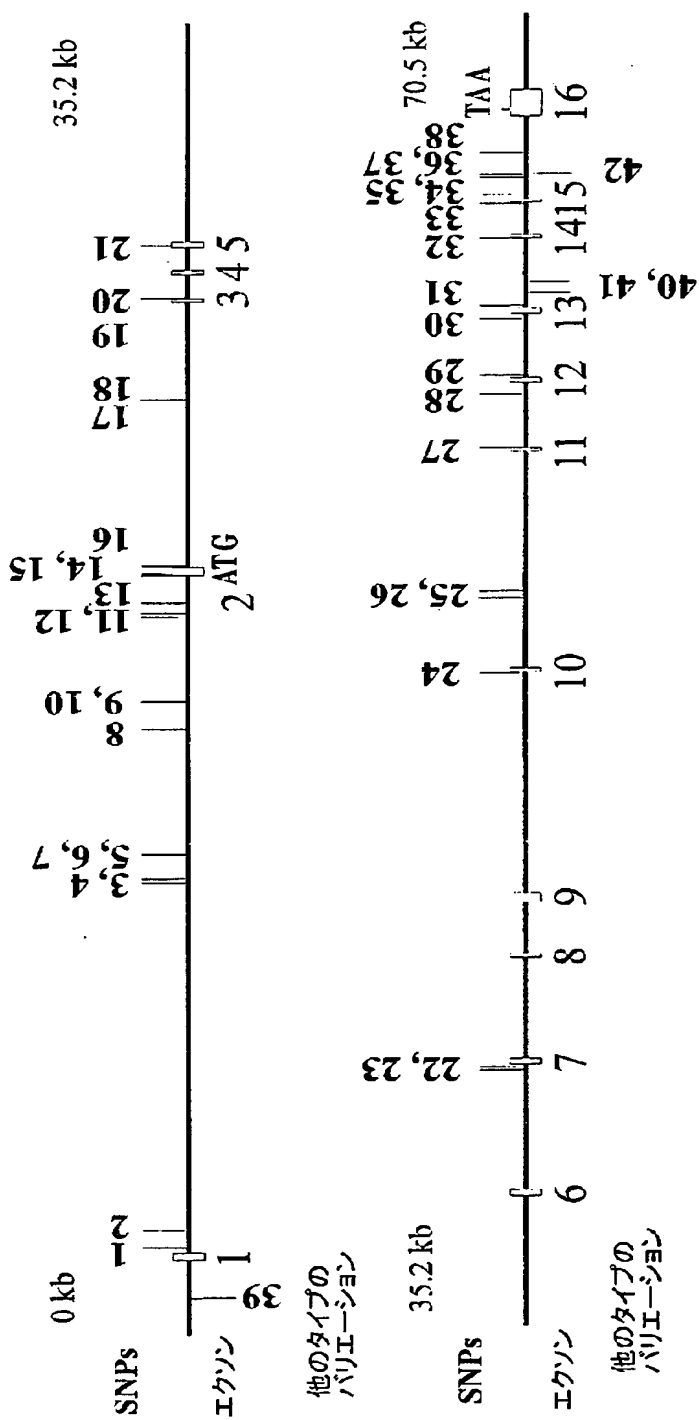
【図 30】



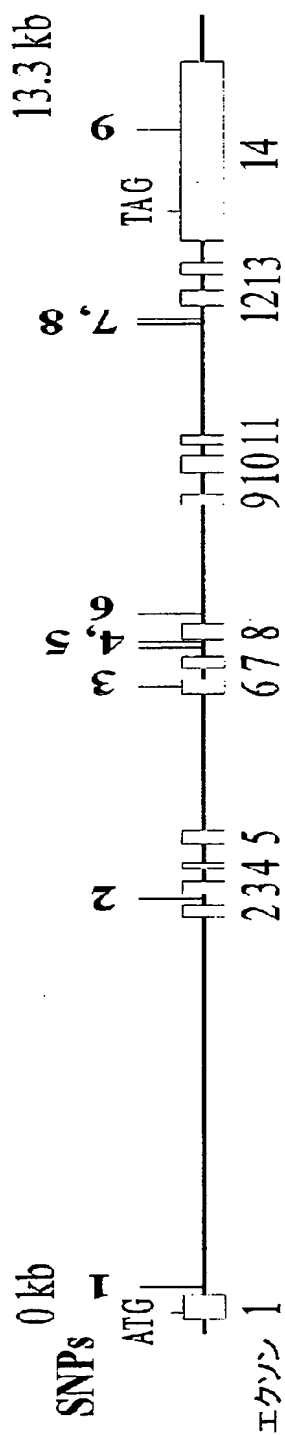
【図 31】



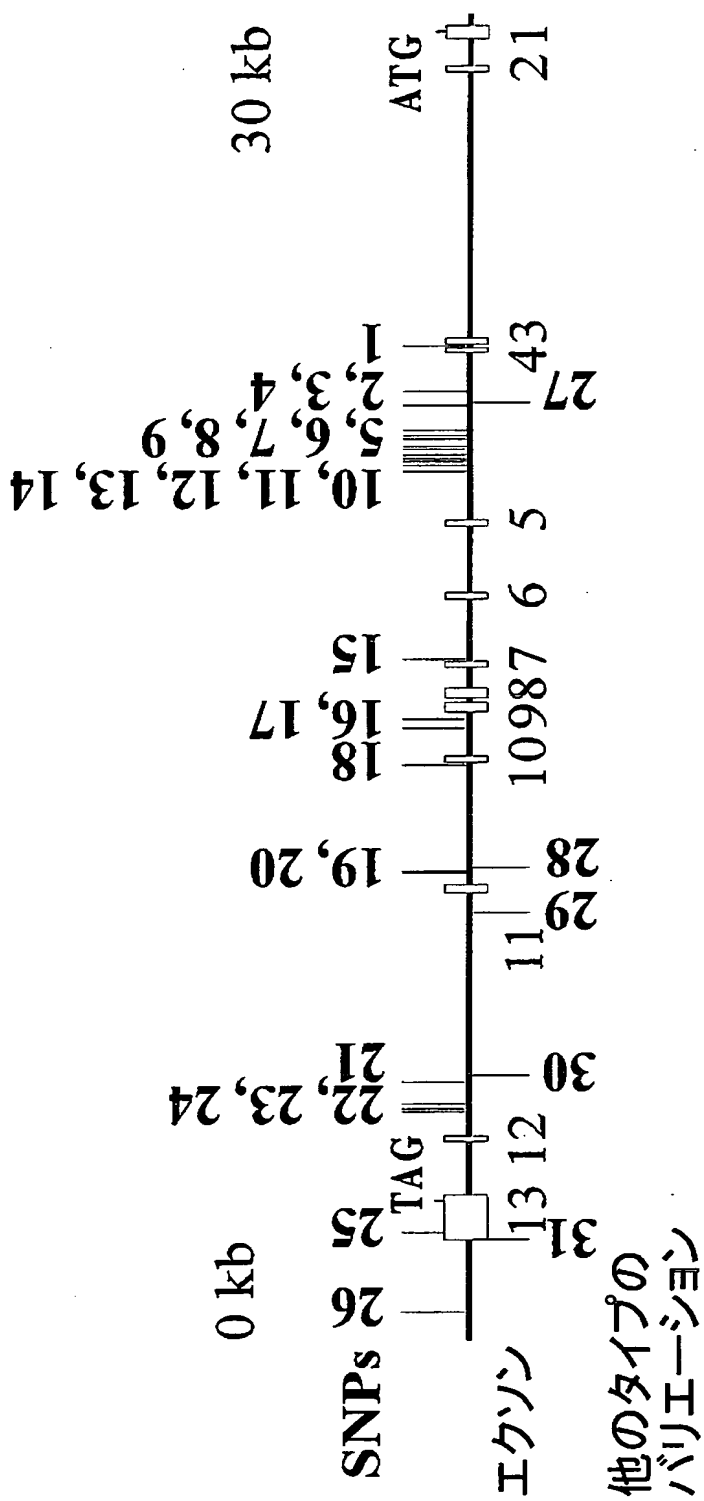
【図 3 2】



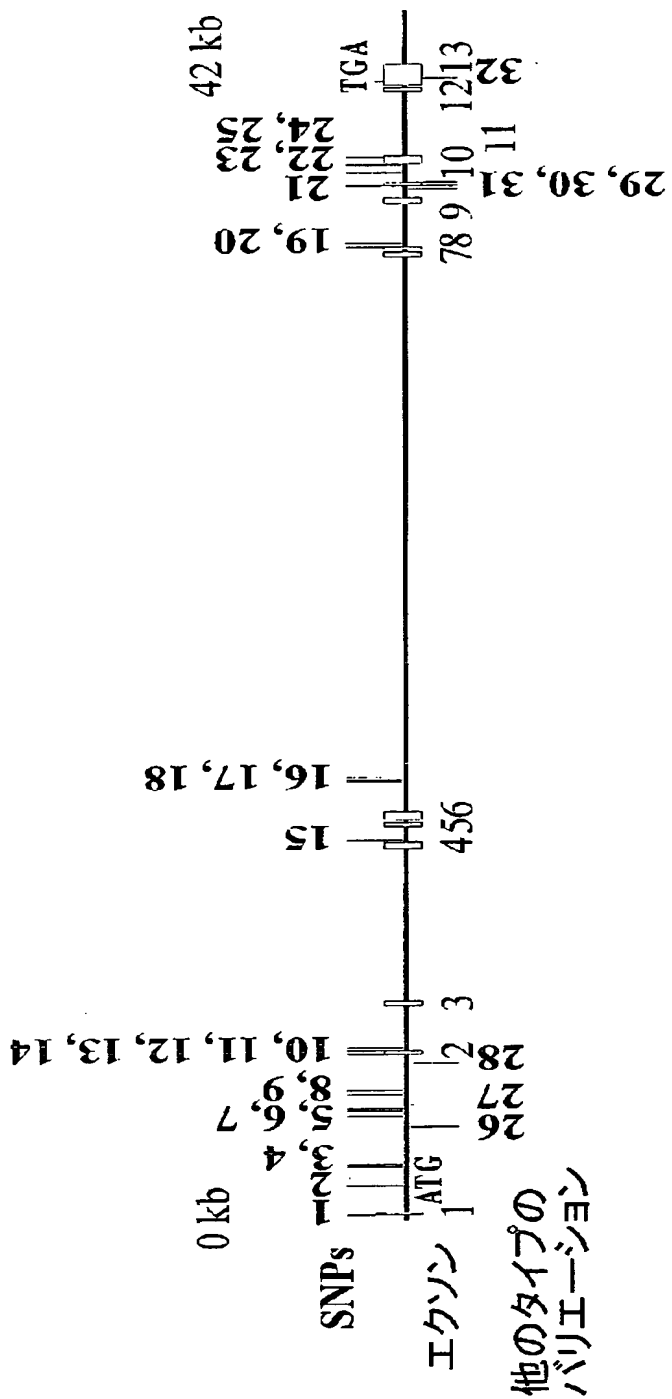
【図 33】



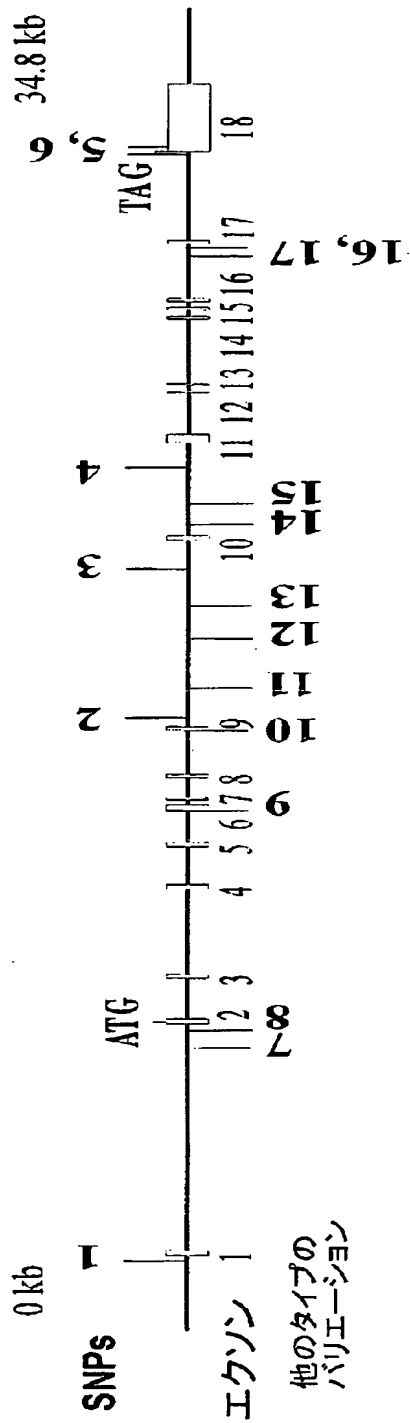
【図 3 4】



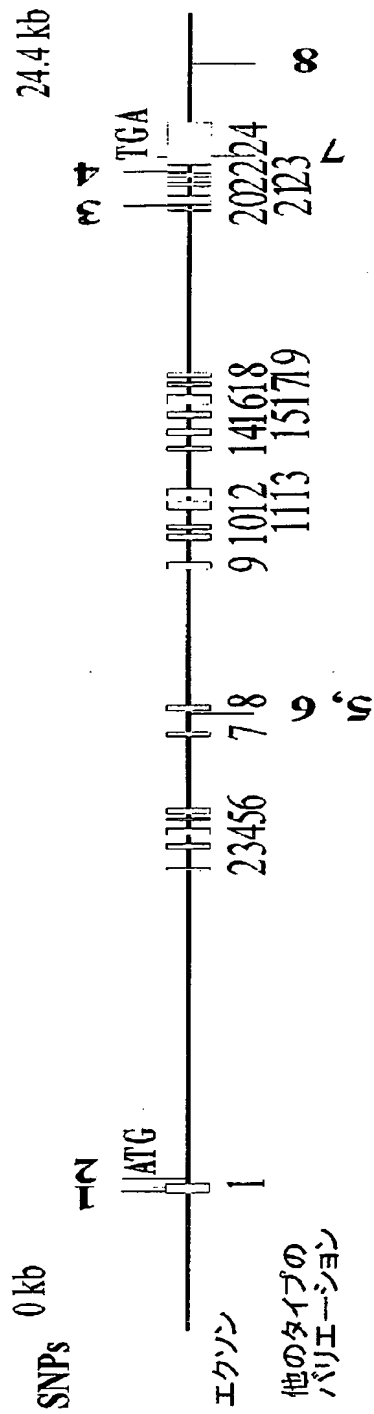
【図 35】



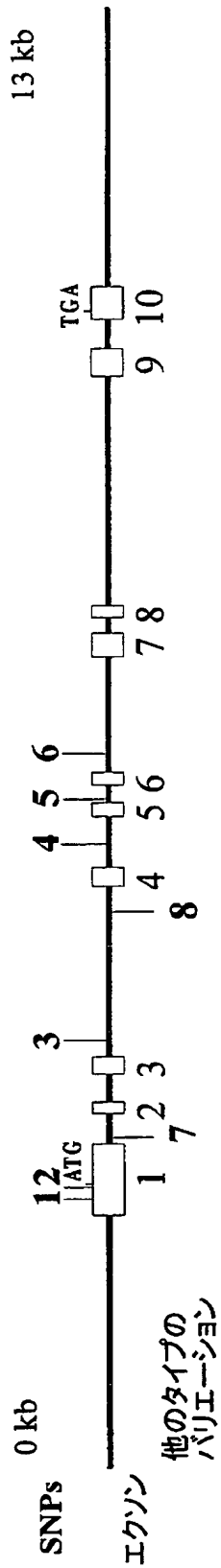
【図 36】



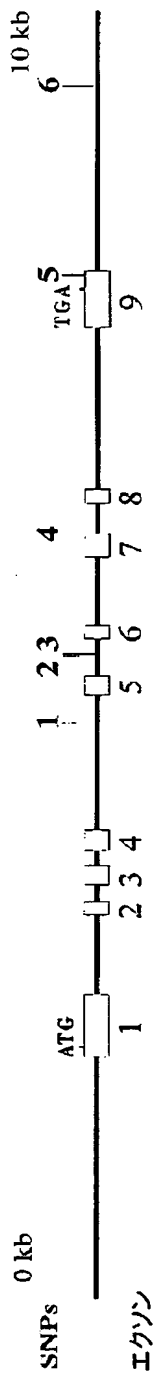
【図 37】



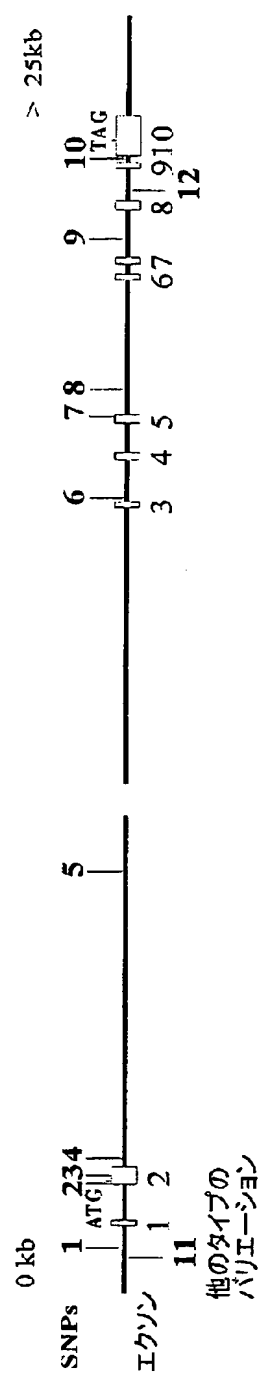
【図 3 8】



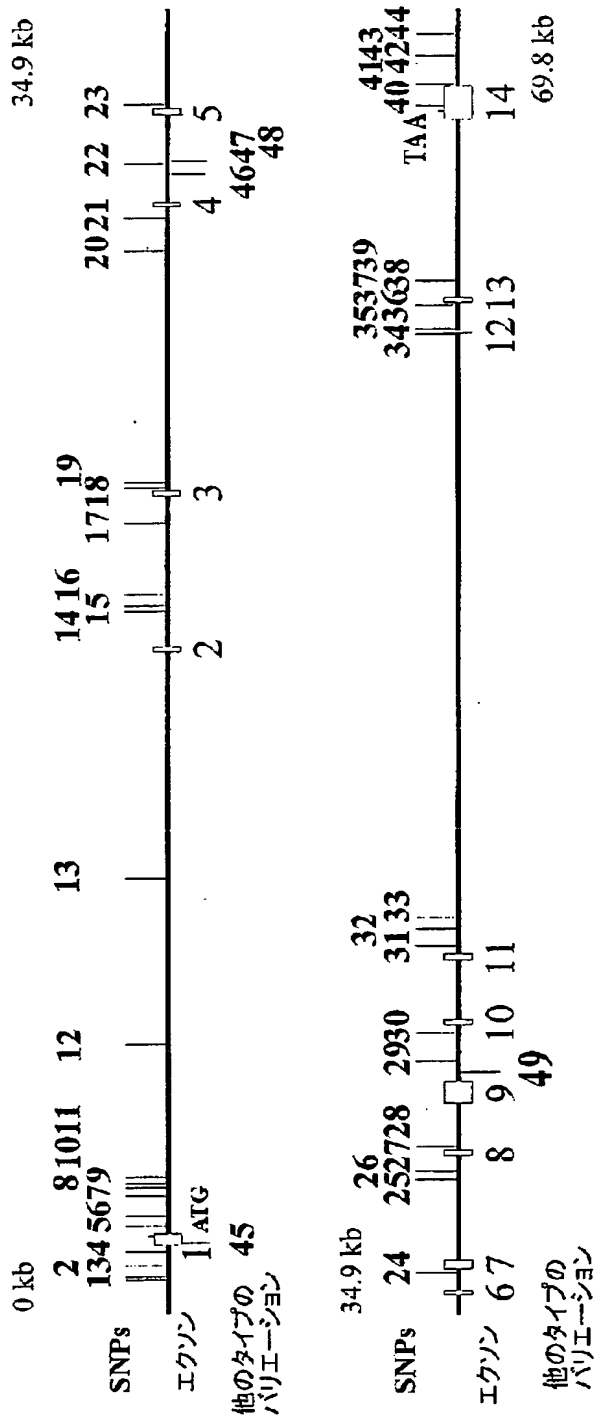
【図 39】



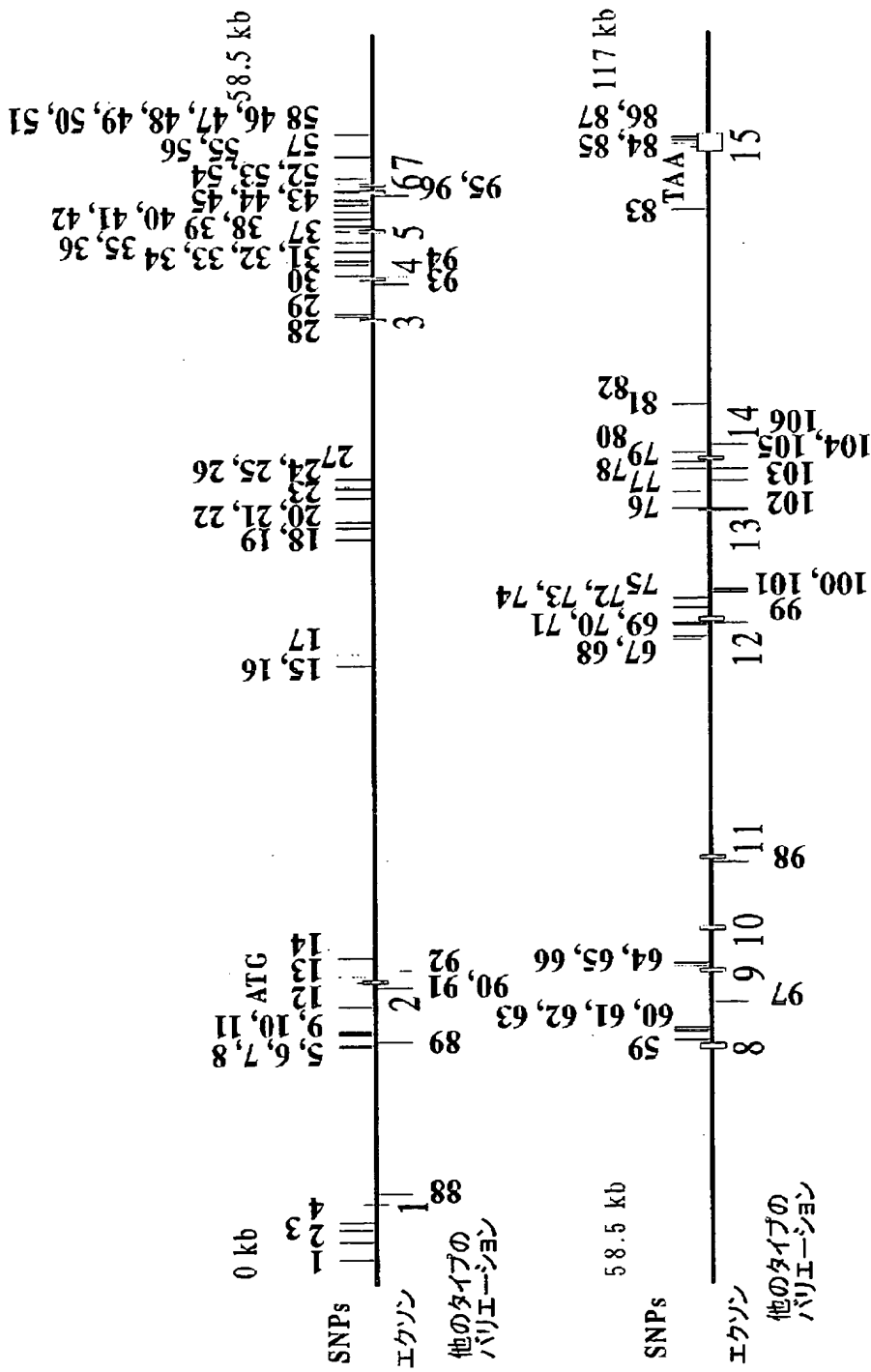
【図 40】



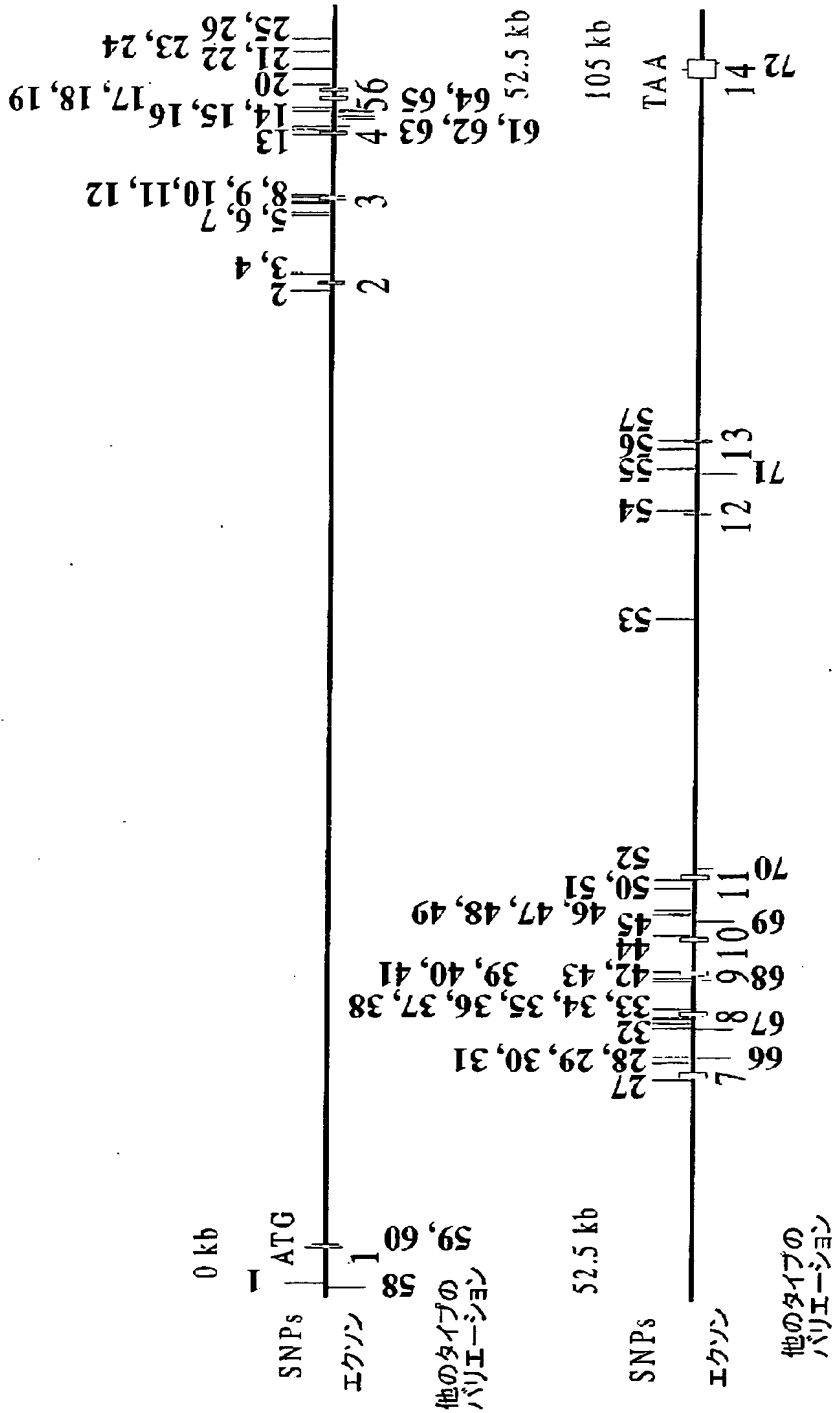
【図 4 1】



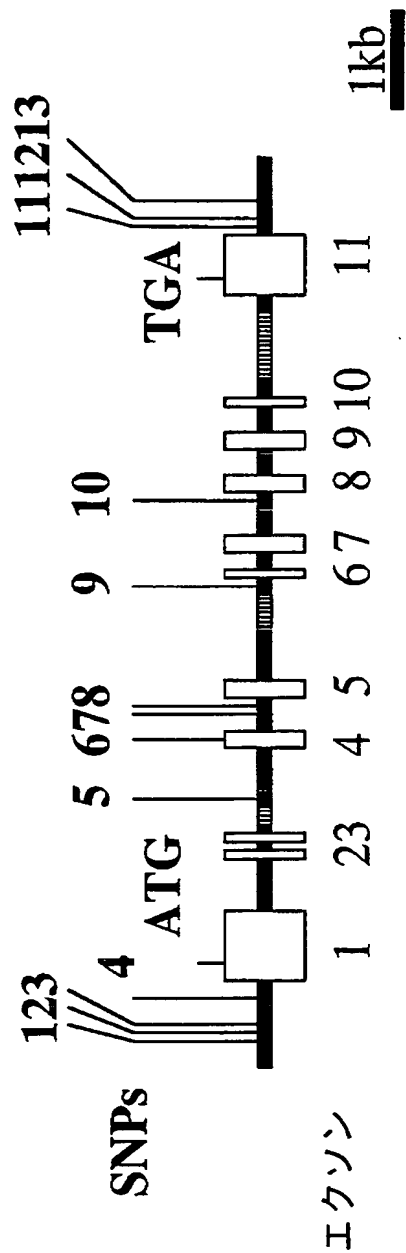
【図 42】



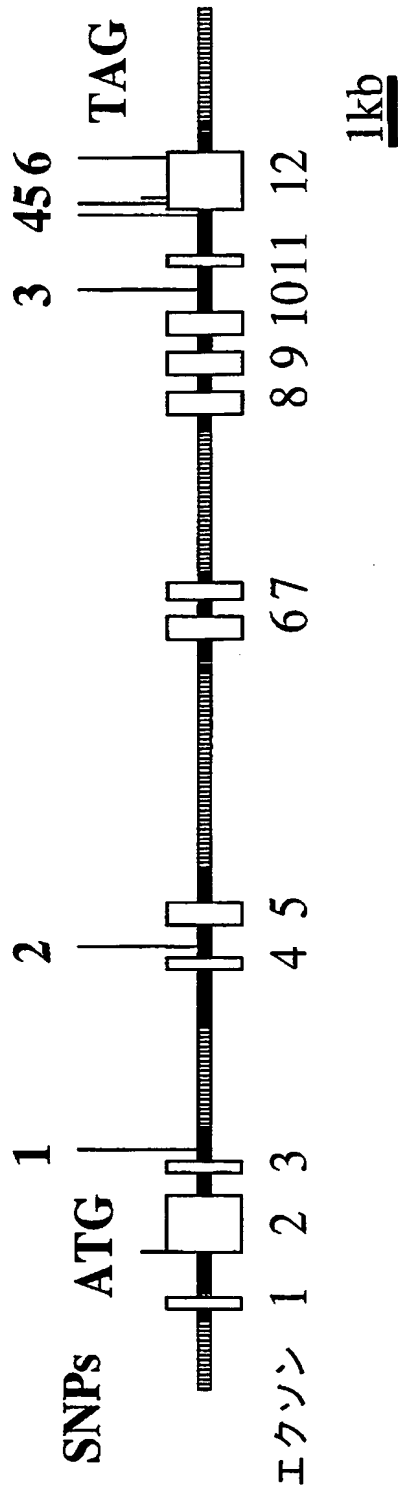
【図 43】



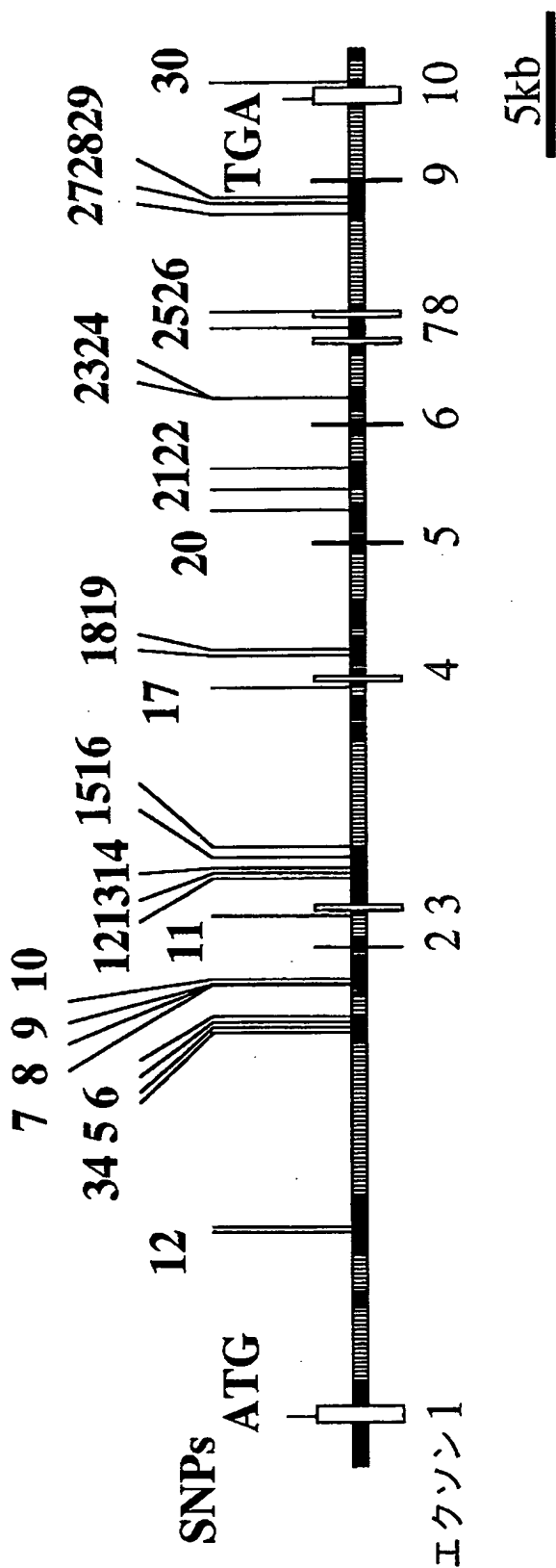
【図 4 4】



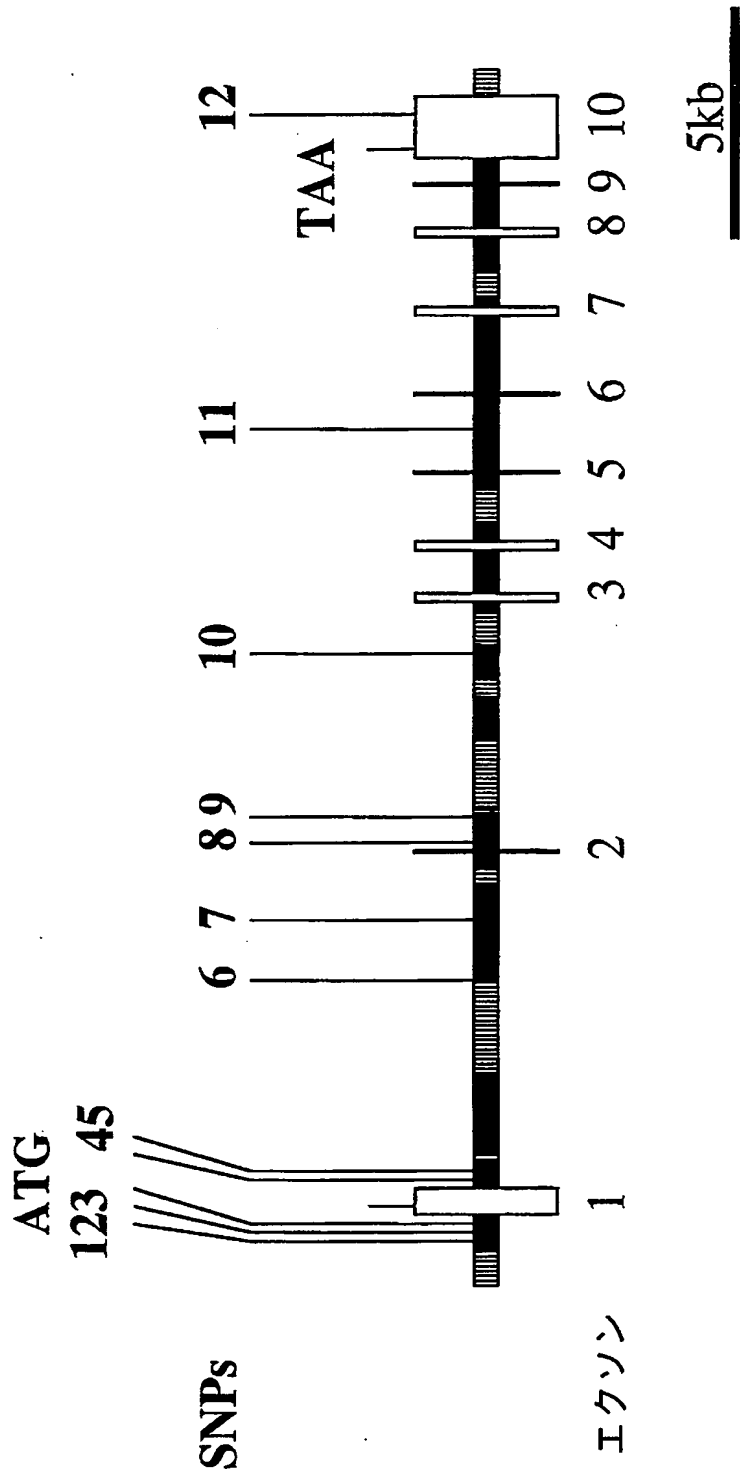
【図 45】



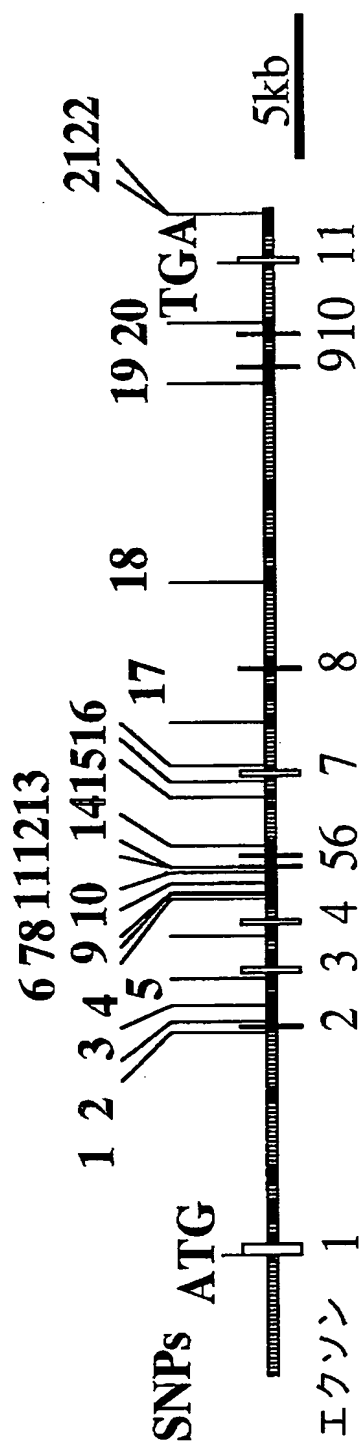
【図 46】



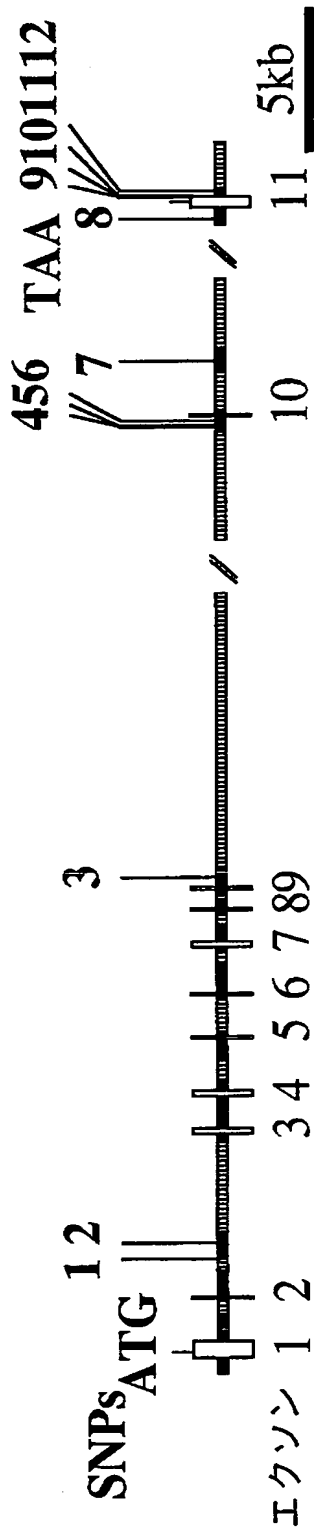
【図 47】



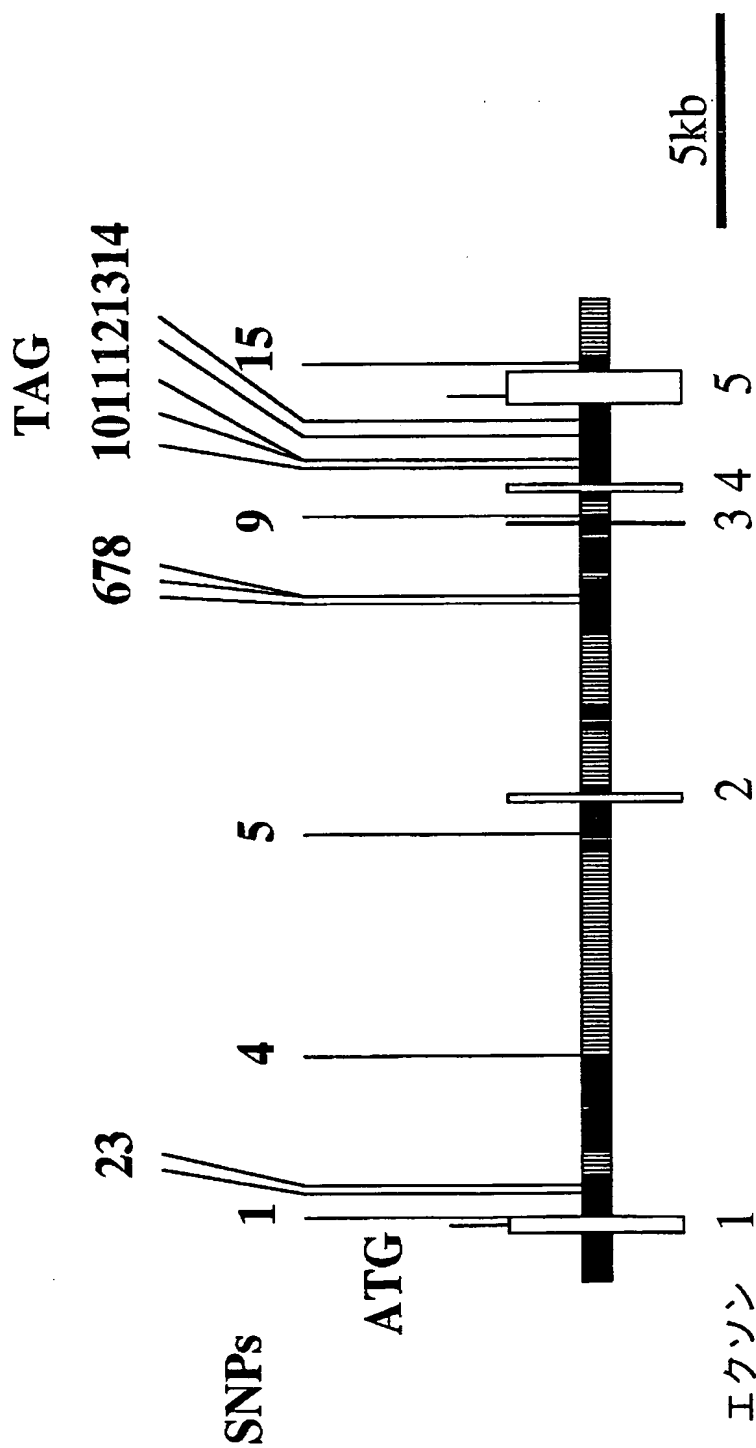
【図 48】



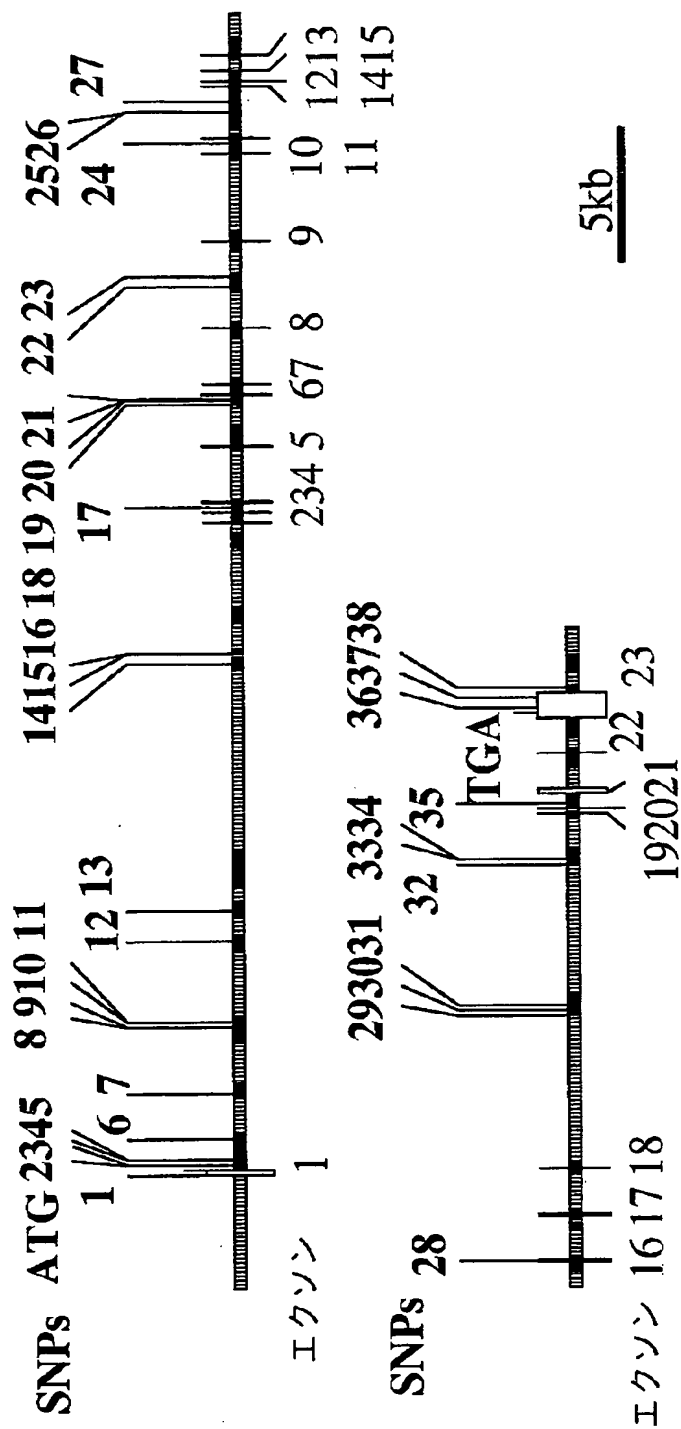
【図 49】



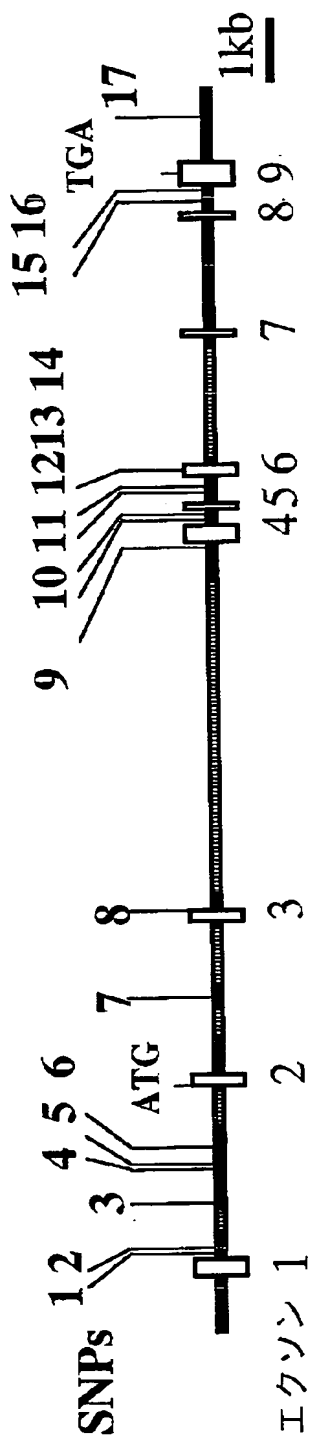
【図 50】



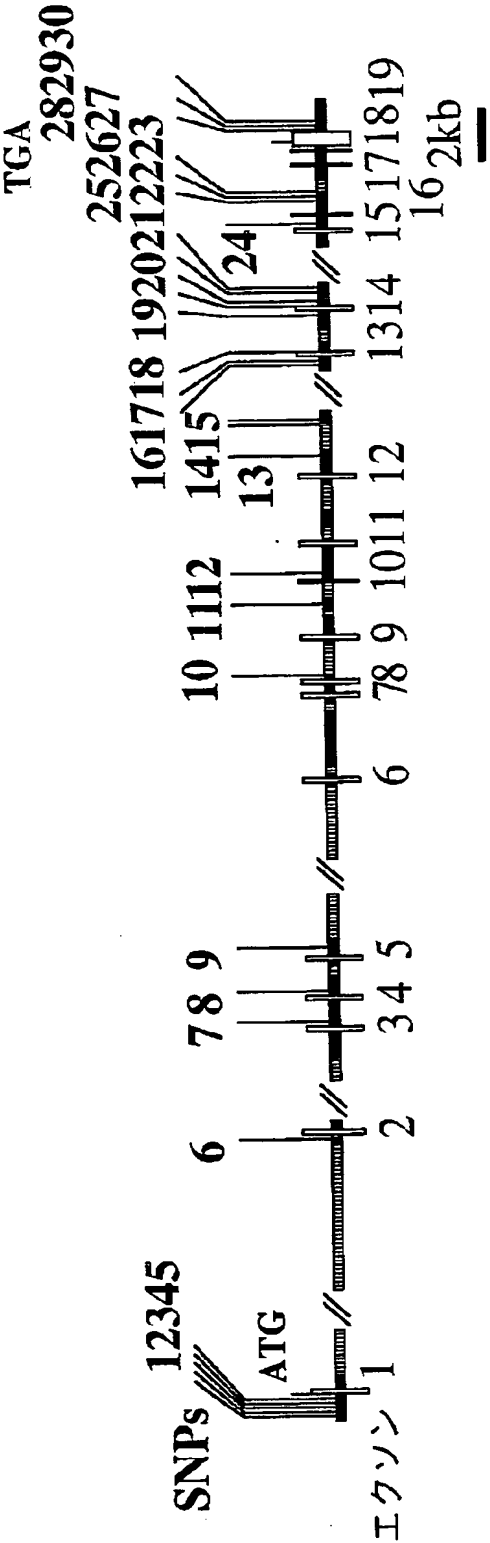
【図 5 1】



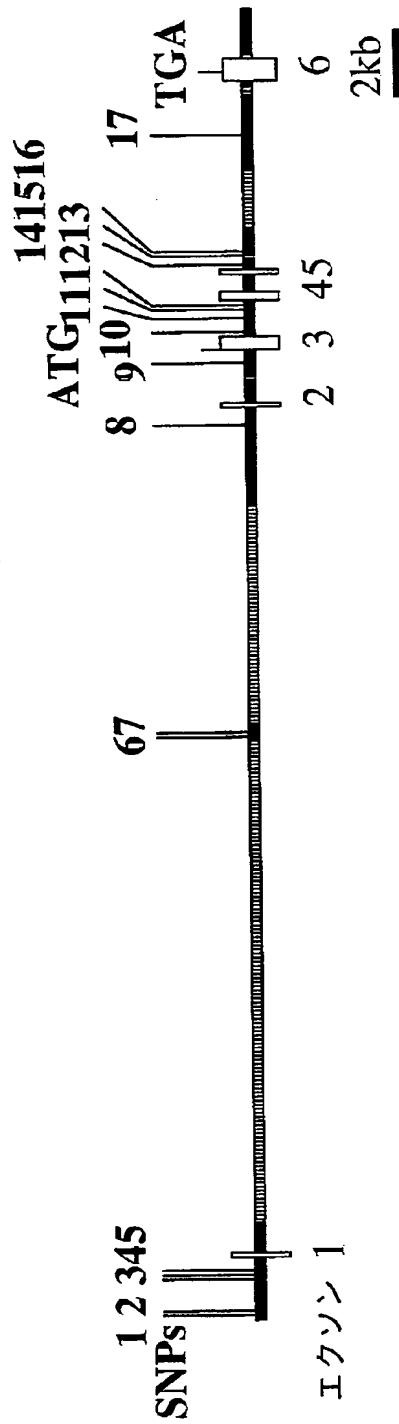
【図 52】



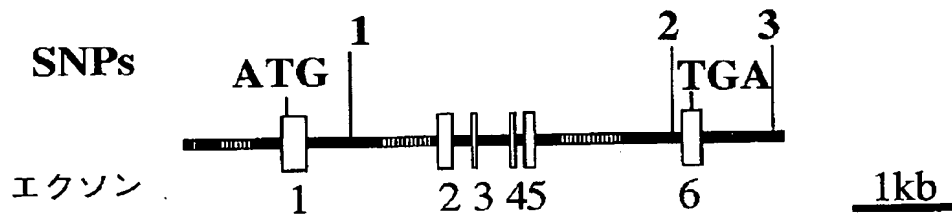
【図 53】



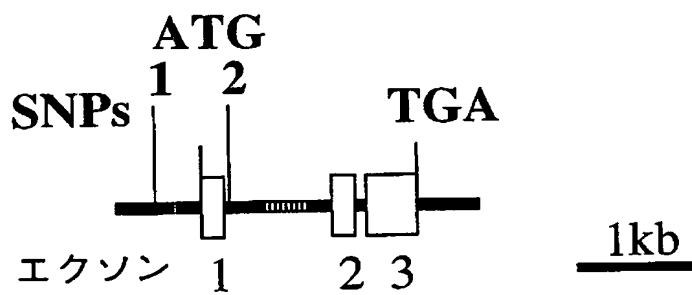
【図 54】



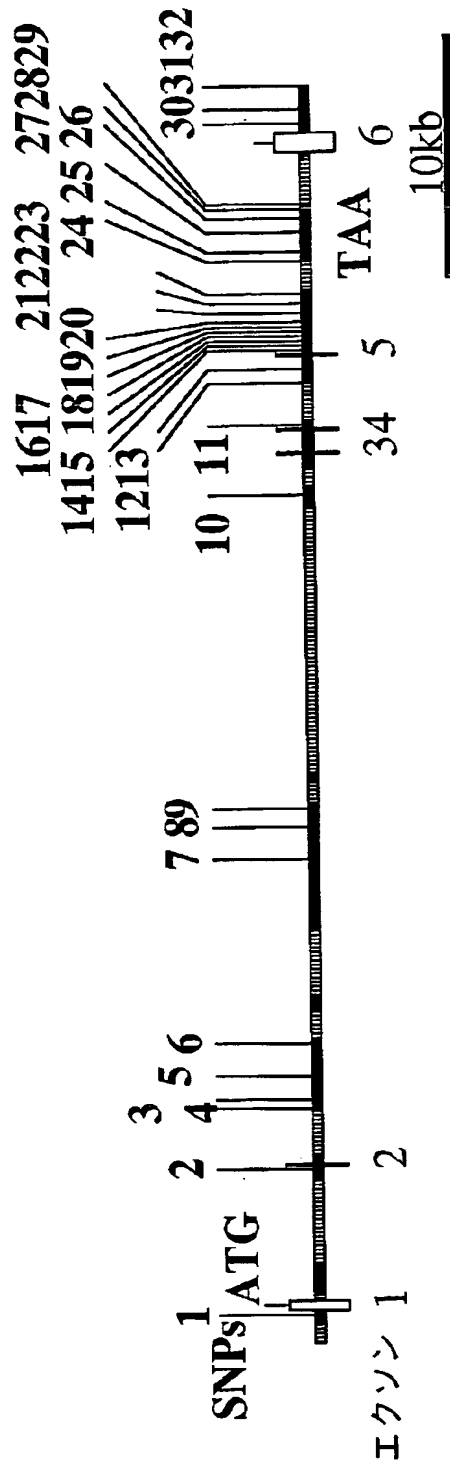
【図 5 5】



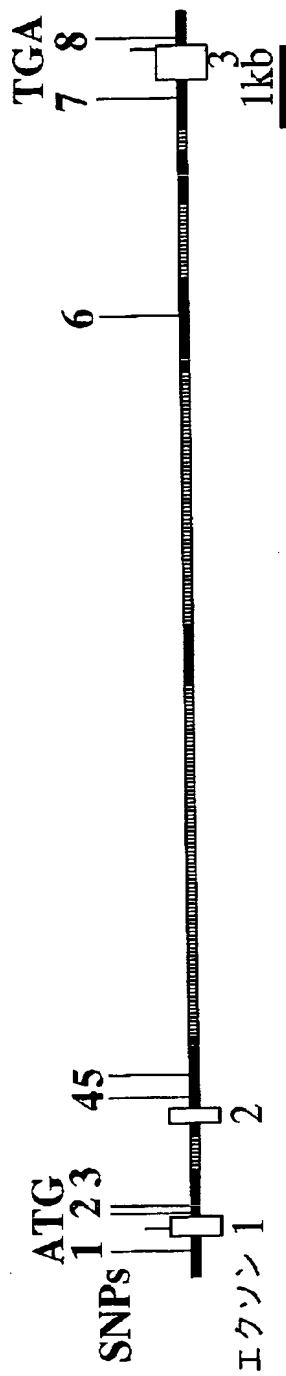
【図 5 6】



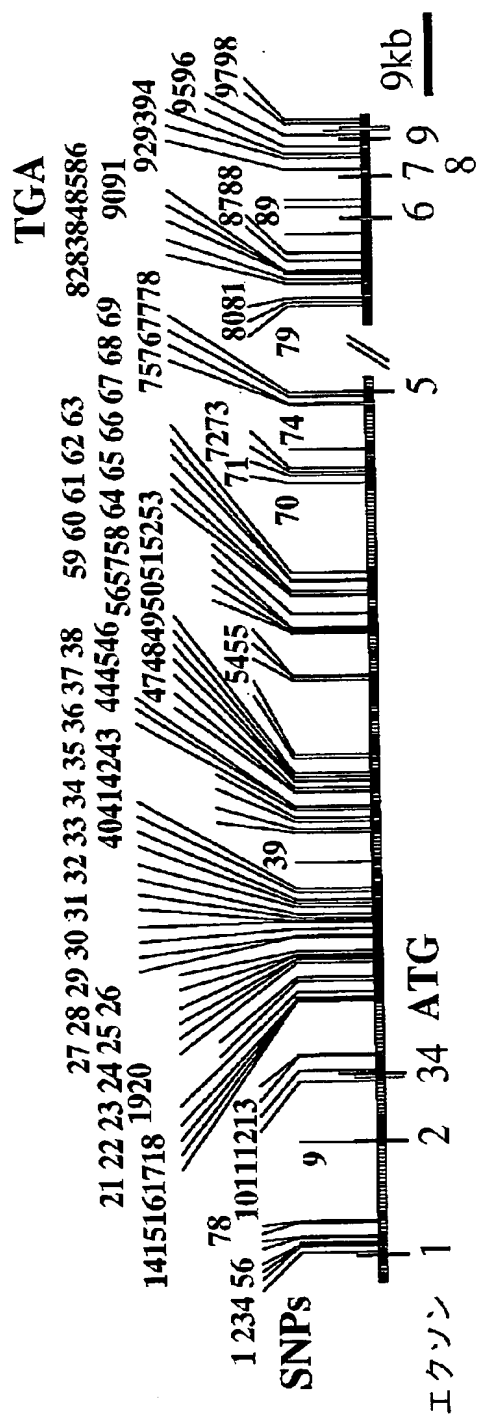
【図 57】



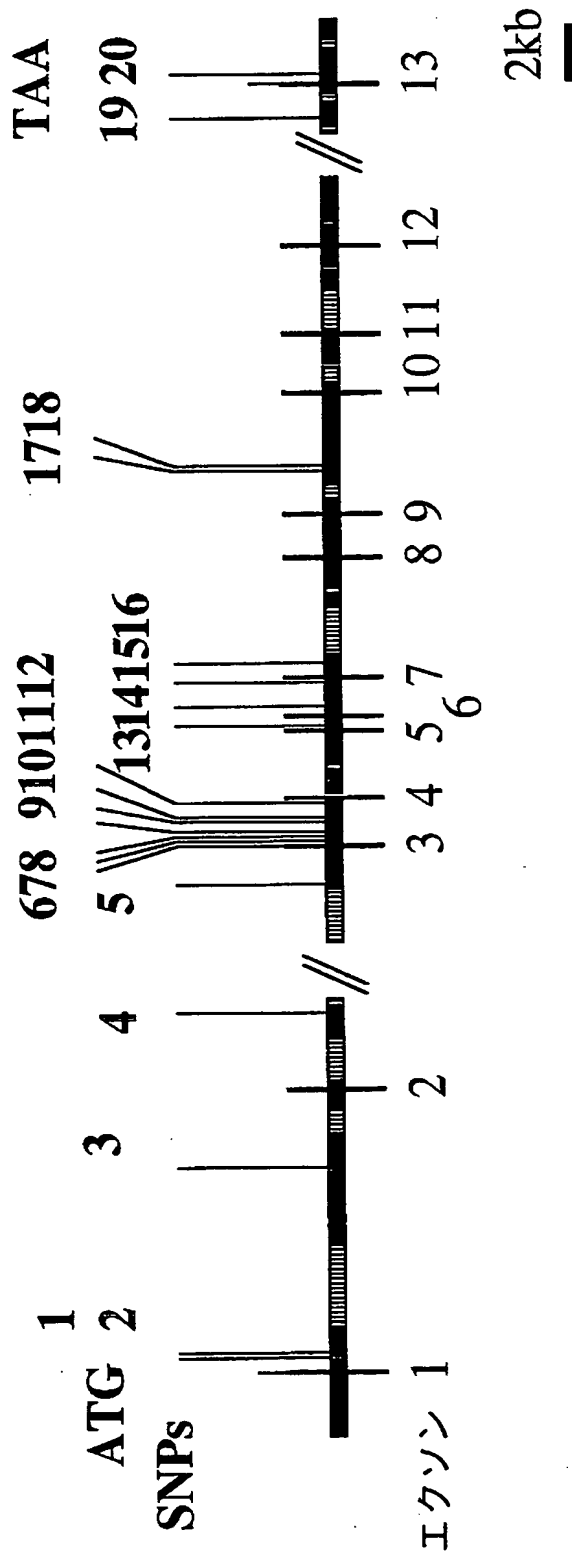
【図 58】



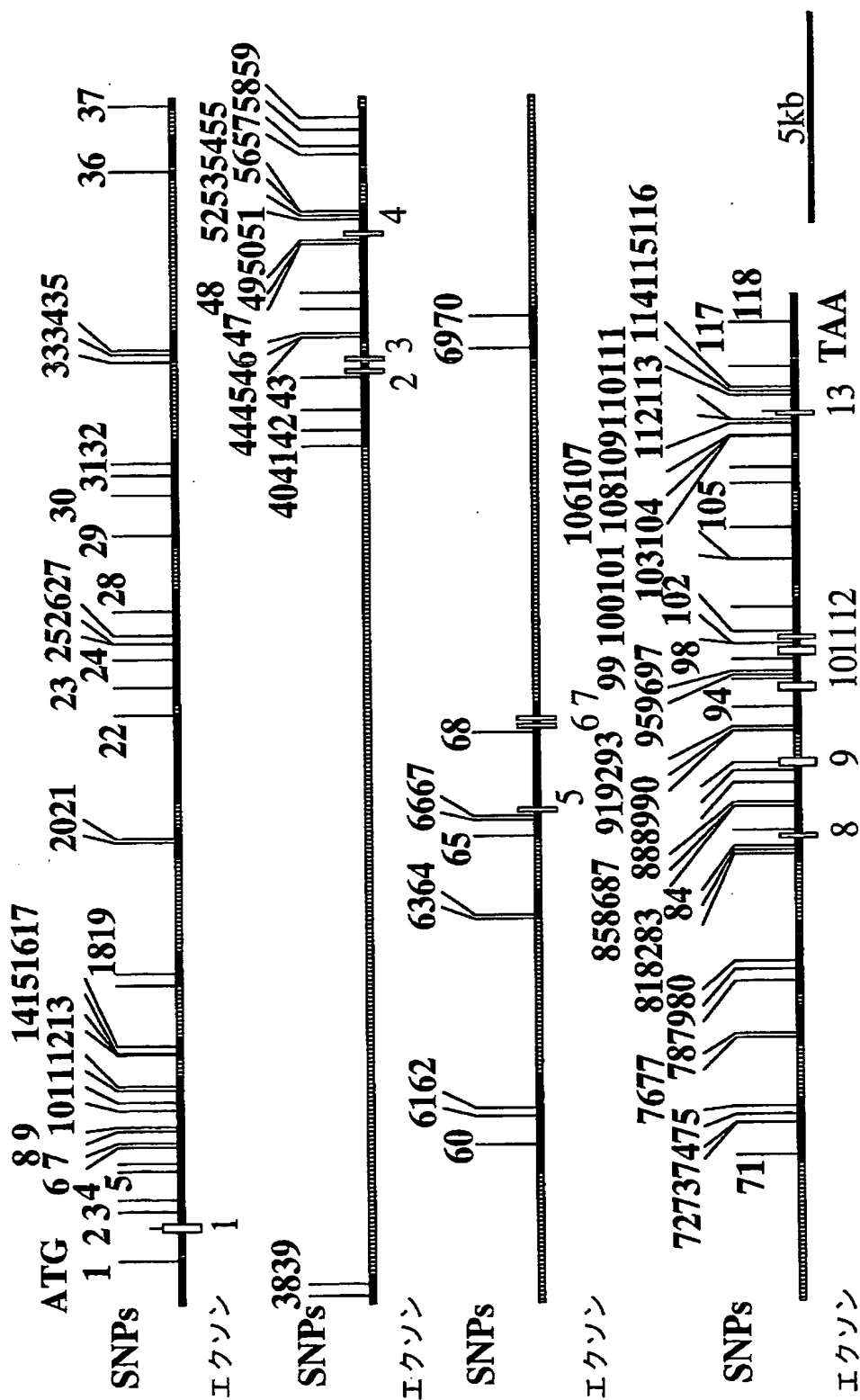
【図 59】



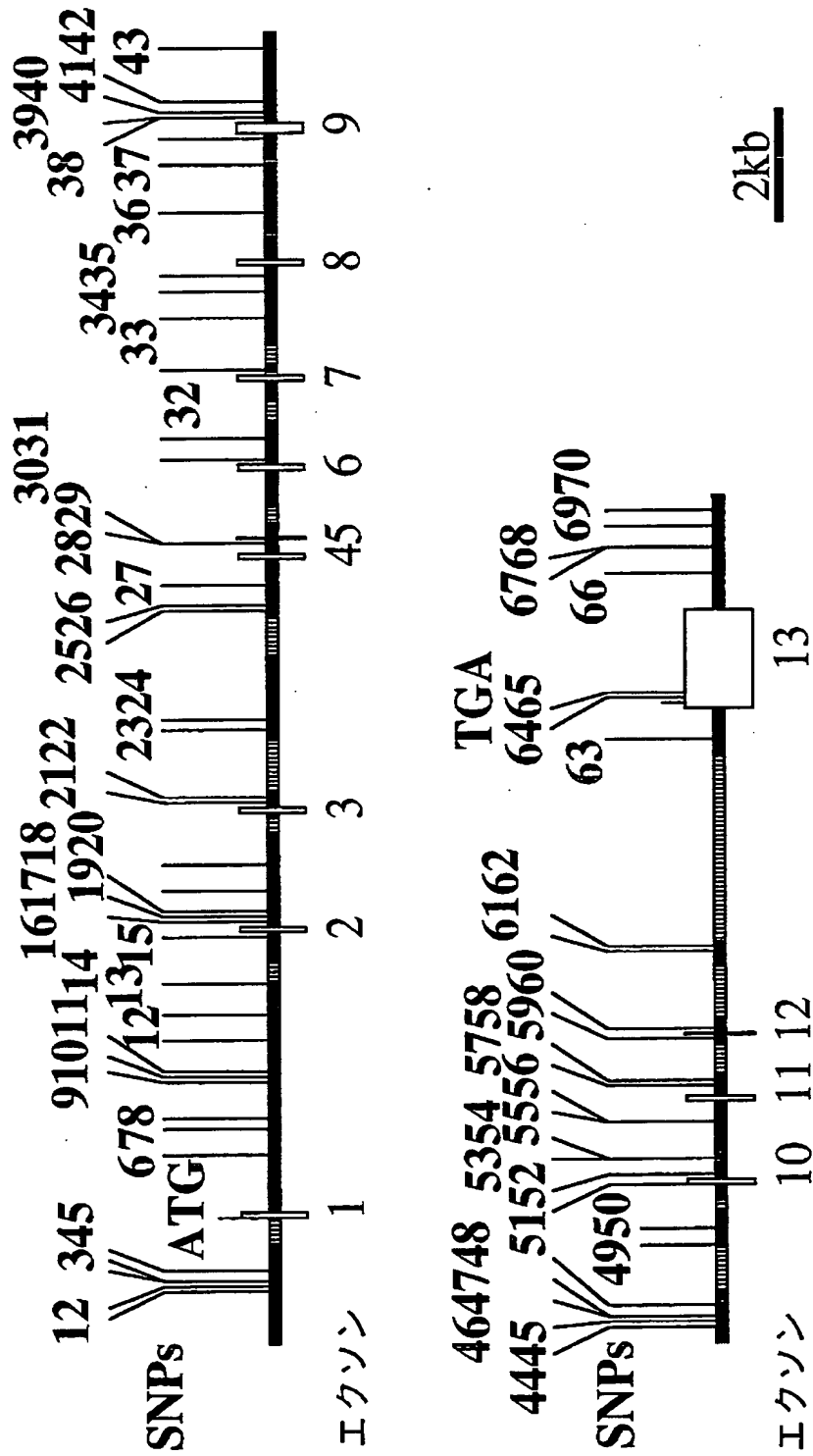
【図 60】



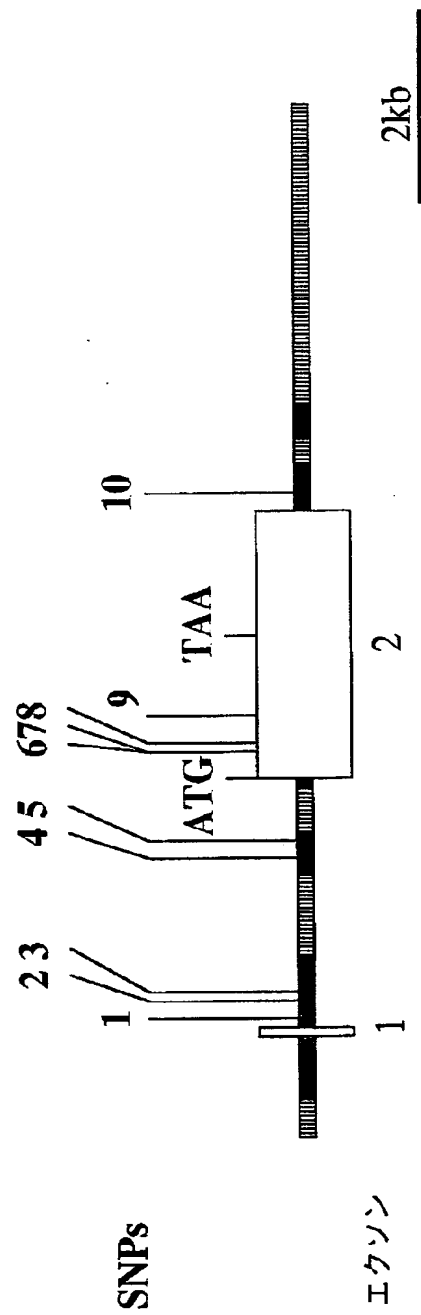
【図 61】



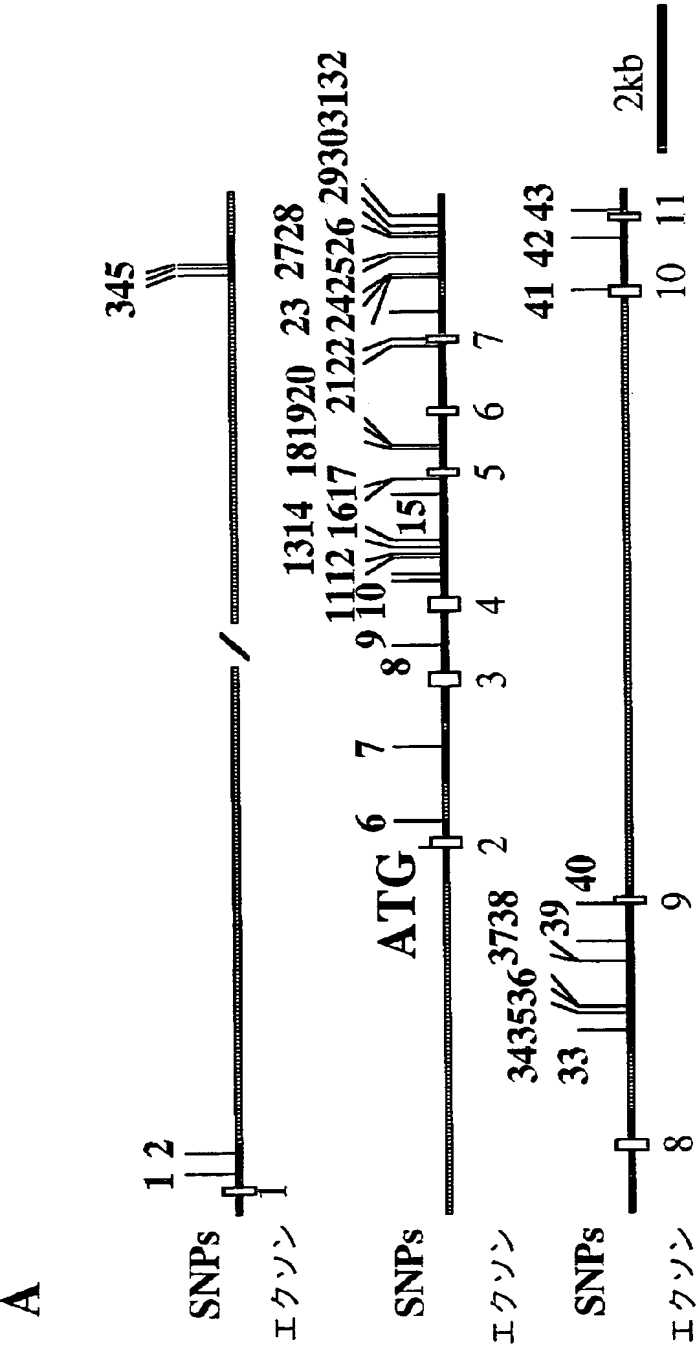
【図 6 2】



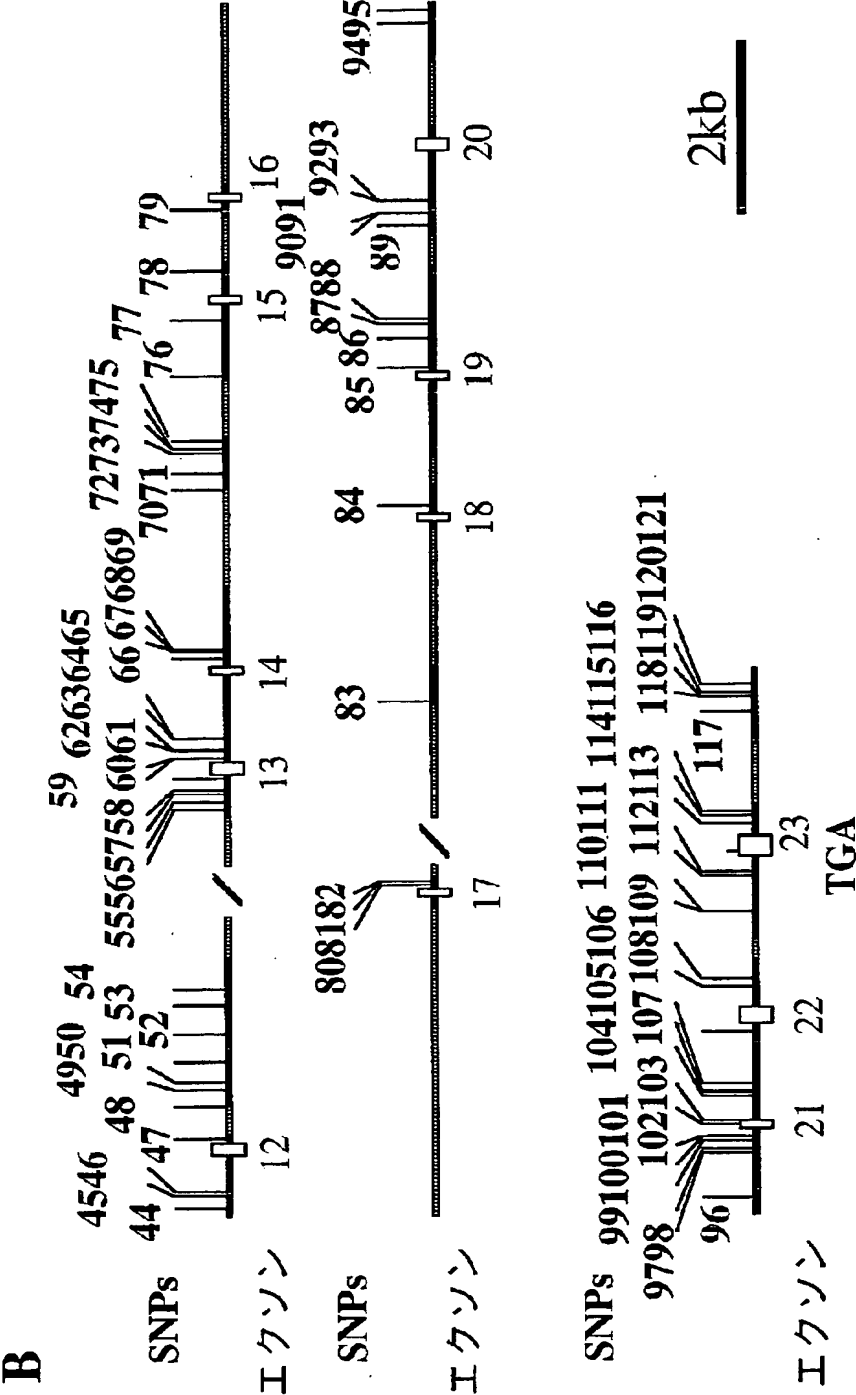
【図 63】



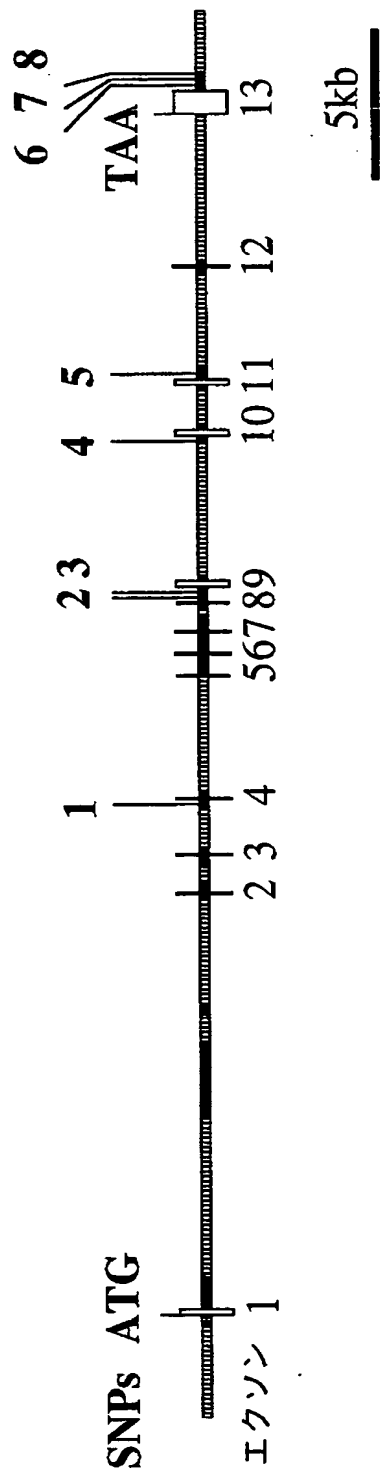
【図 6 4 A】



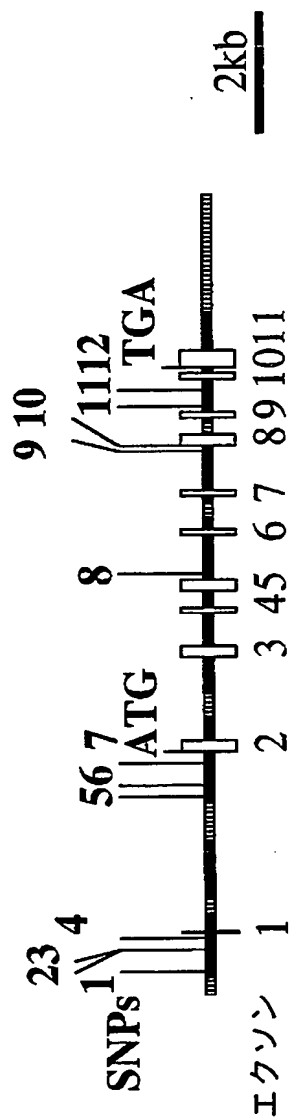
【図 6 4 B】



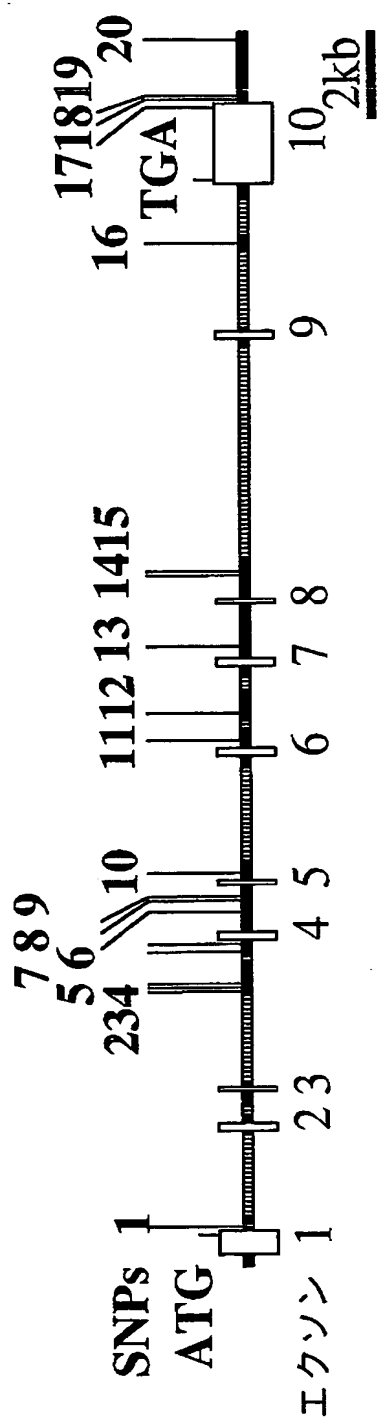
【図 65】



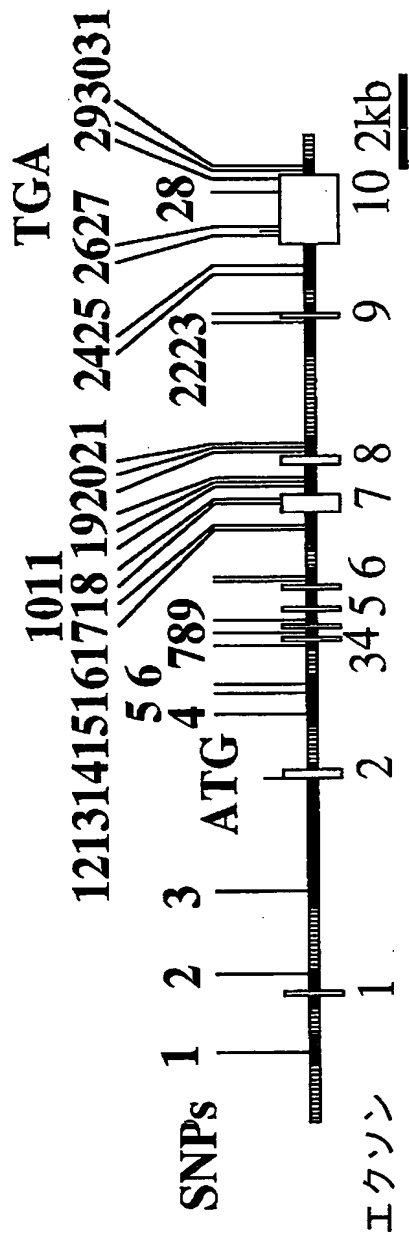
【図66】



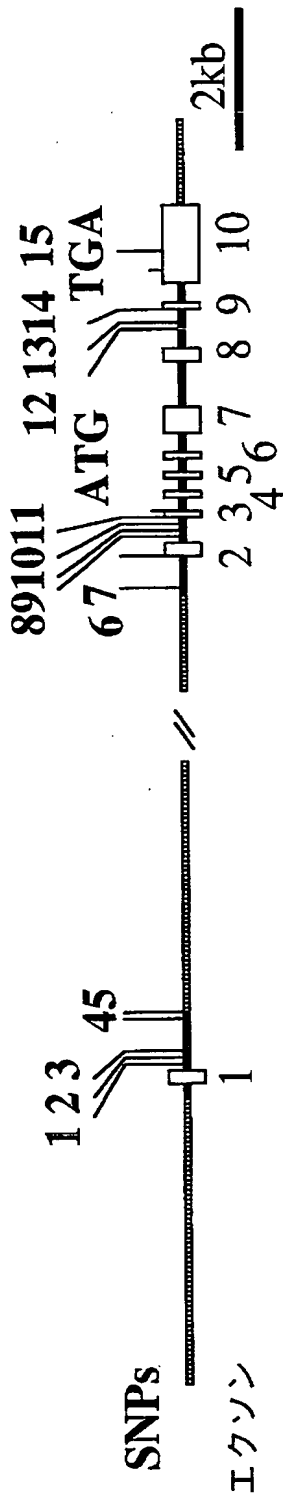
【図 67】



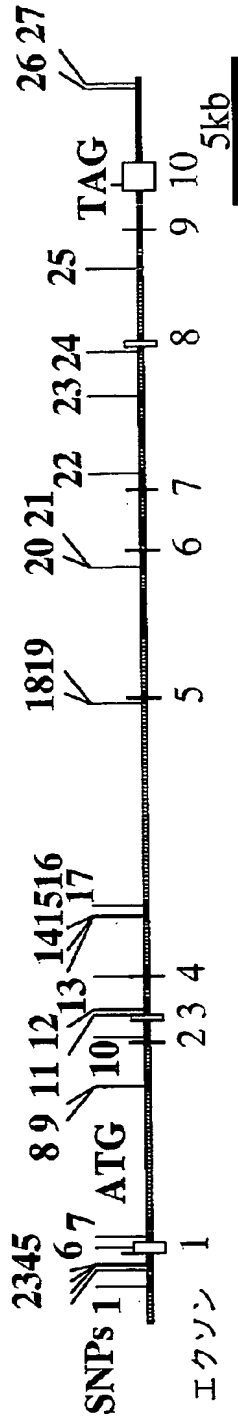
【図 68】



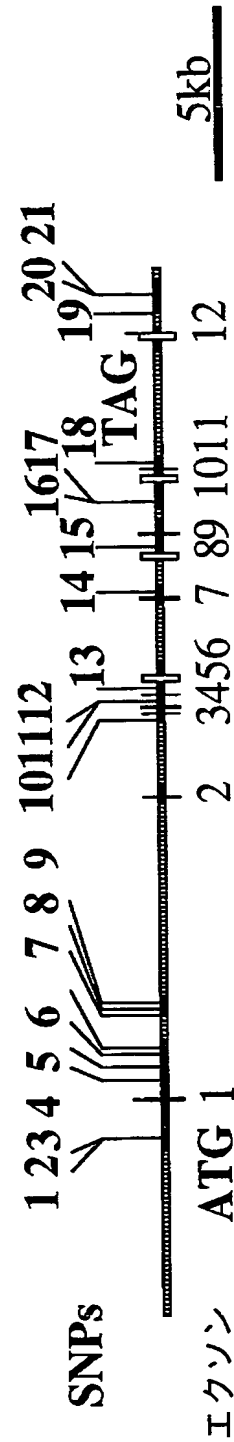
【図 69】



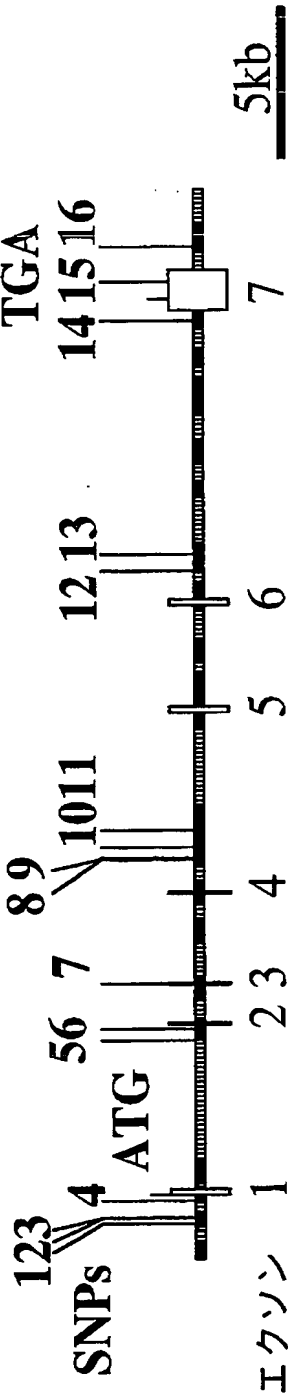
【図 70】



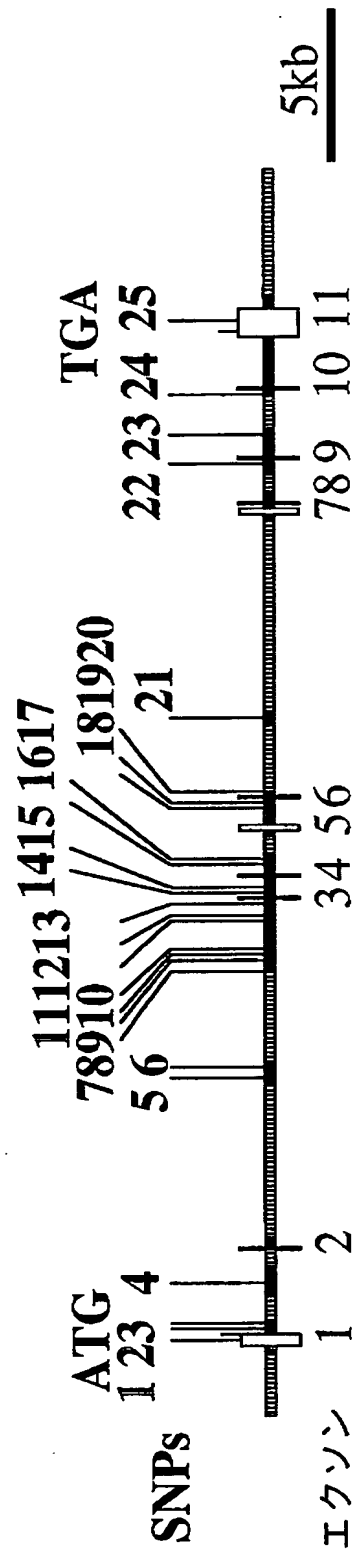
【図 7 1】



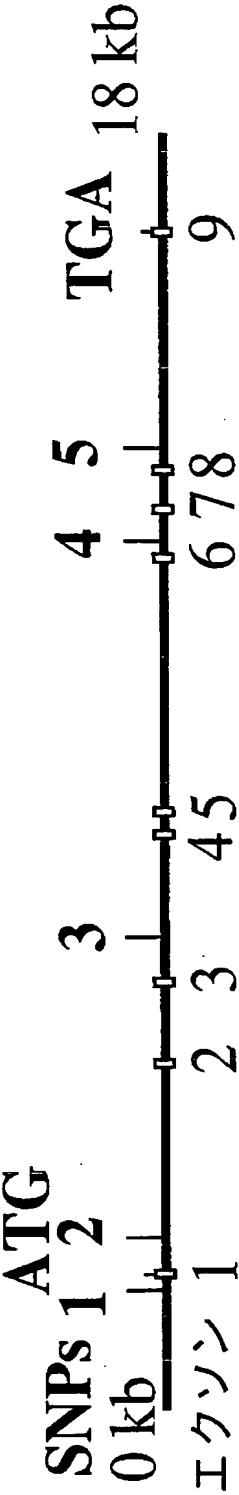
【図 7 2】



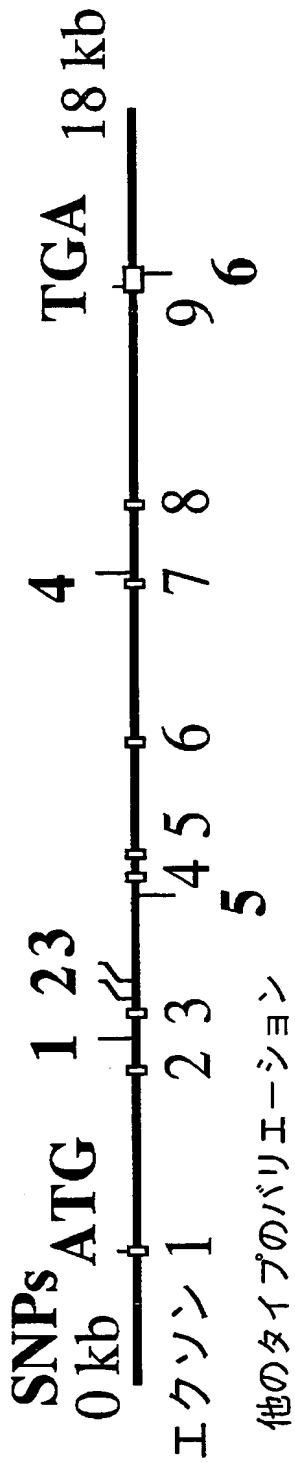
【図 73】



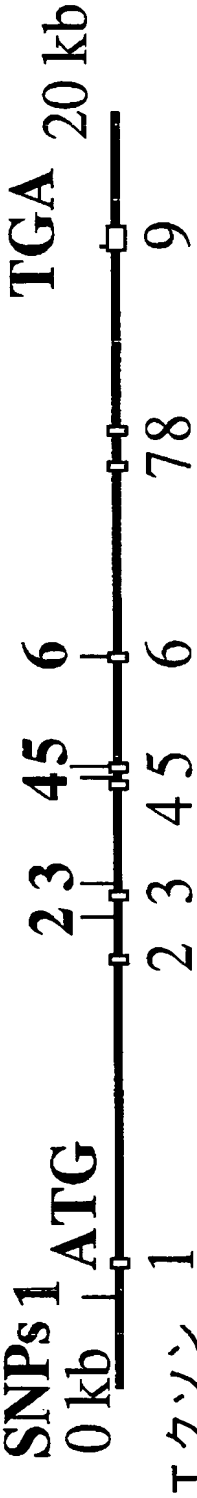
【図 7 4】



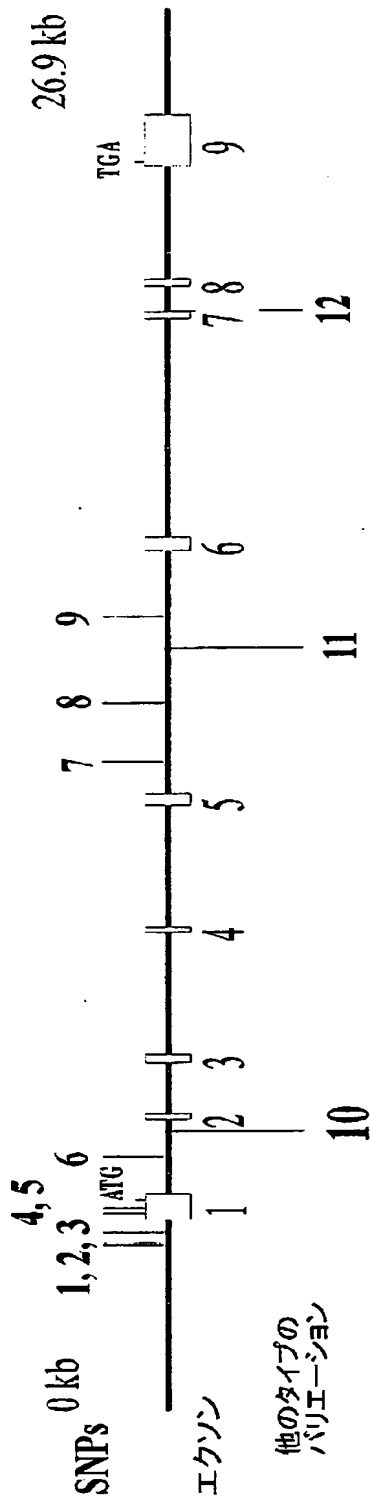
【図 75】



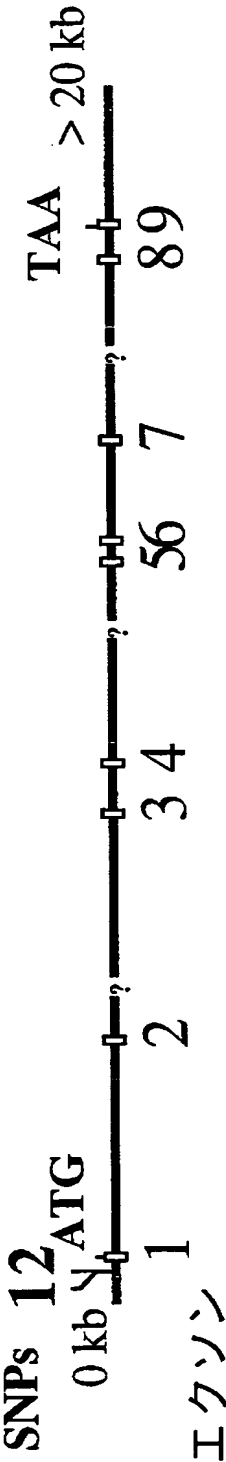
【図 76】



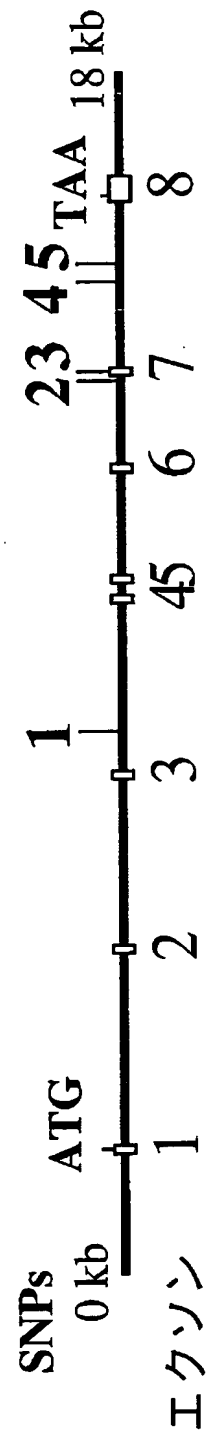
【図 77】



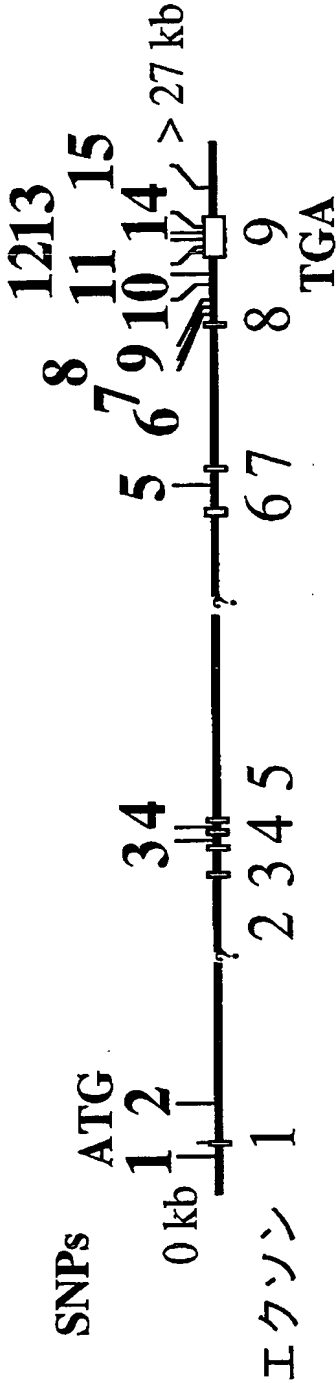
【図 78】



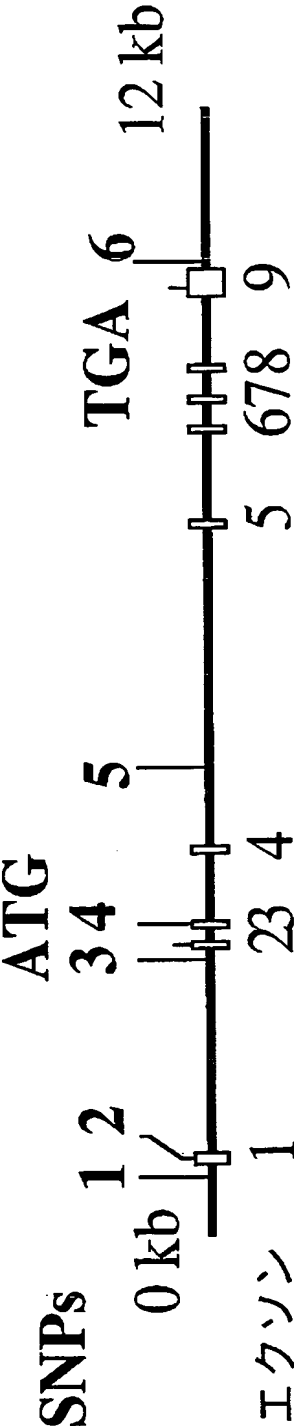
【図 79】



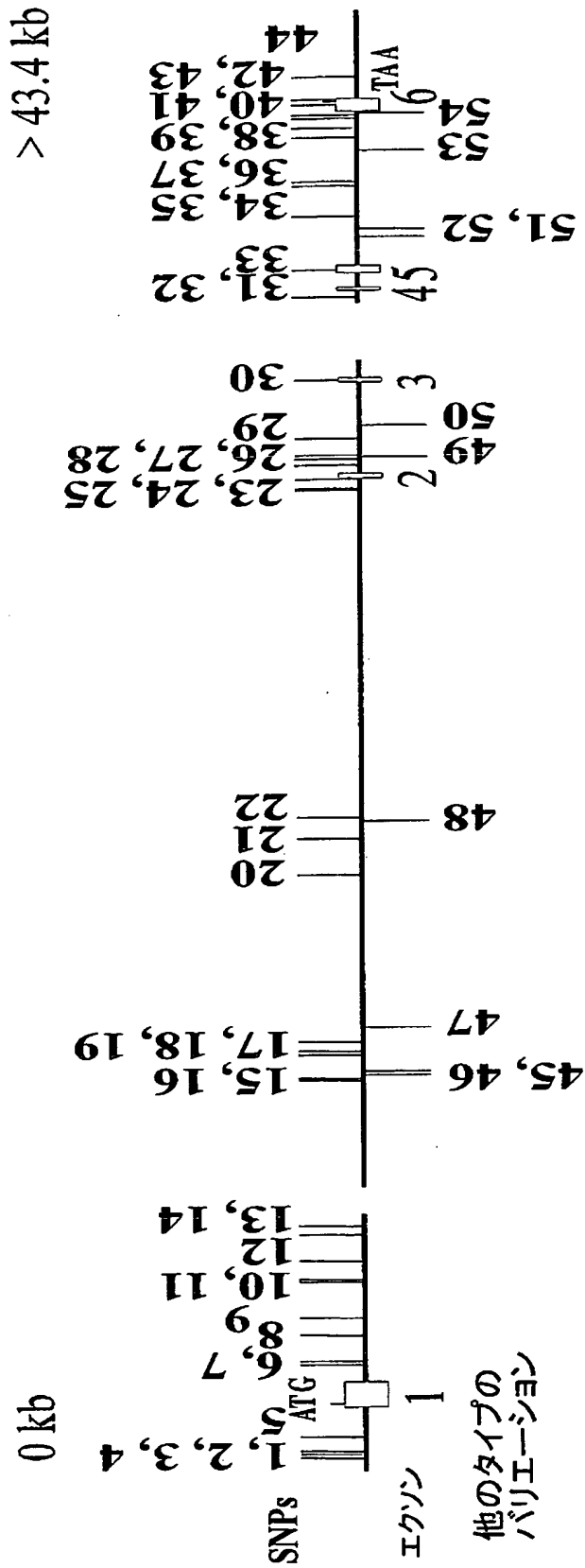
【図 80】



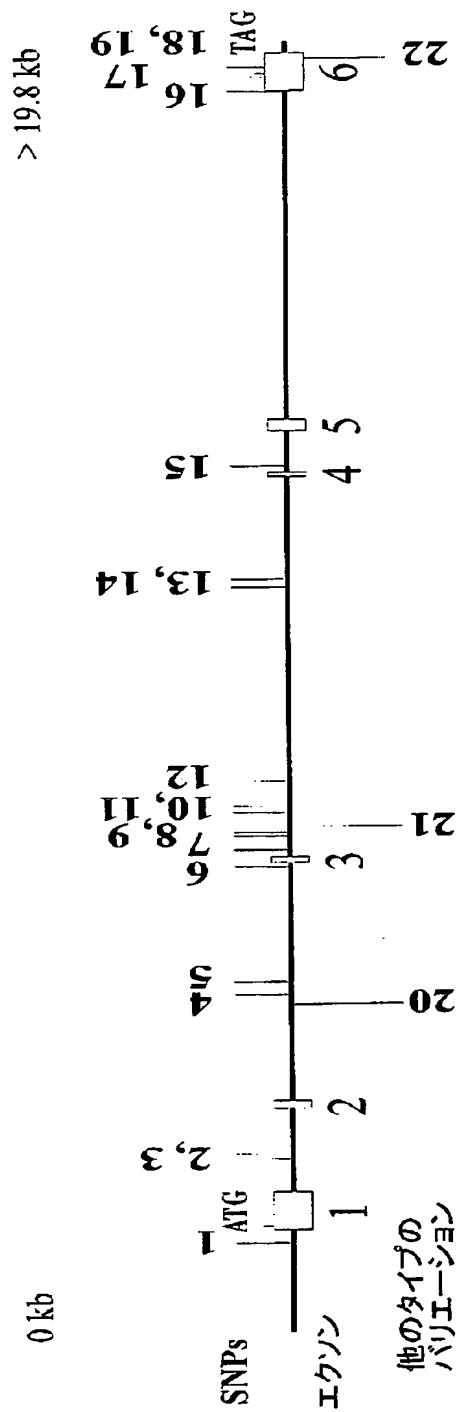
【図 8 1】



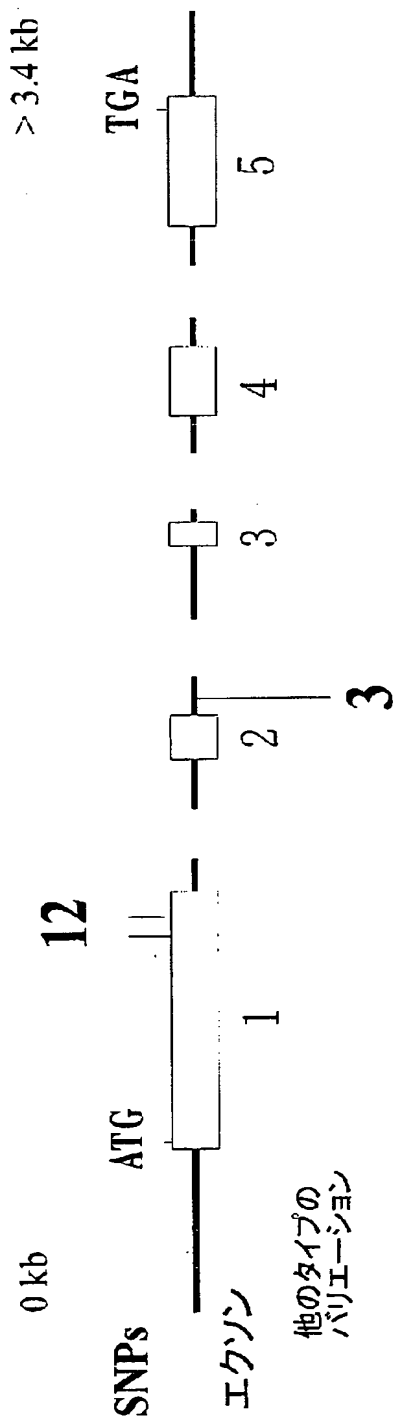
【図 8 3】



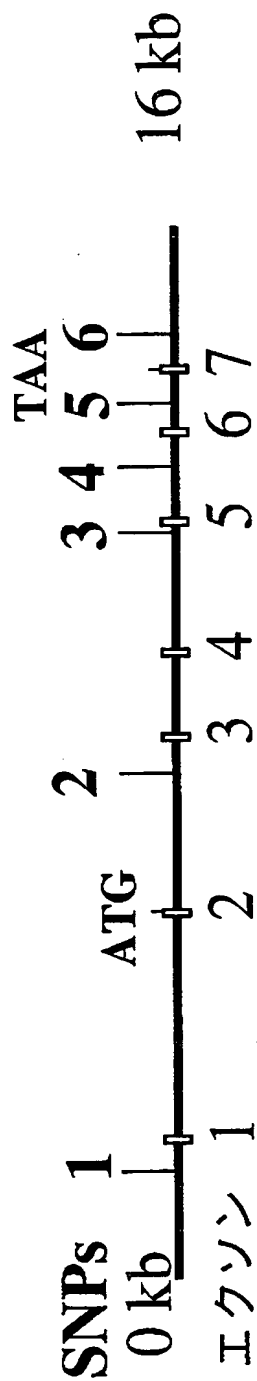
【図 84】



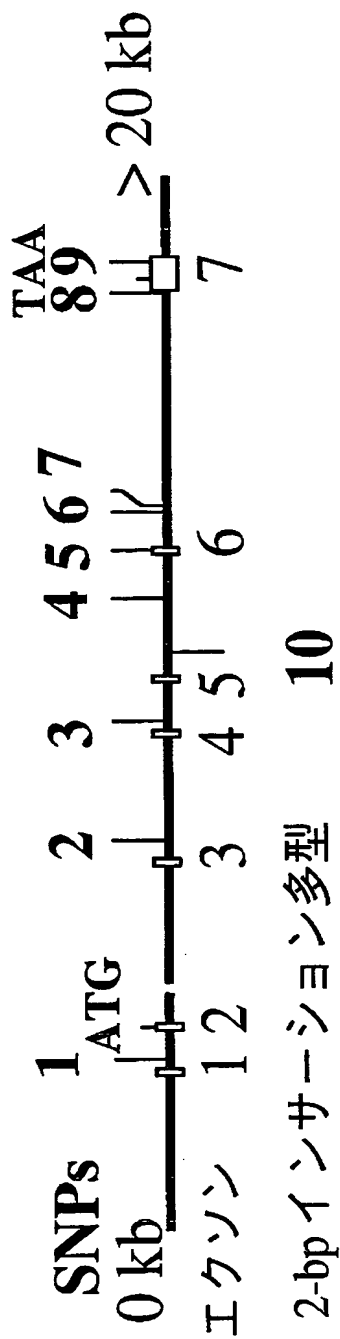
【図 85】



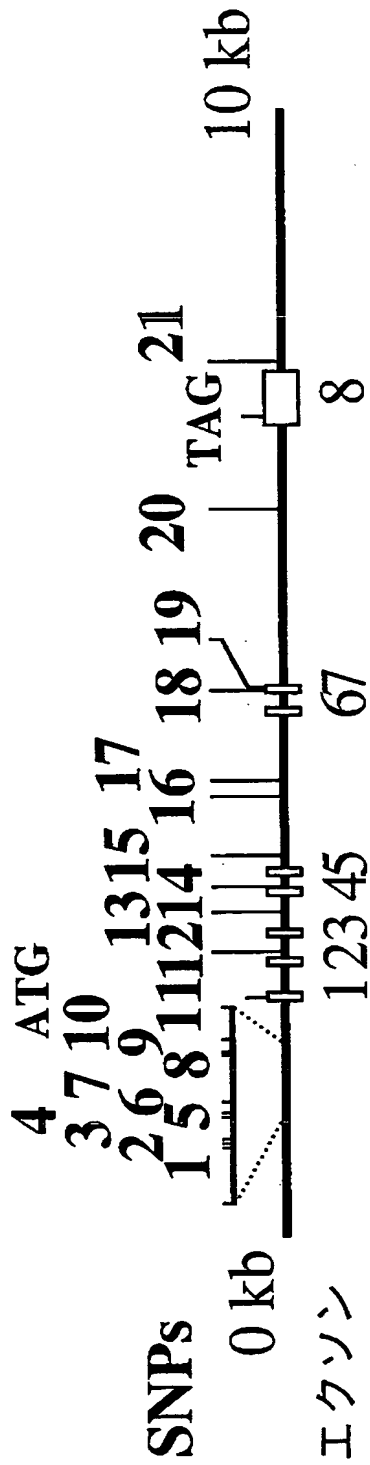
【図 86】



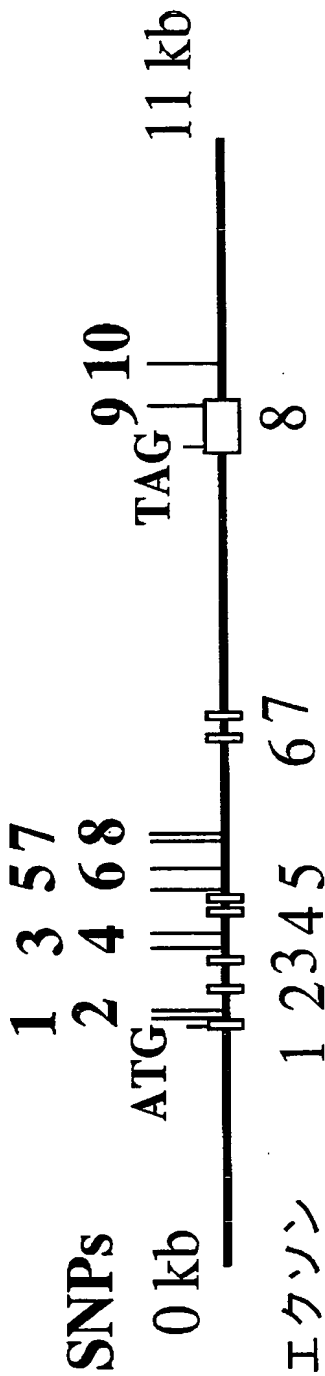
【図 87】



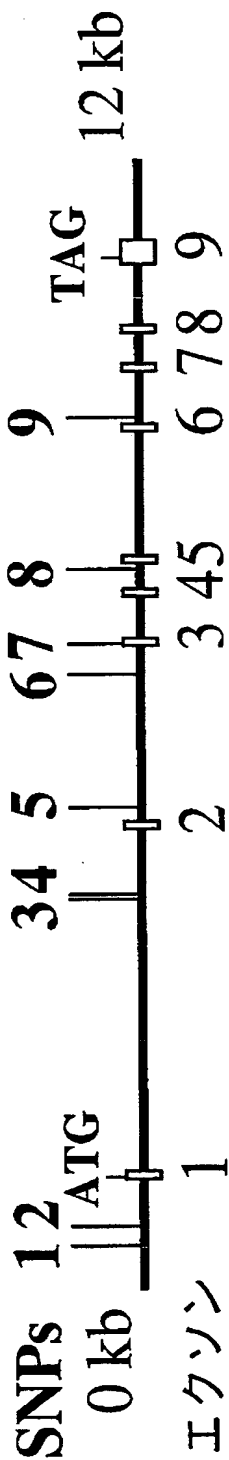
【図 88】



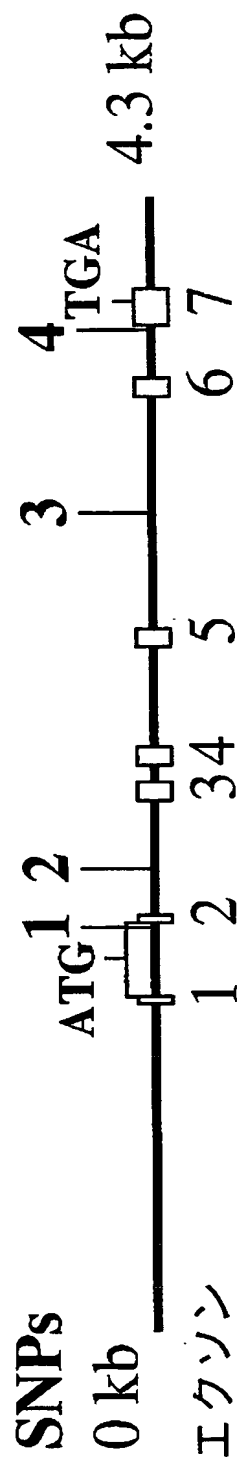
【図 89】



【図 9 0】



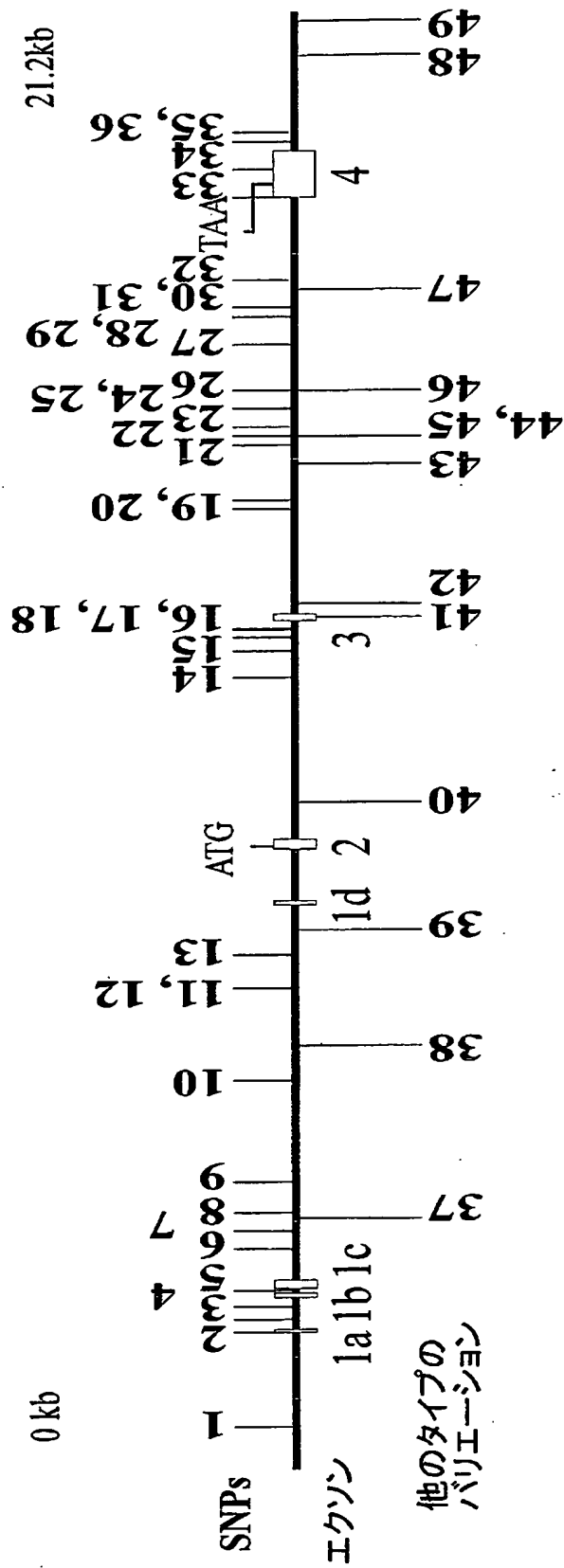
【図 91】



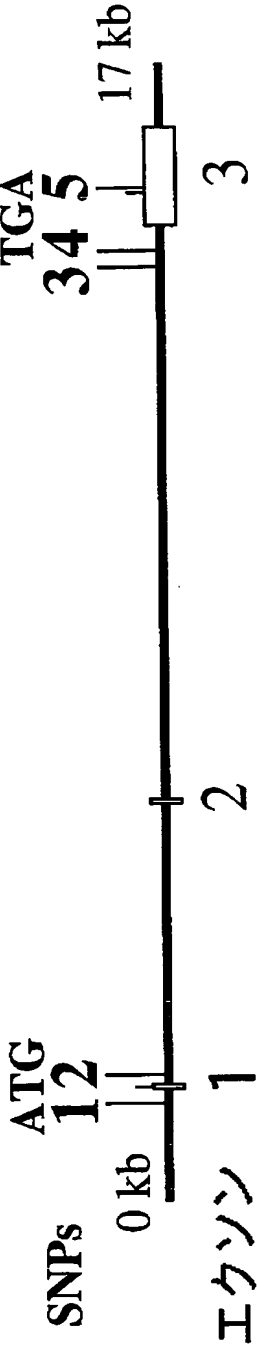
【図 9 2】



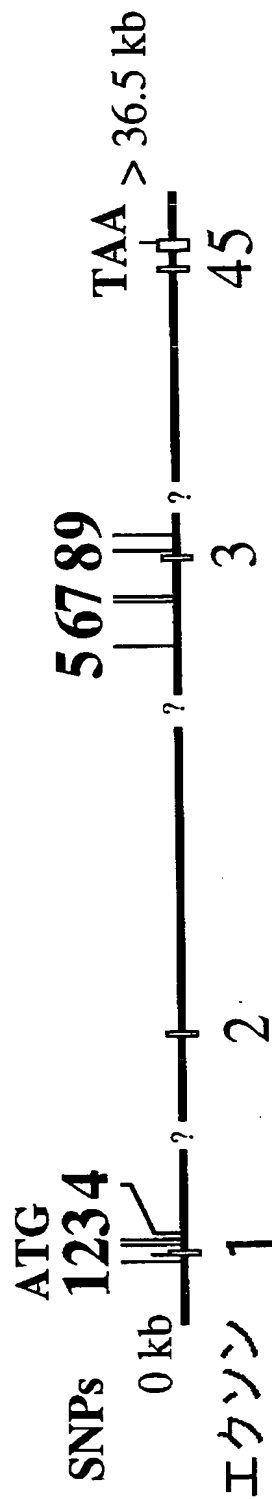
【図 9 3】



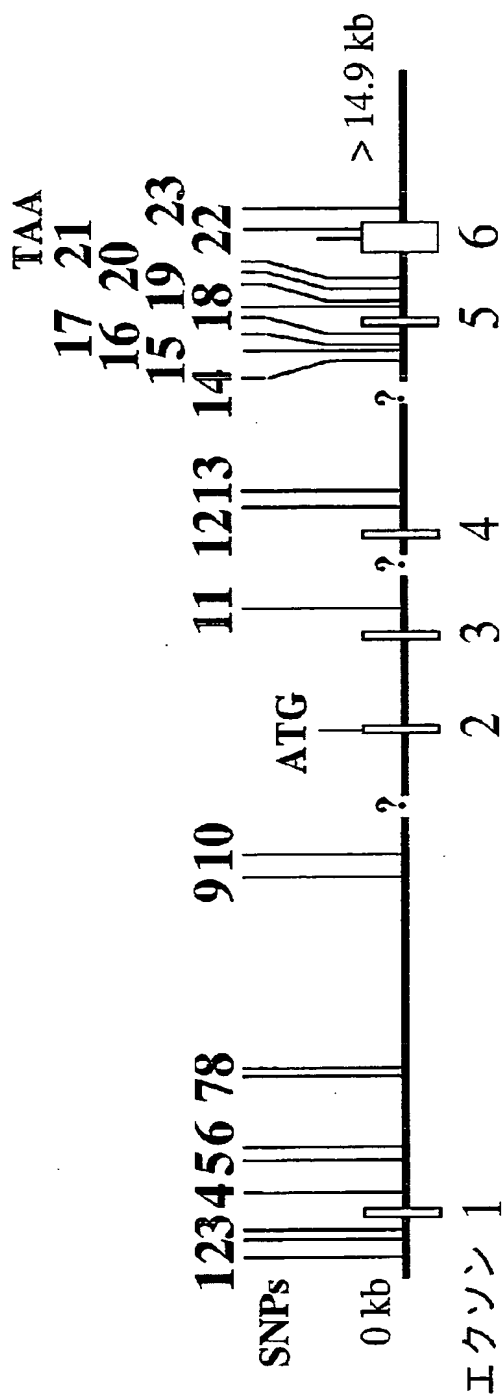
【図 9 4】



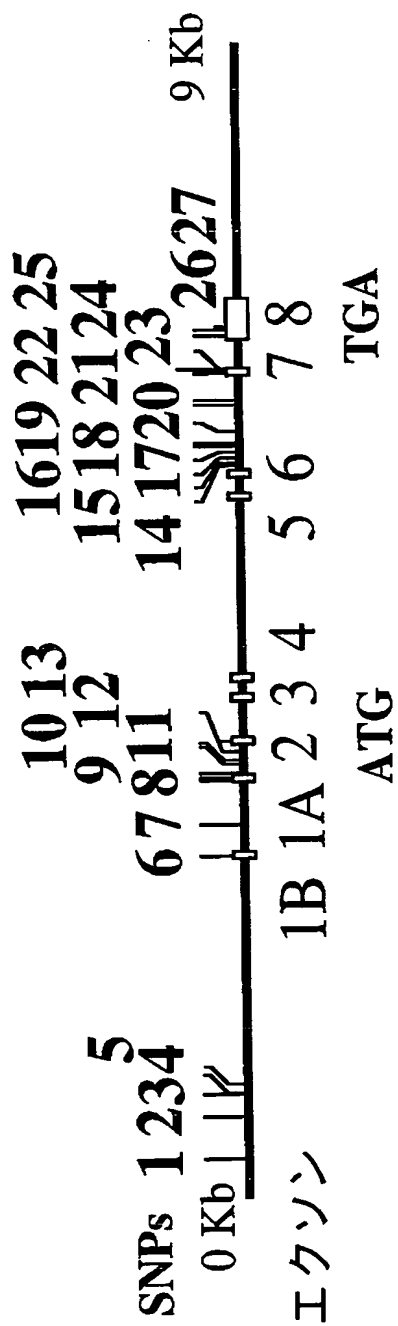
【図 95】



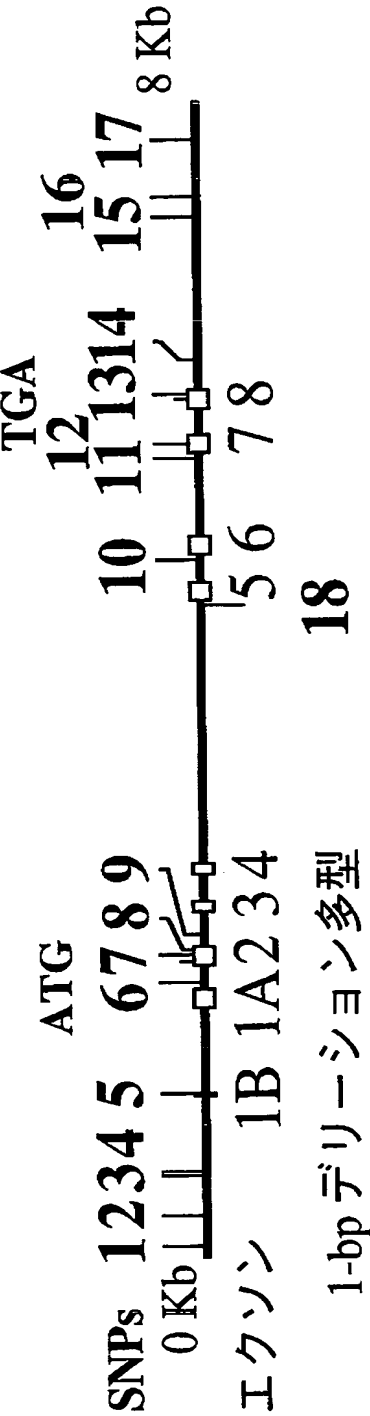
【図 96】



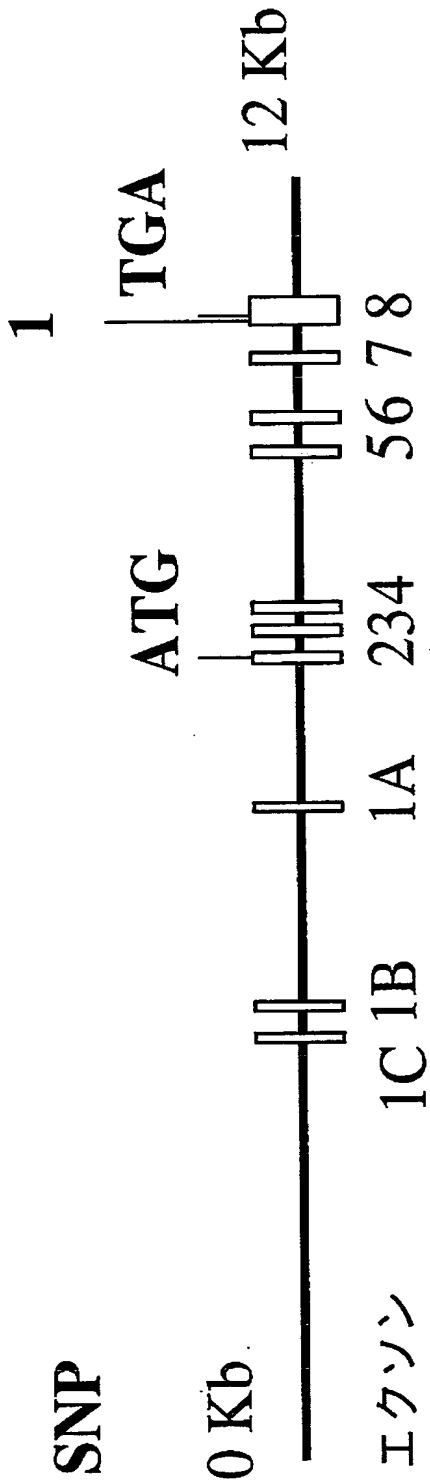
【図 97】



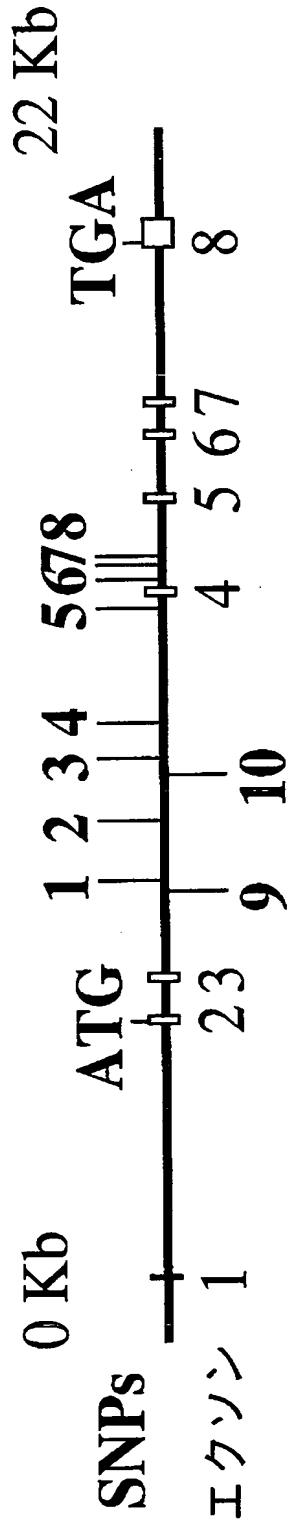
【図 98】



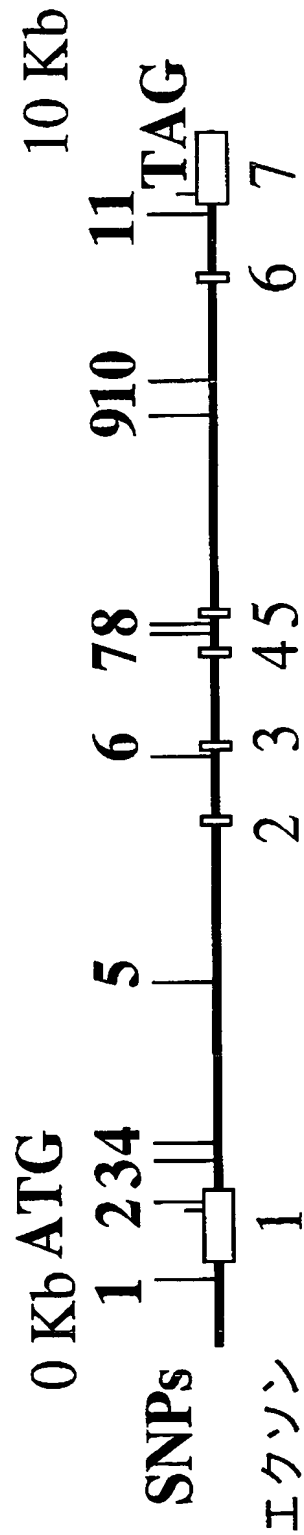
【図 9 9】



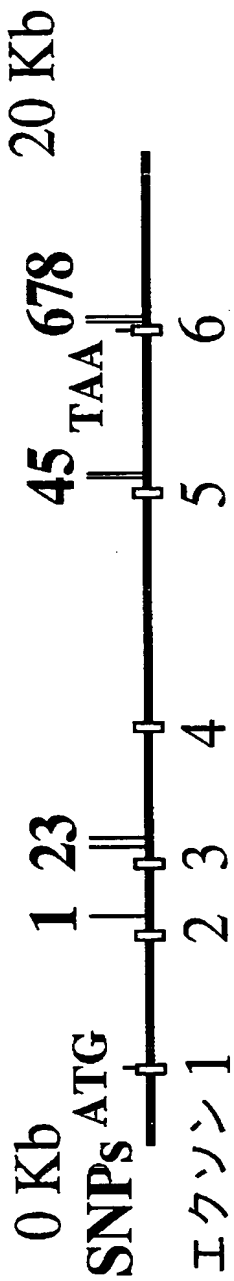
【図 100】



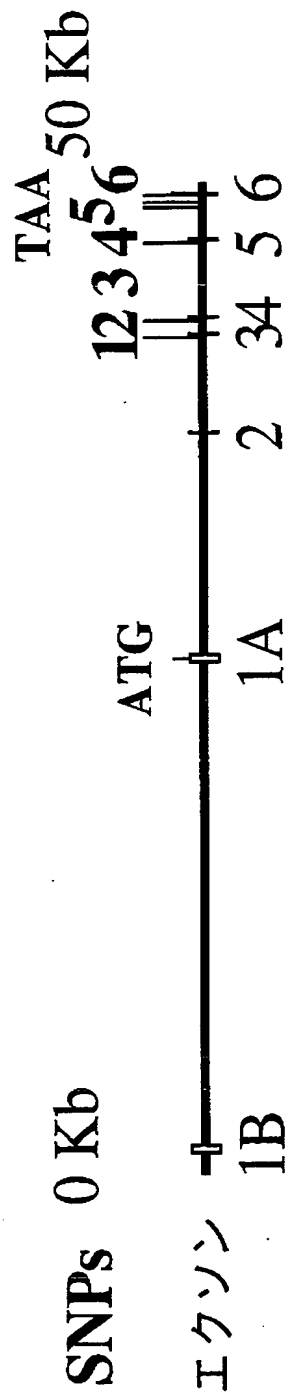
【図 1 0 1】



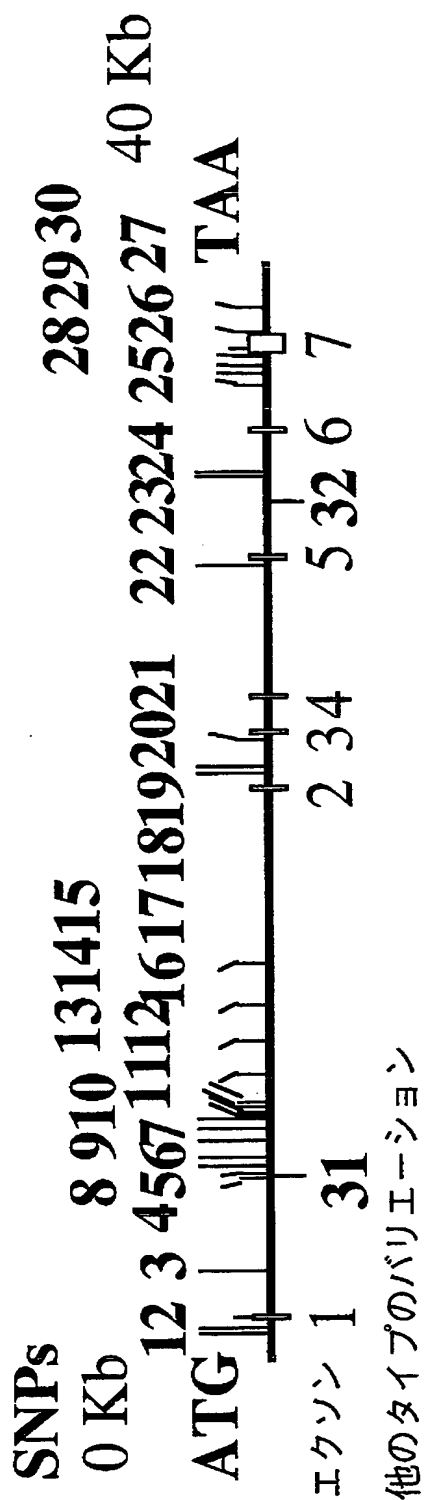
【図 1 0 2】



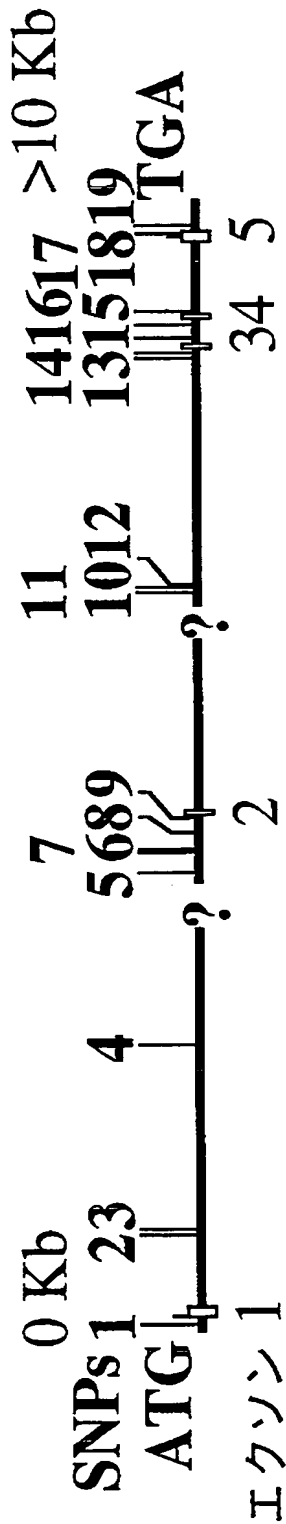
【図 1 0 3】



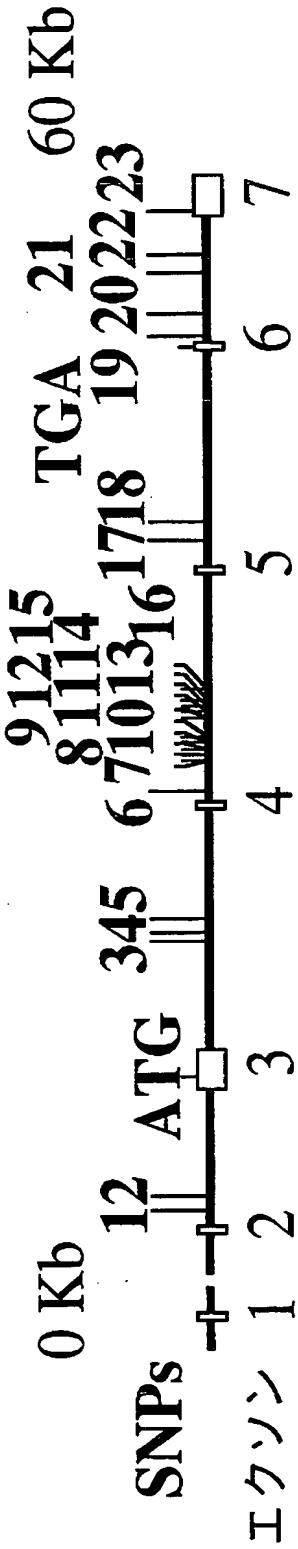
【図 104】



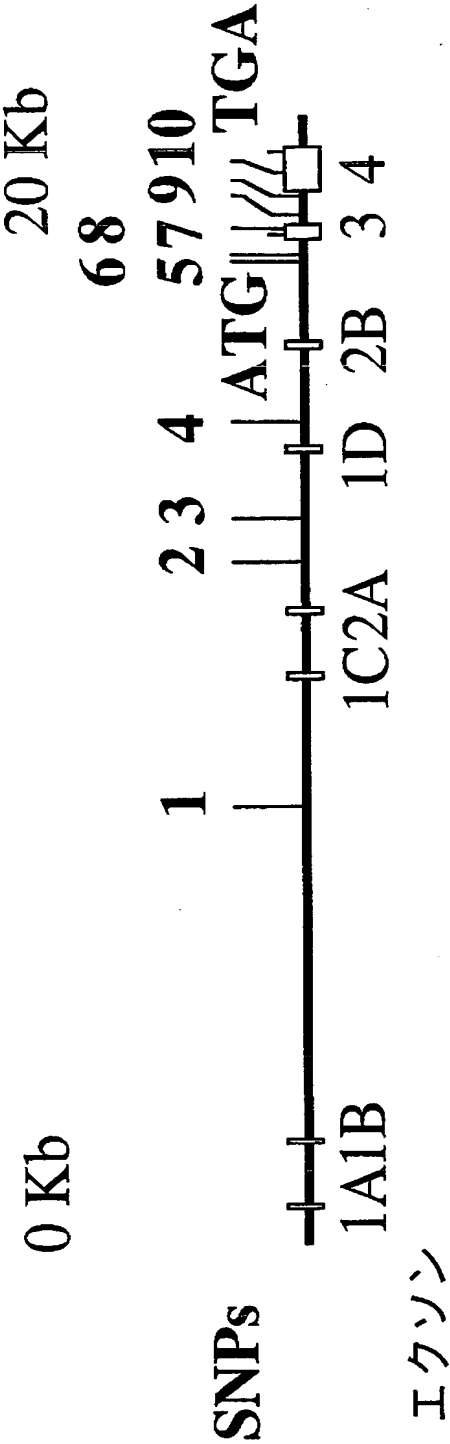
【図 105】



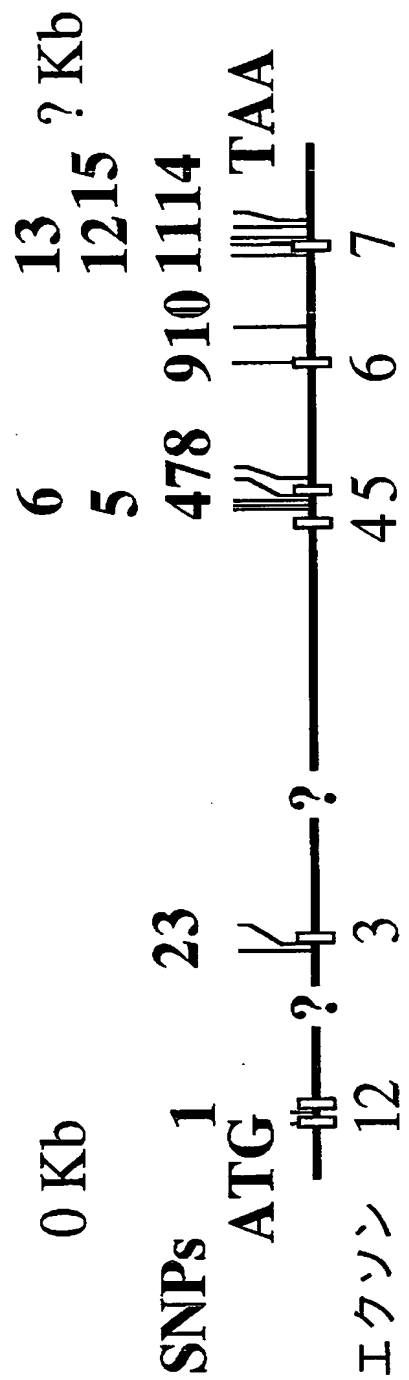
【図 106】



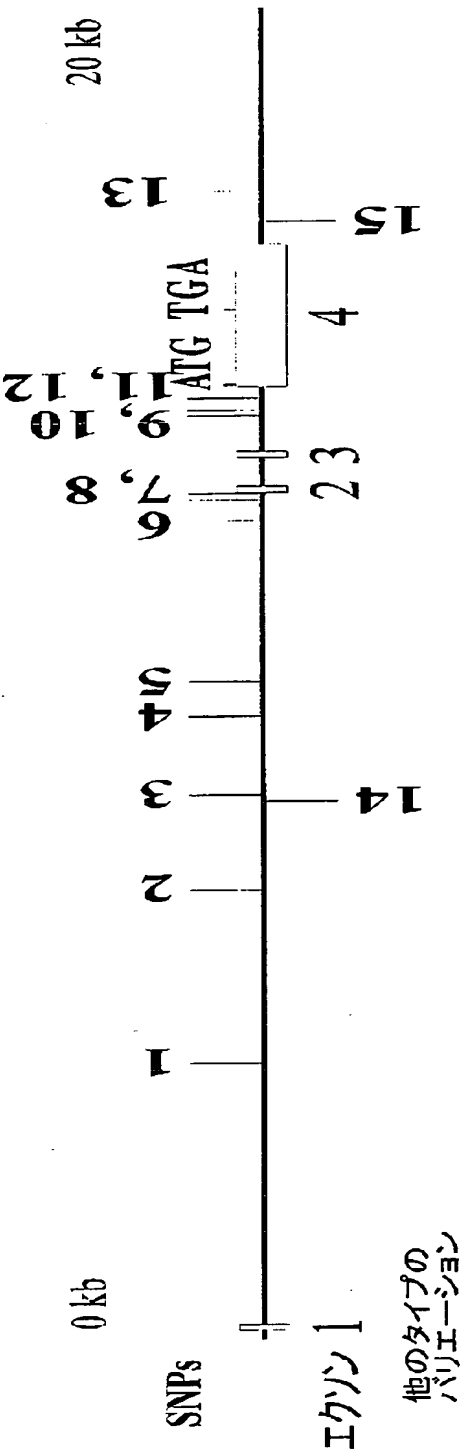
【図 1 0 7】



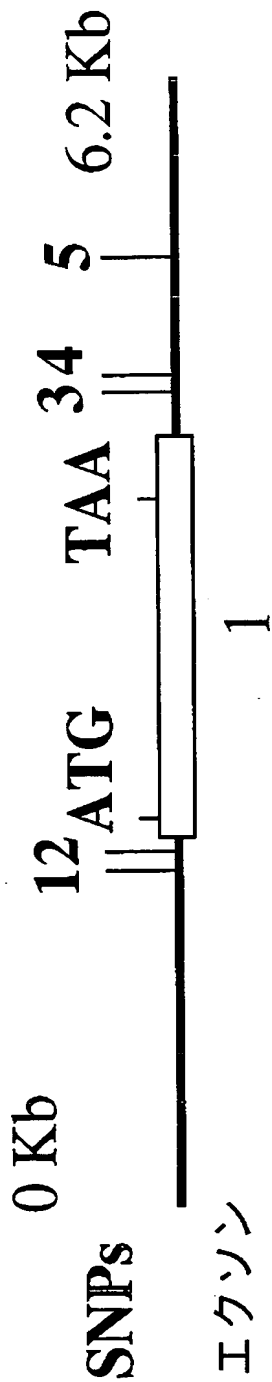
【図 1 0 8】



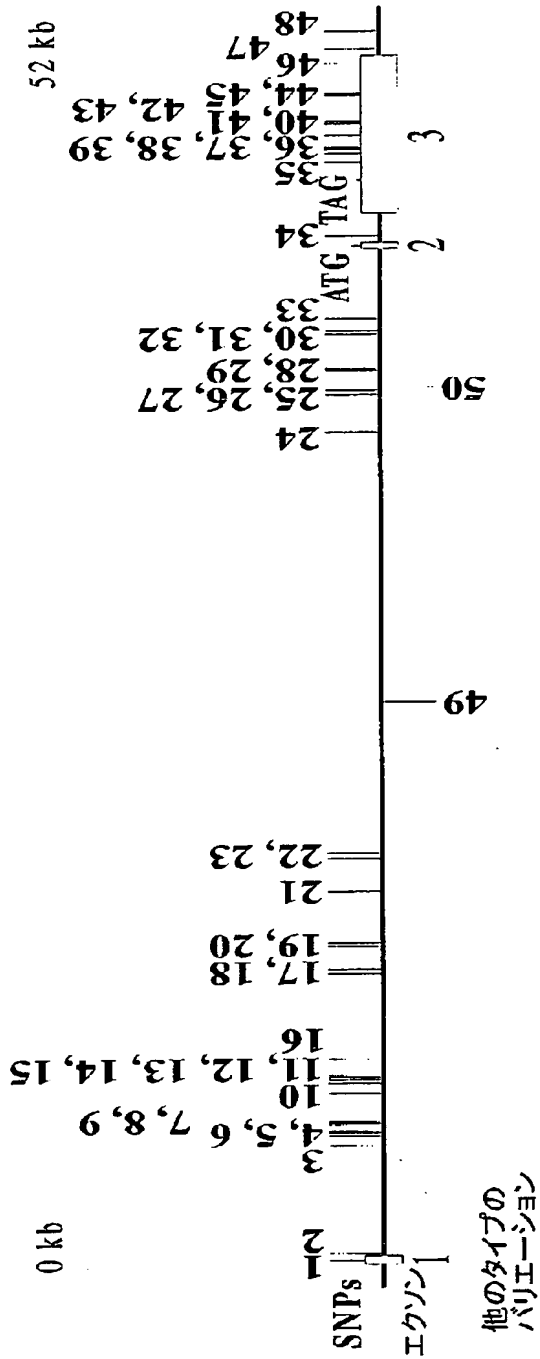
【図109】



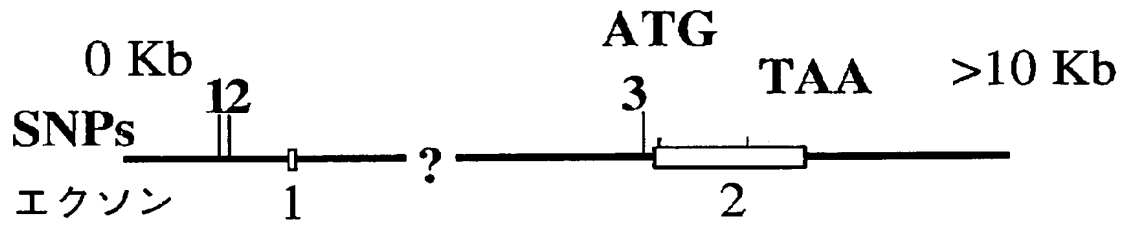
【図 110】



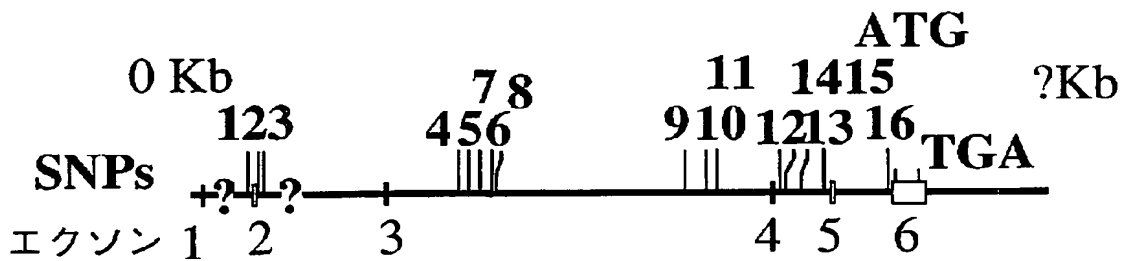
【図 111】



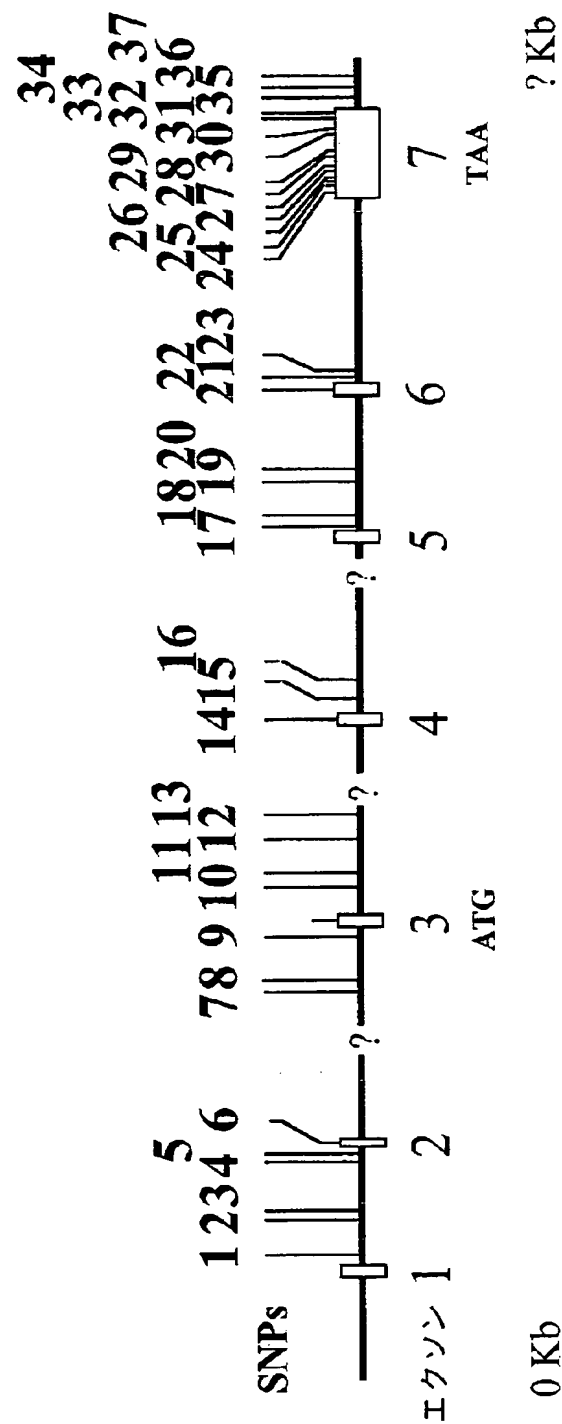
【図 1 1 2】



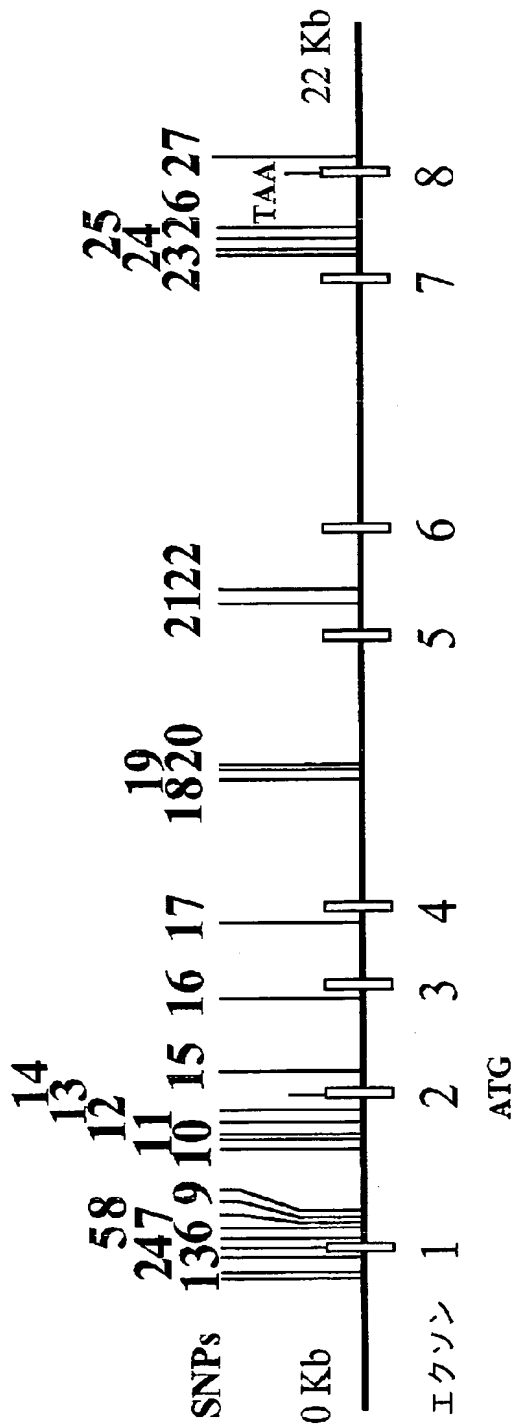
【図 1 1 3】



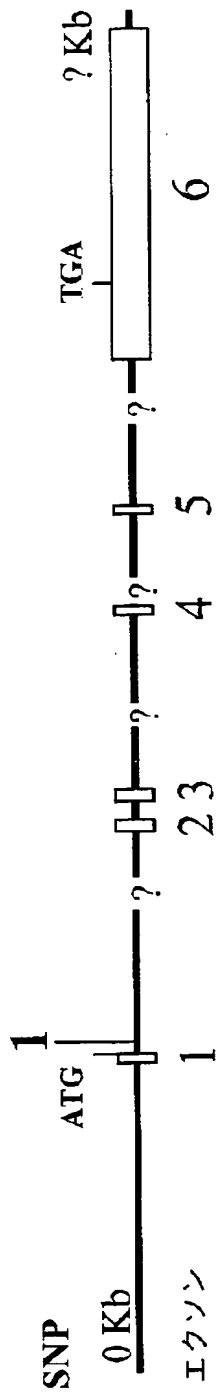
【図 114】



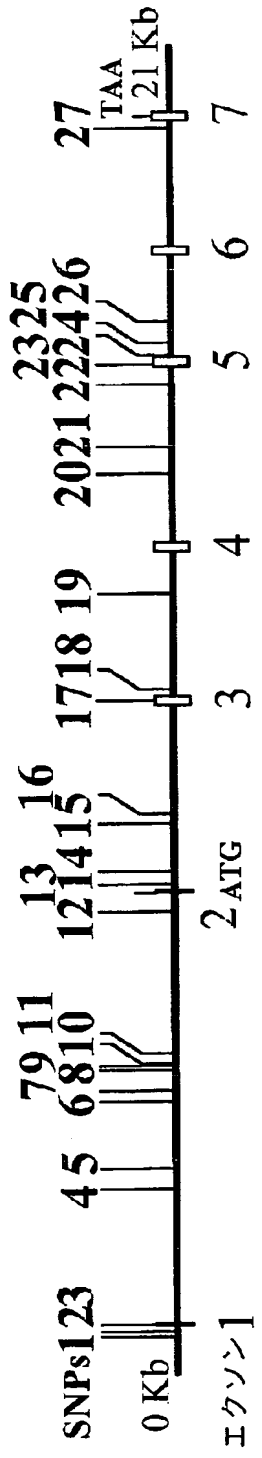
【図 115】



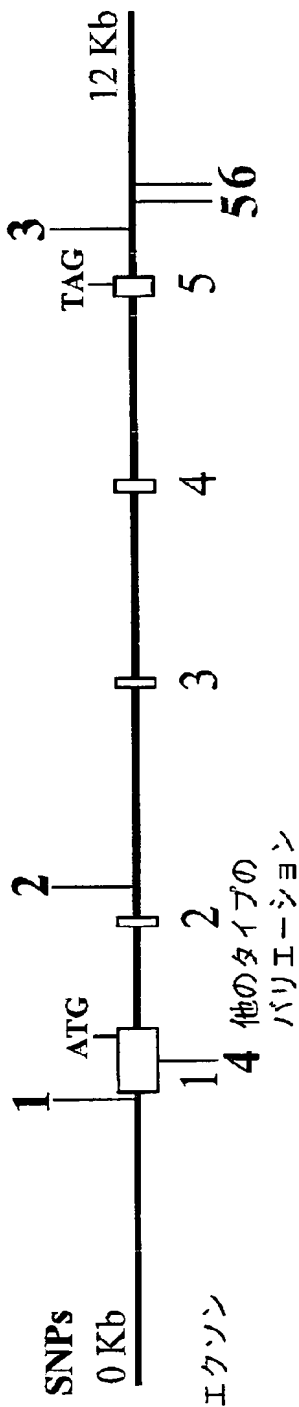
【図 116】



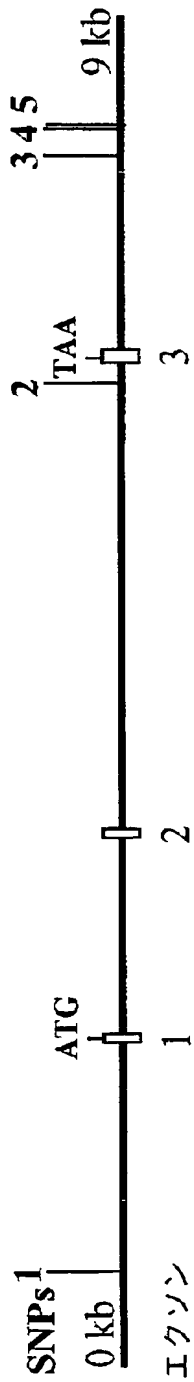
【図 117】



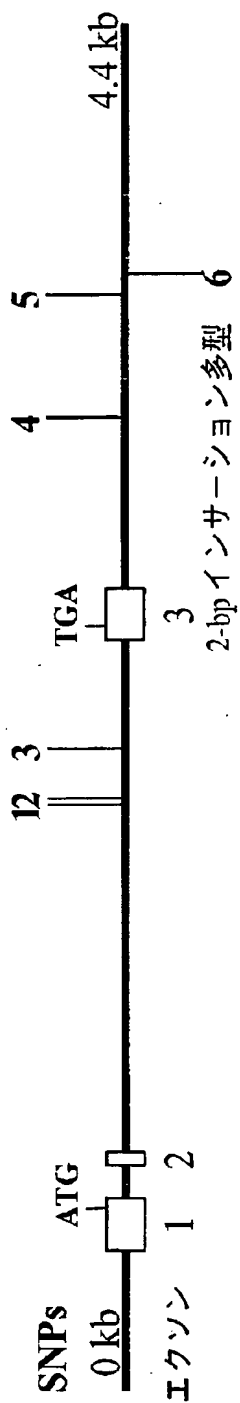
【図 118】



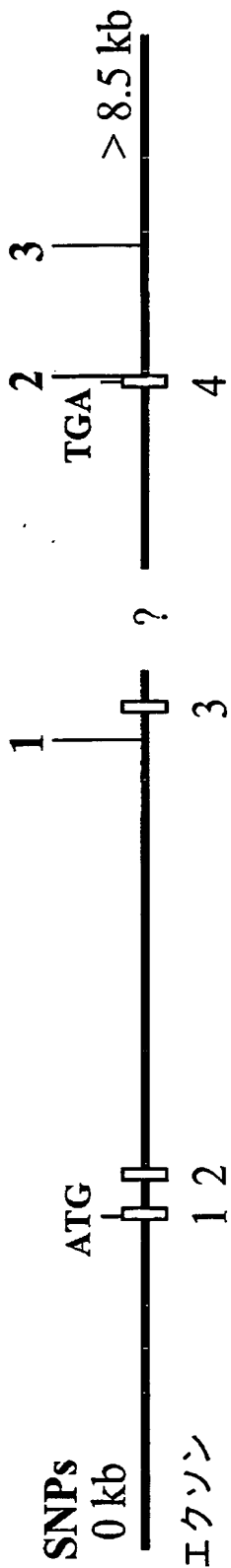
【図 119】



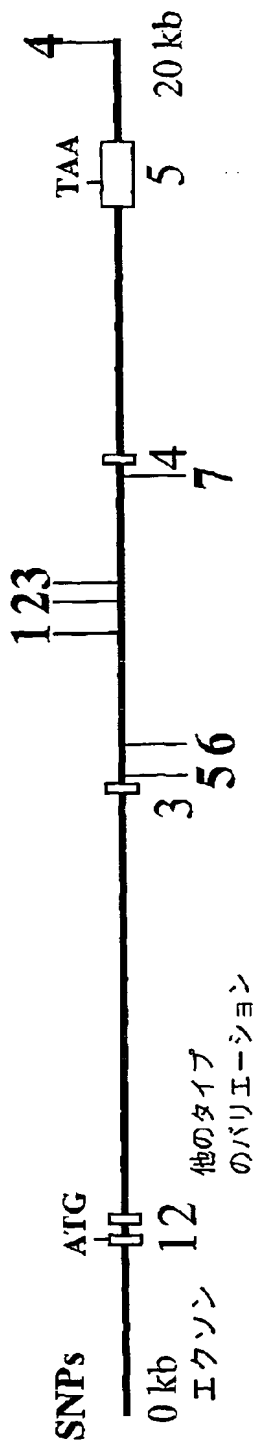
【図 120】



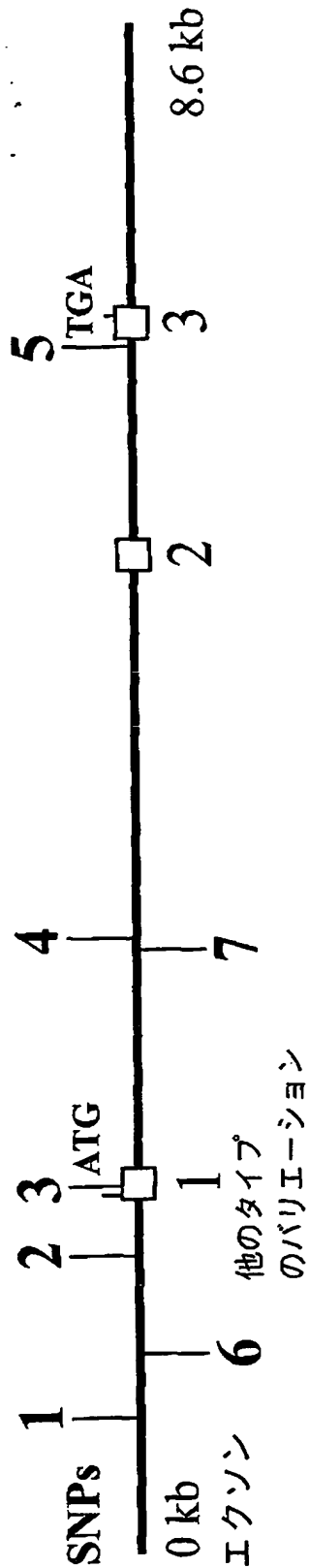
【図 121】



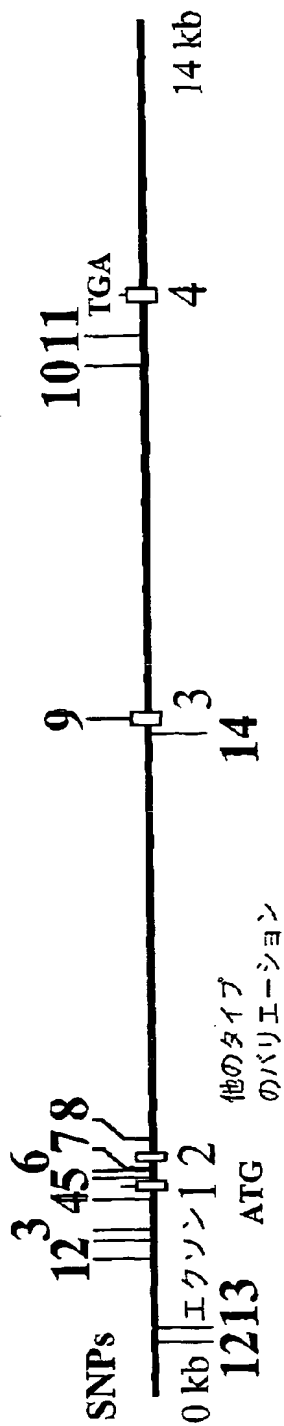
【図 122】



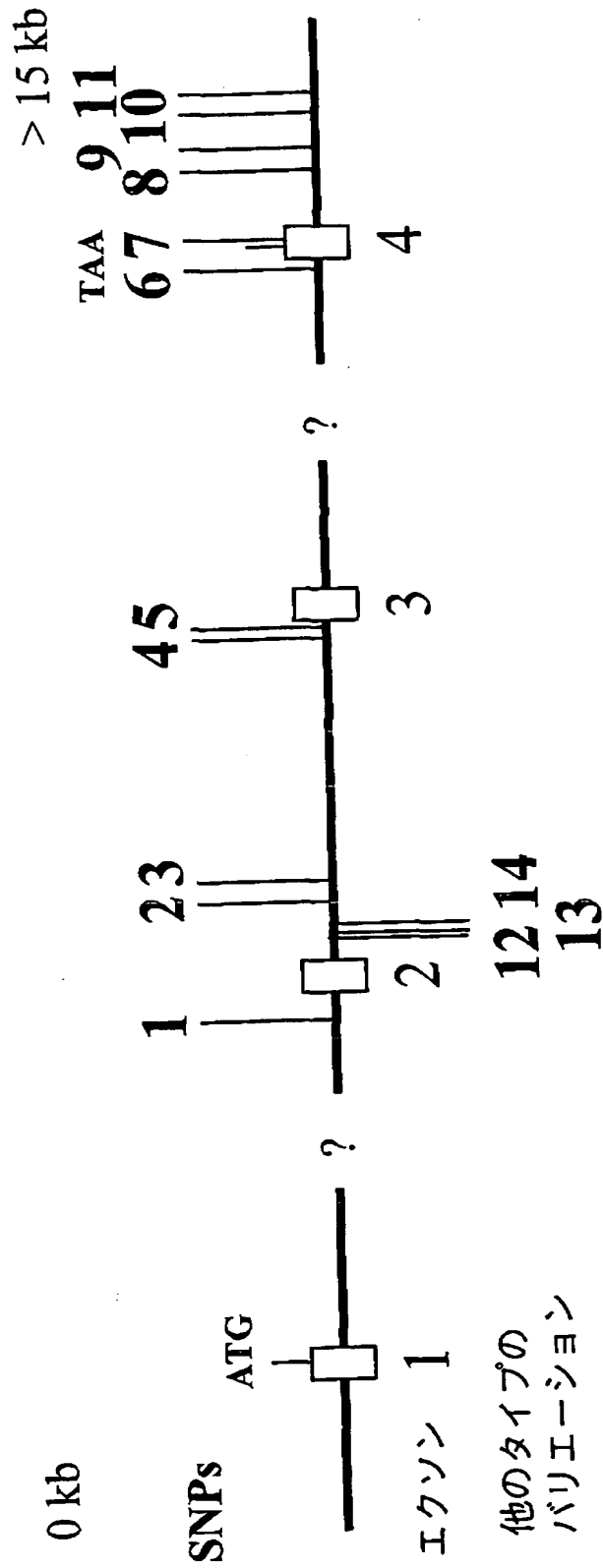
【図 123】



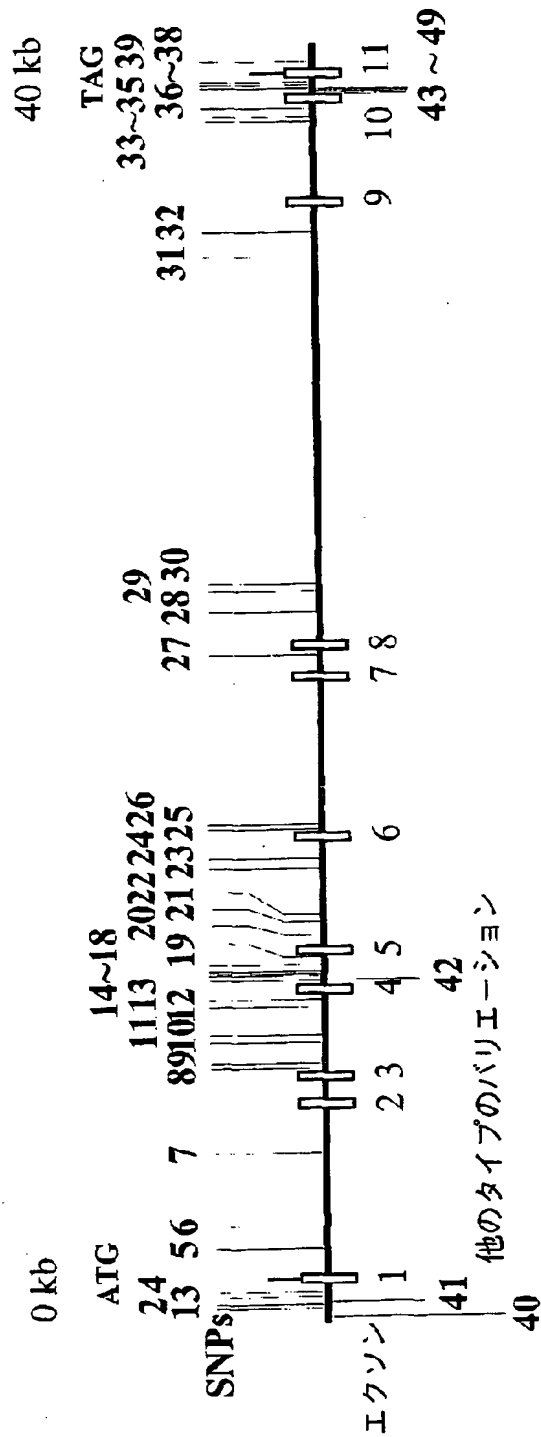
【図 124】



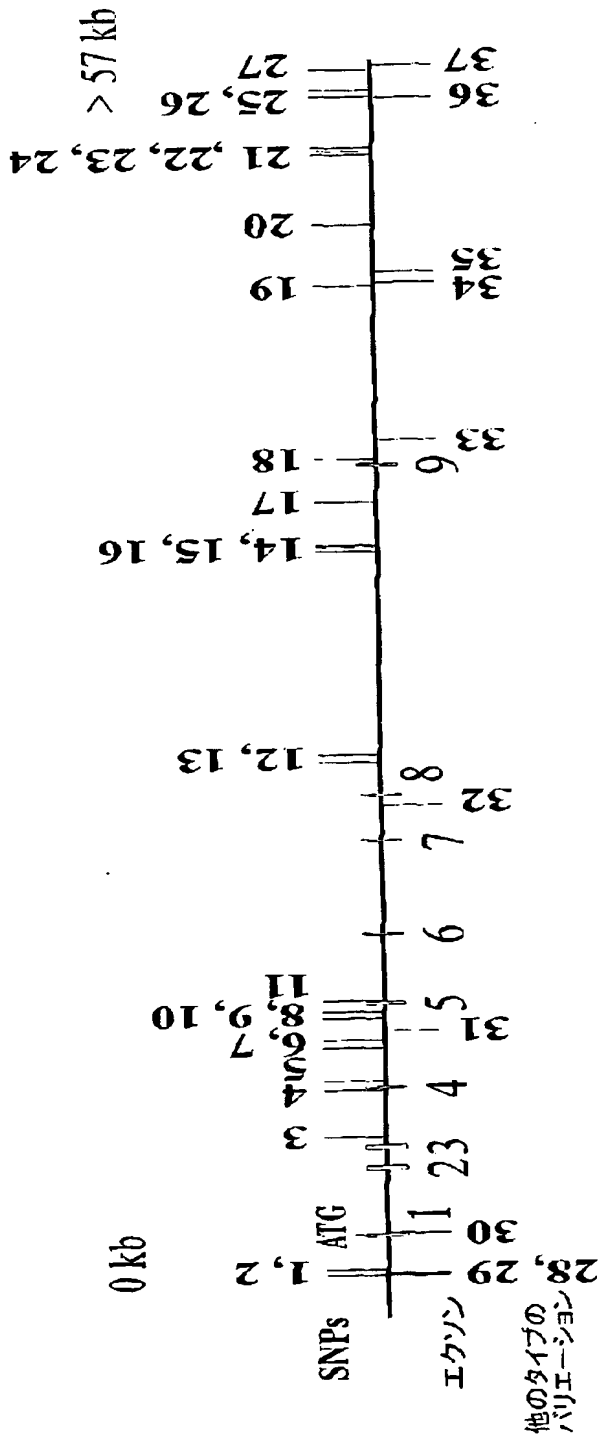
【図 125】



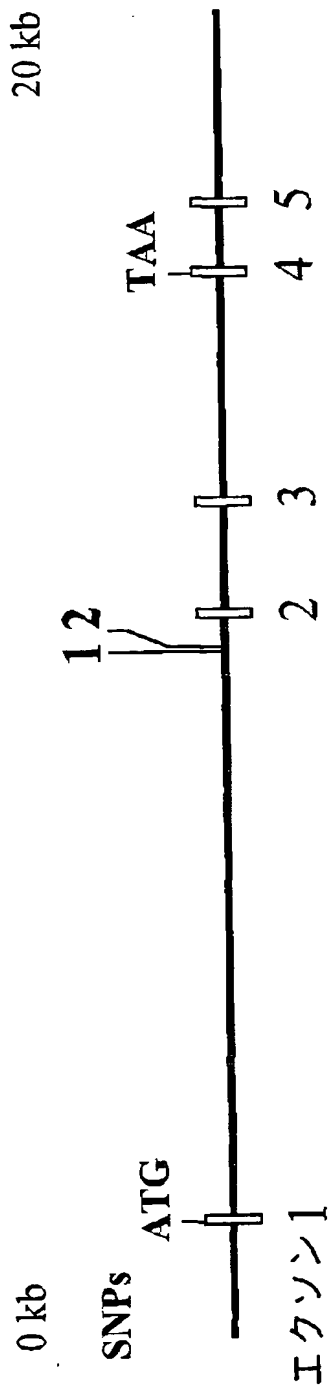
【図 126】



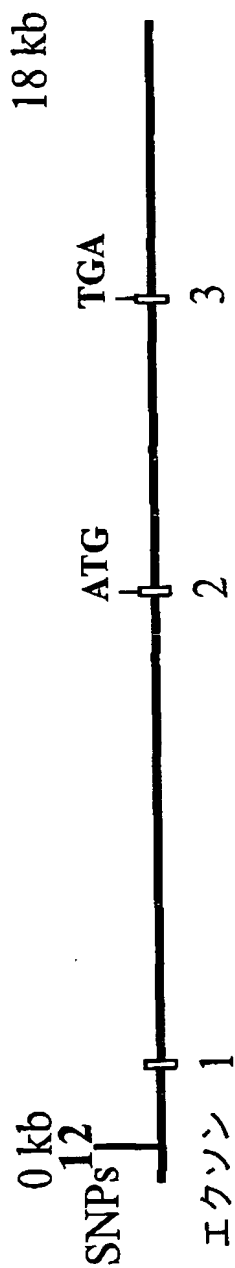
【図 127】



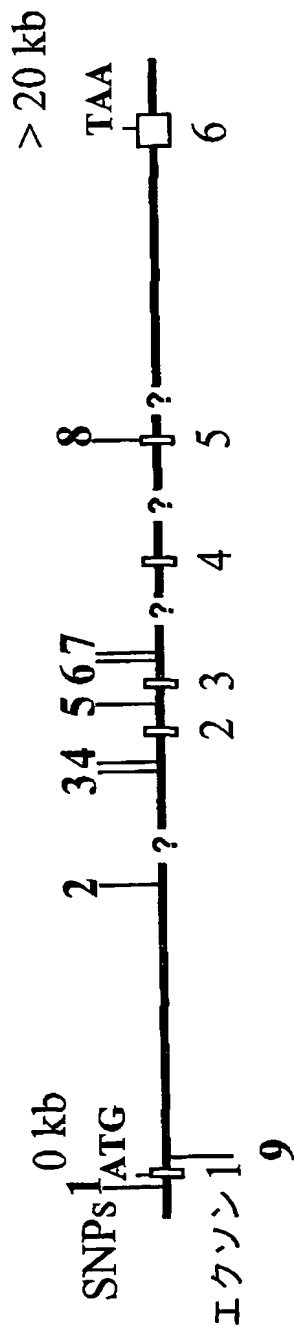
【図 128】



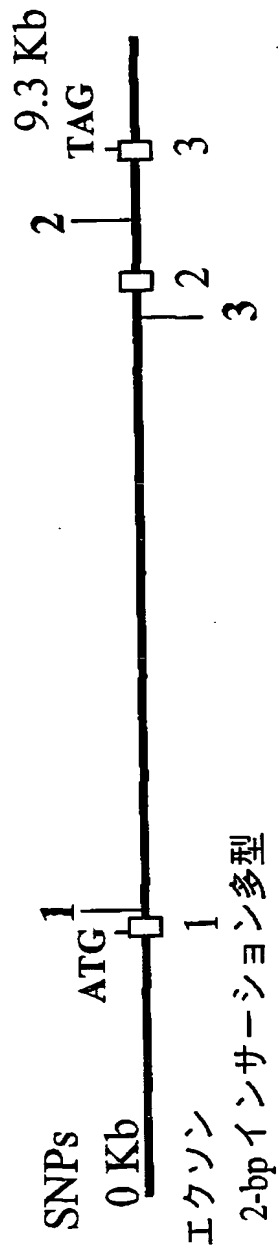
【図 129】



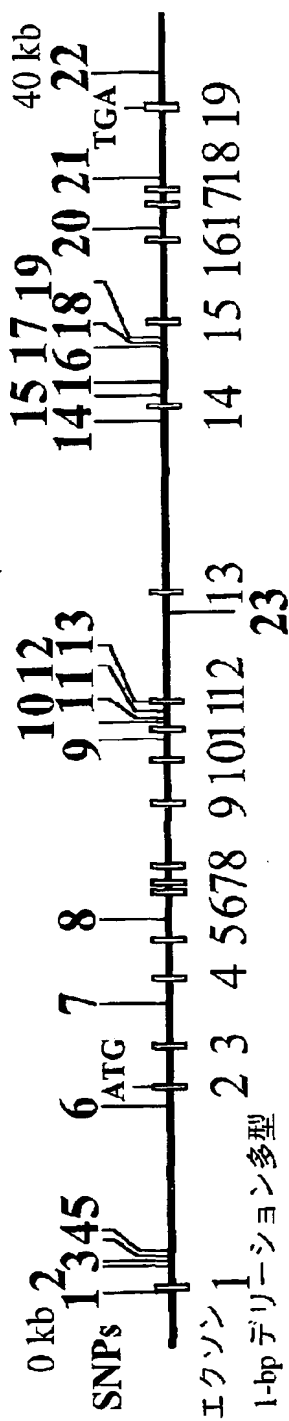
【図 1 3 0】



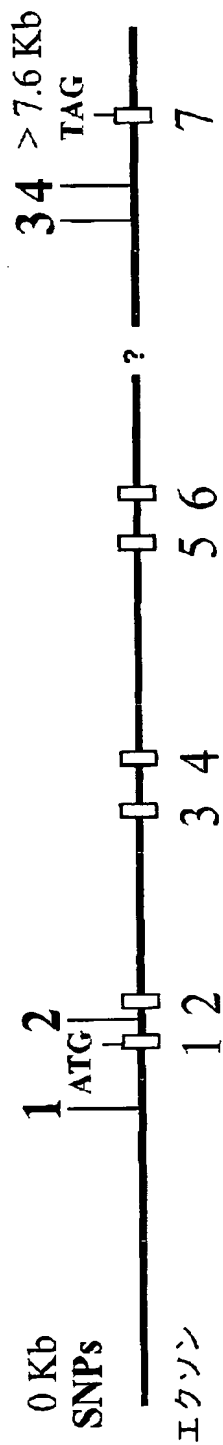
【図 131】



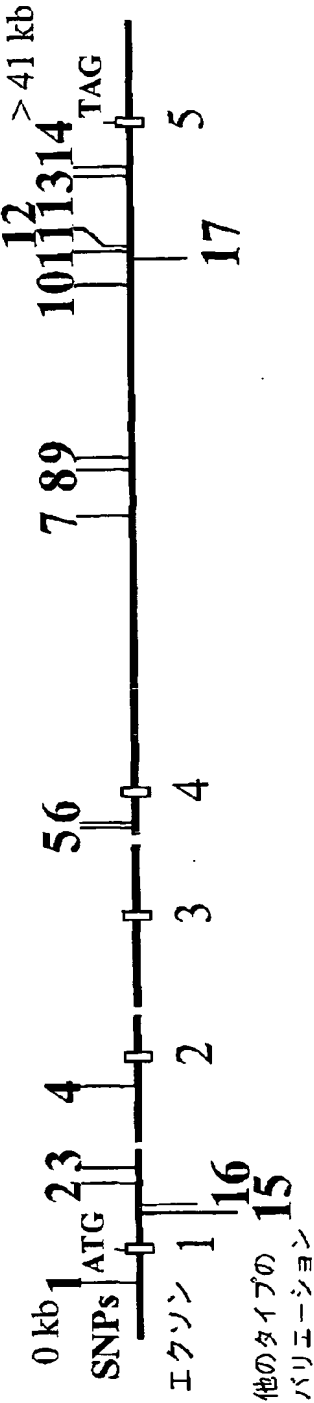
【図 132】



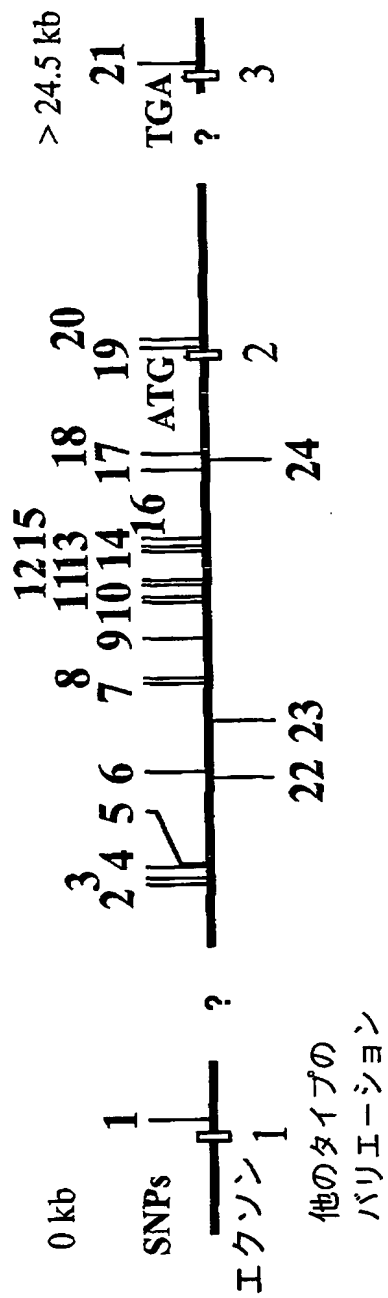
【図 133】



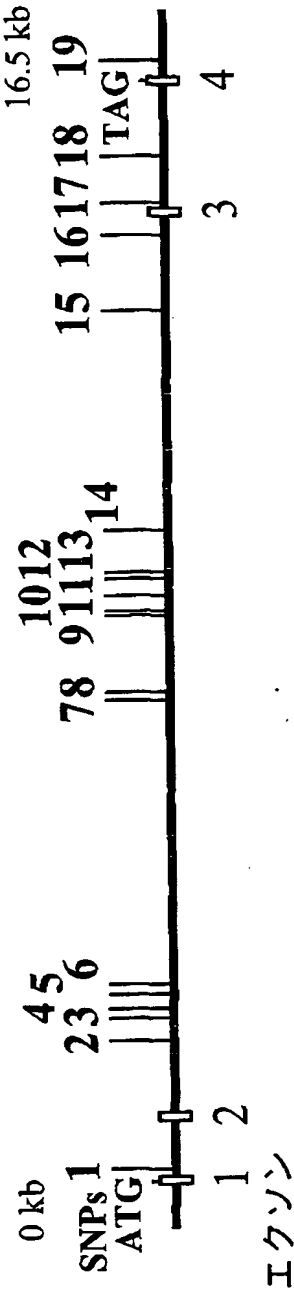
【図 134】



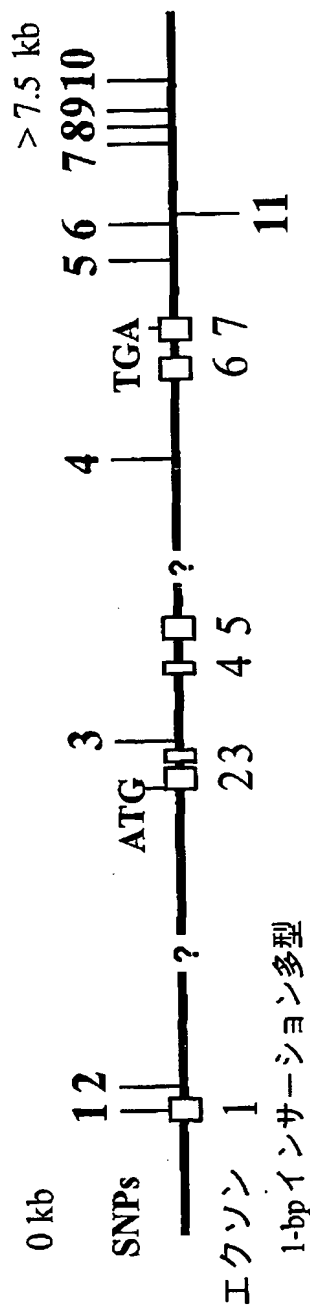
【図 135】



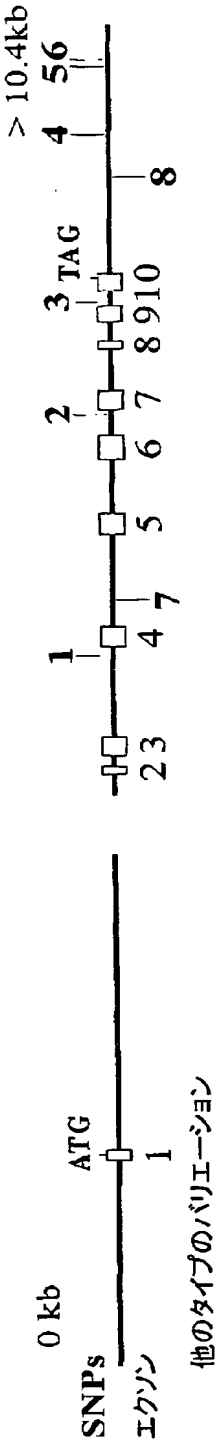
【図 136】



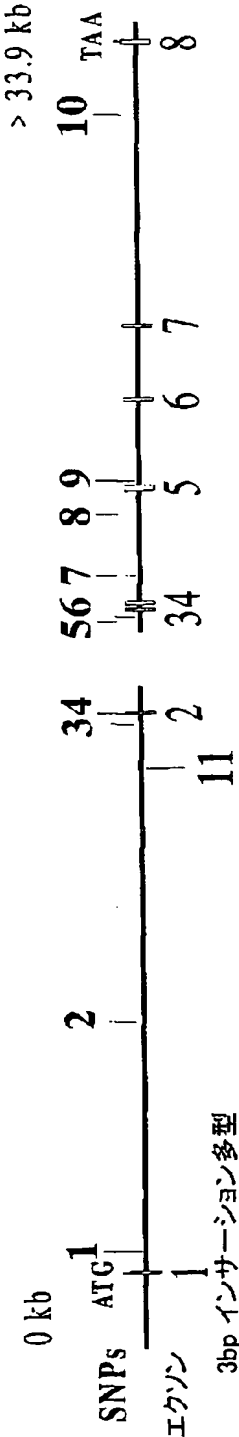
【図 137】



【図 138】



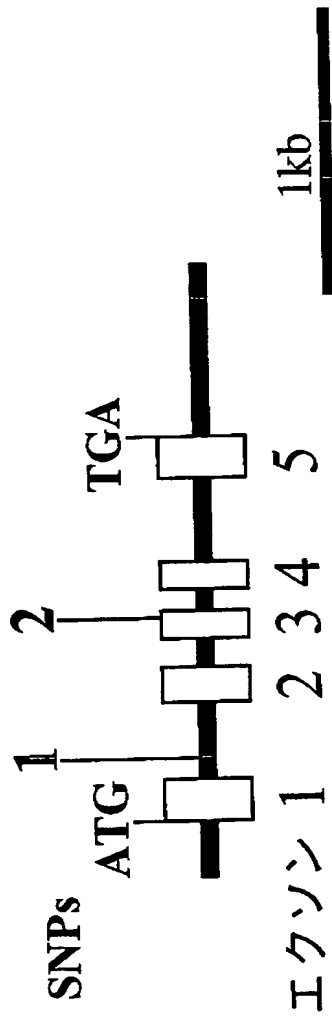
【図 139】



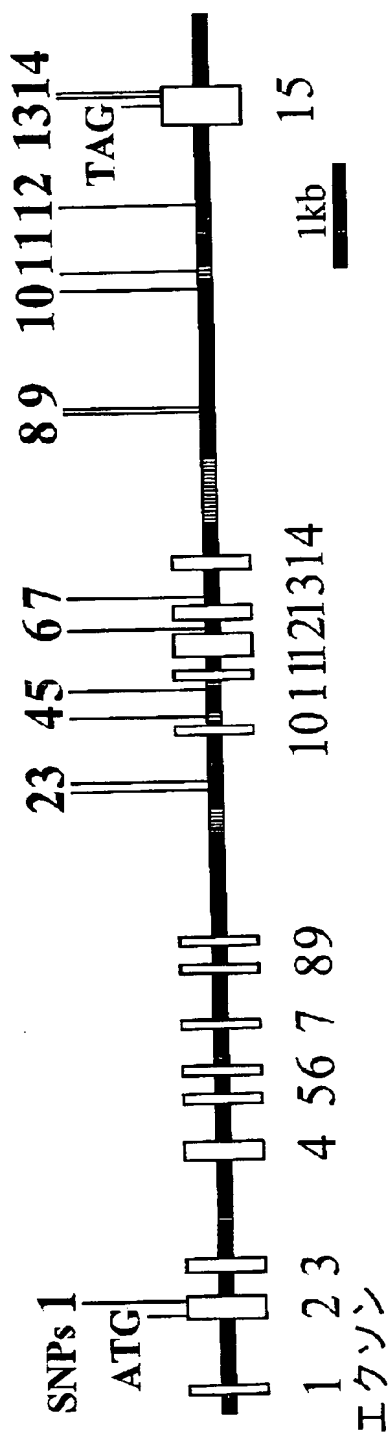
【図 140】



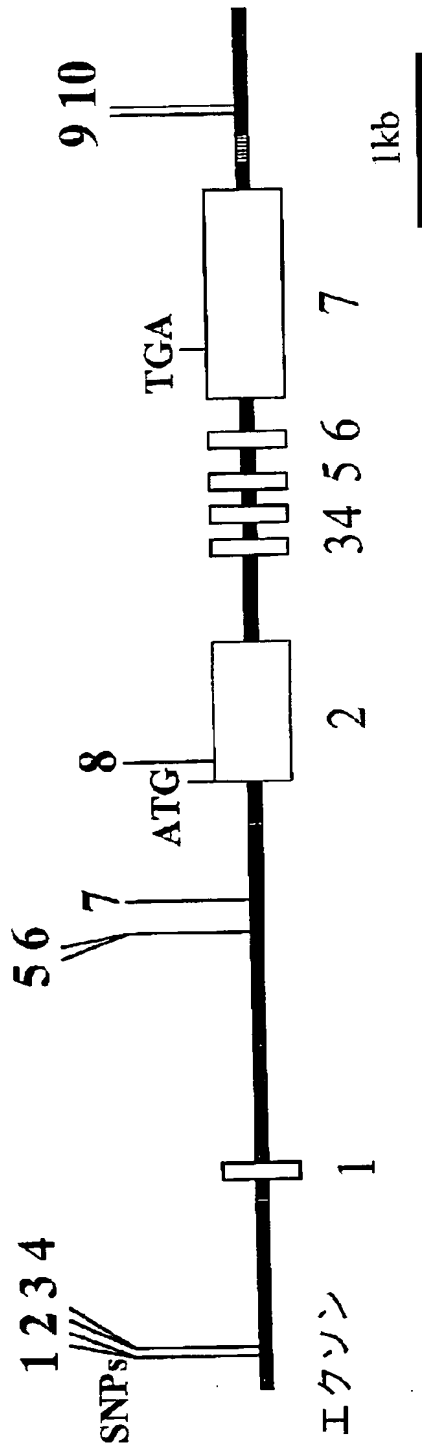
【図 1 4 1】



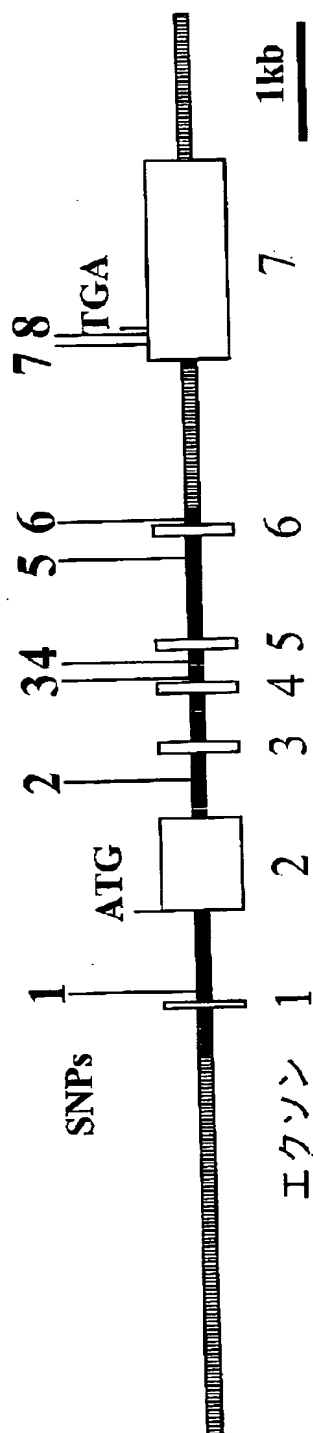
【図 142】



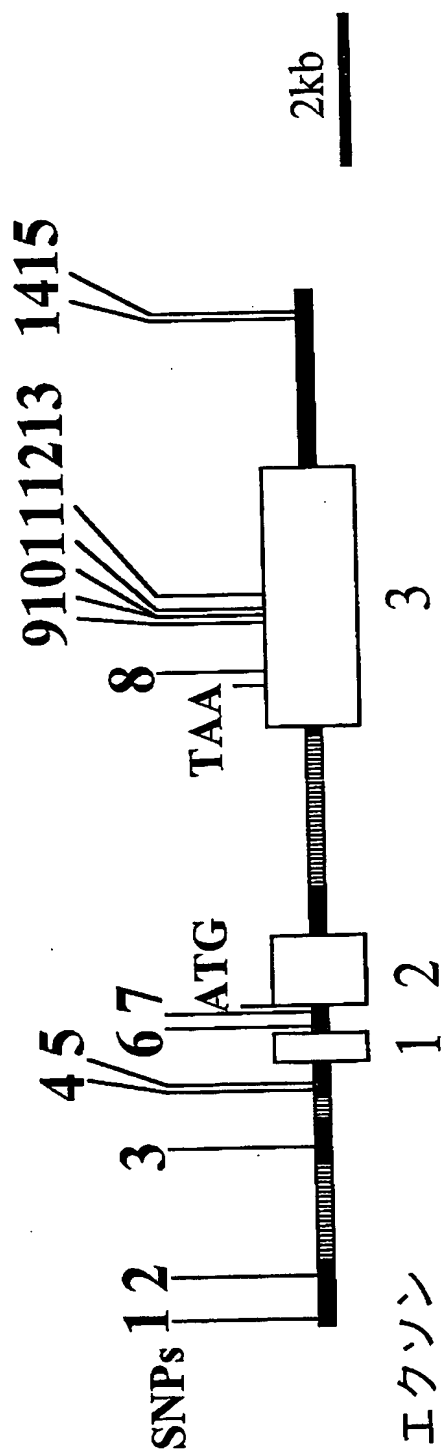
【図 143】



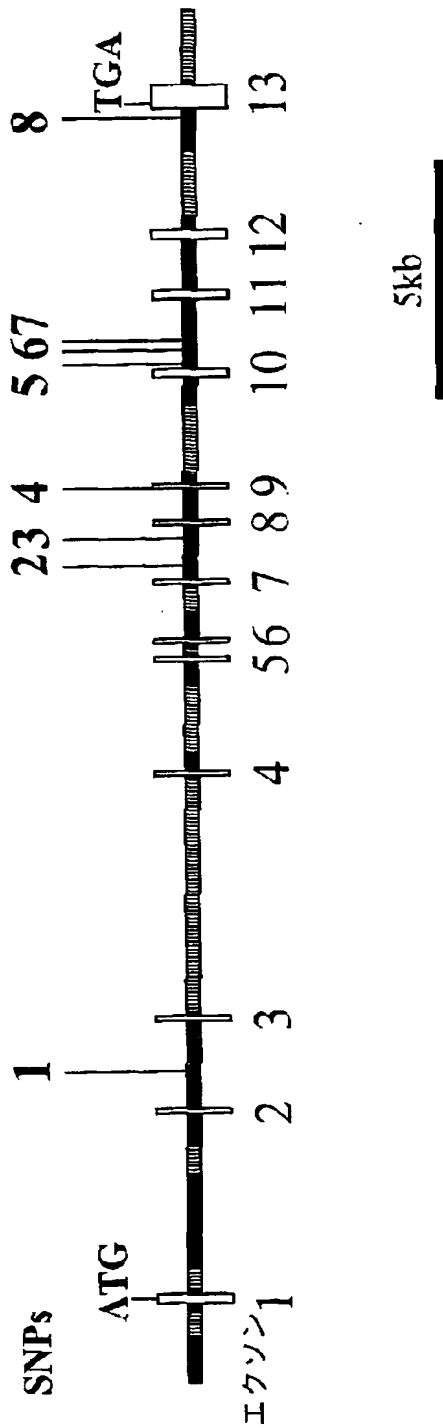
【図 144】



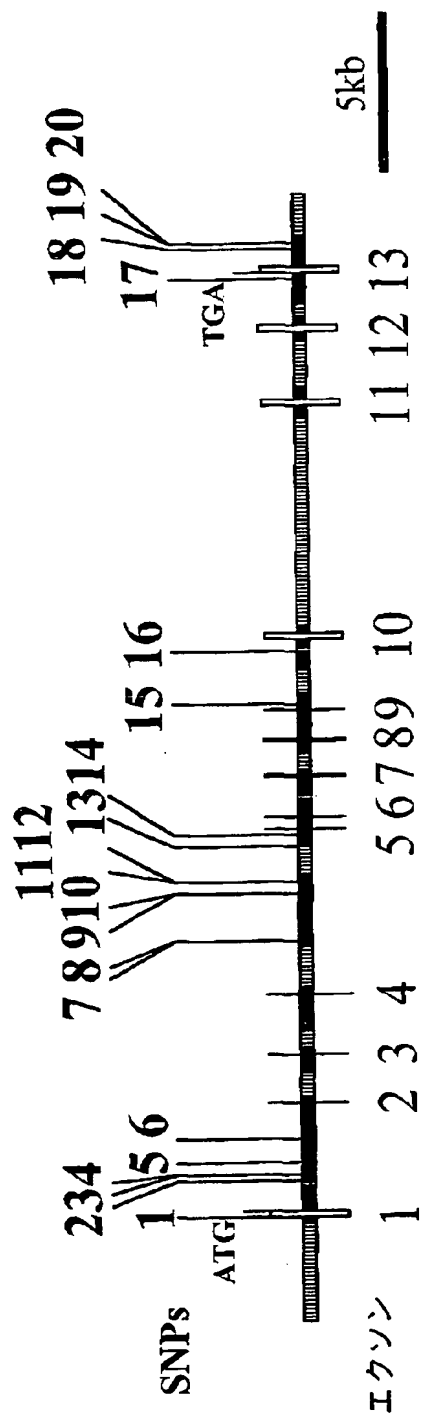
【図 145】



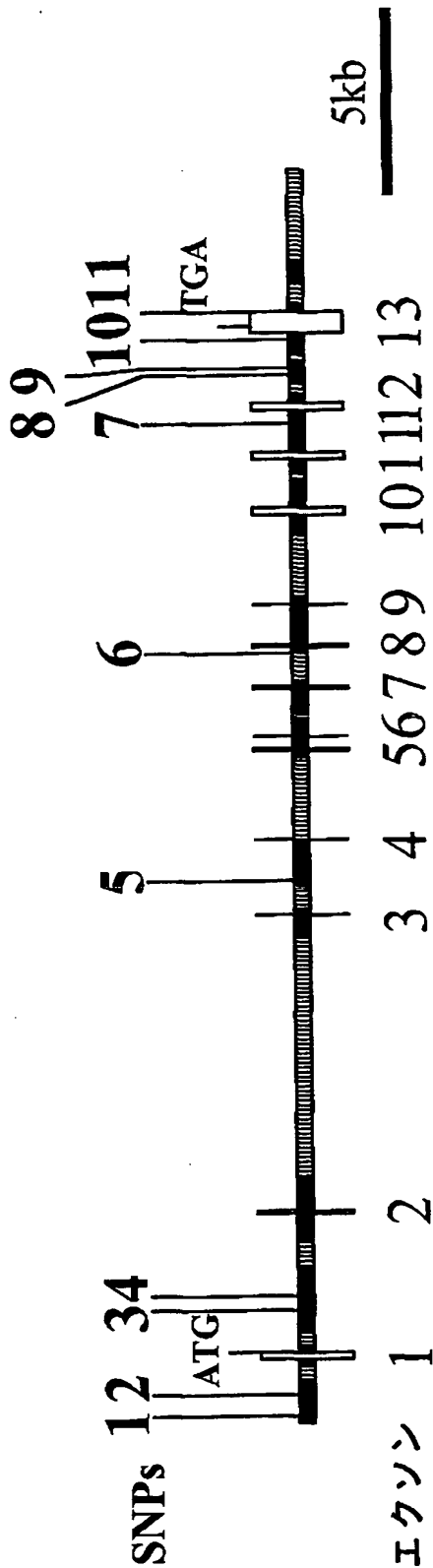
【図 146】



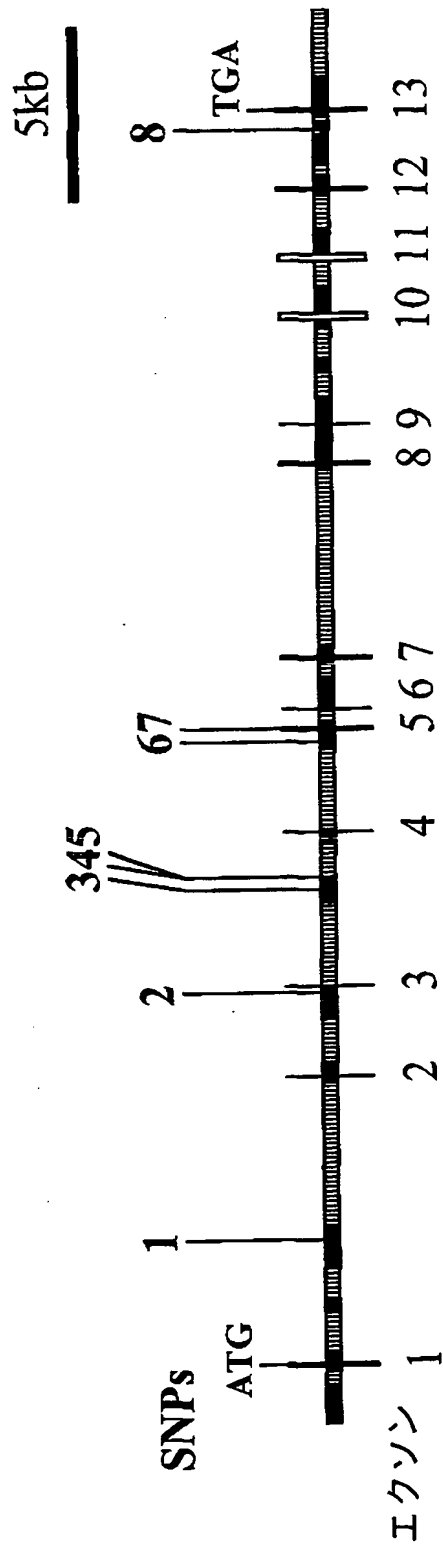
【図 147】



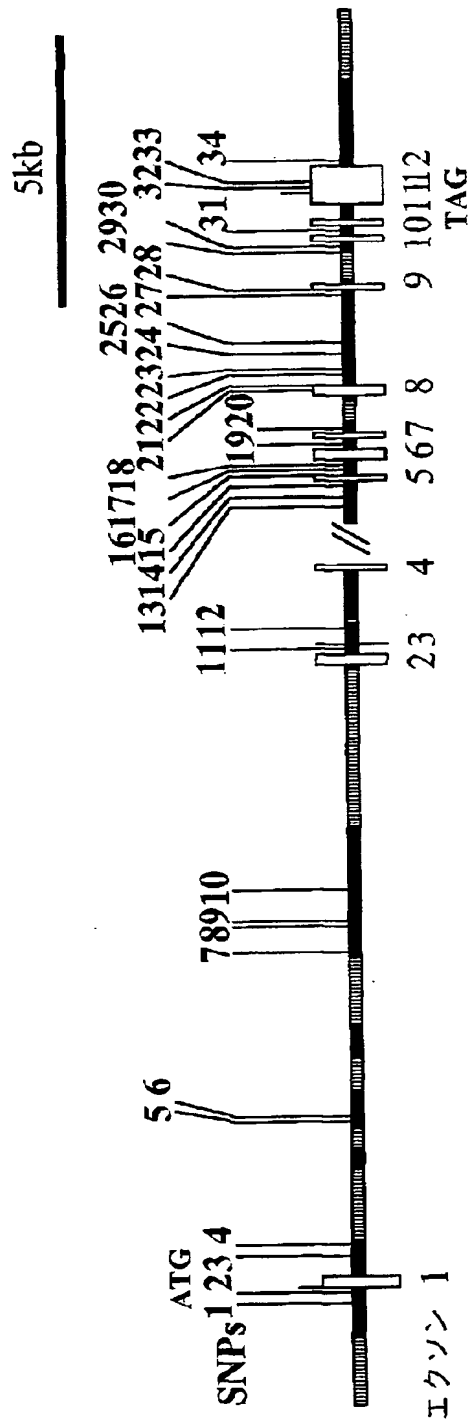
【図 148】



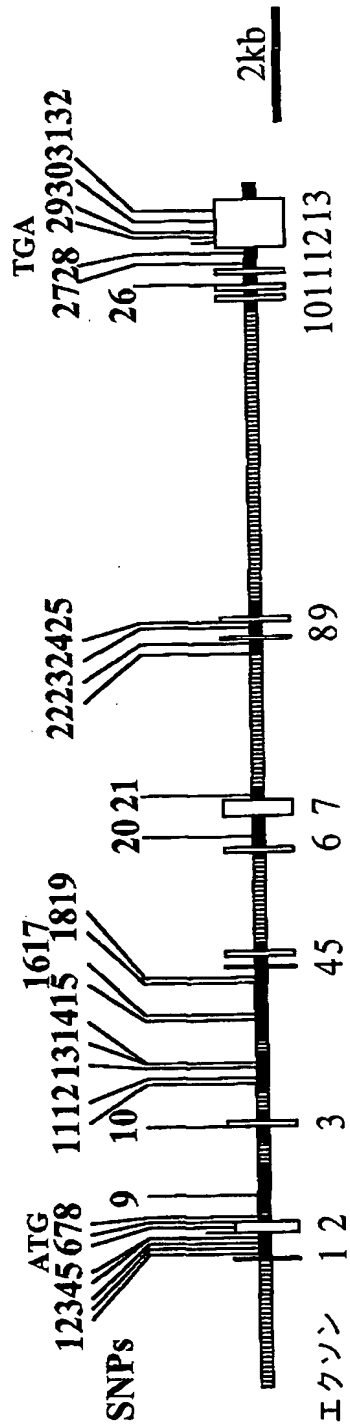
【図 149】



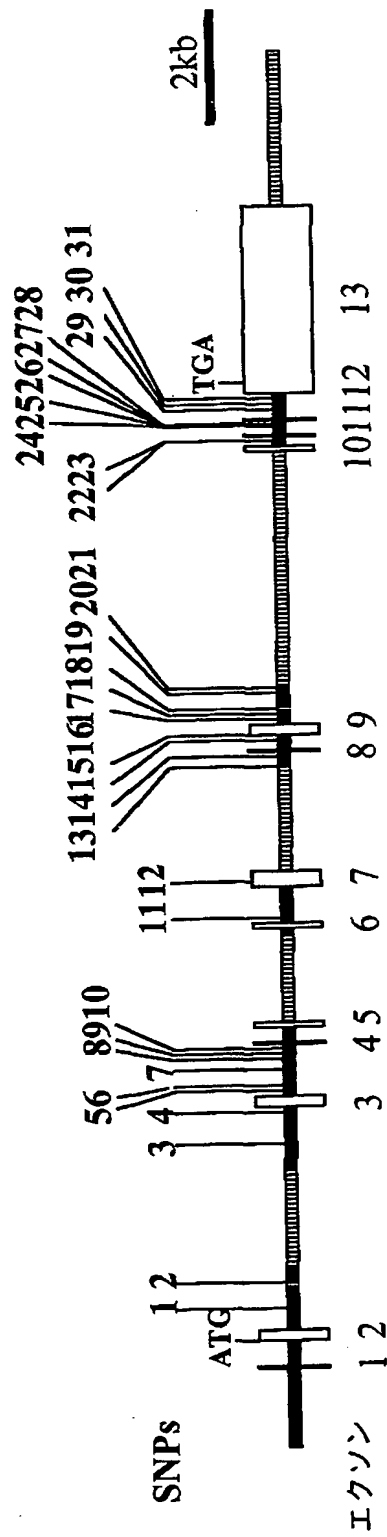
【図 150】



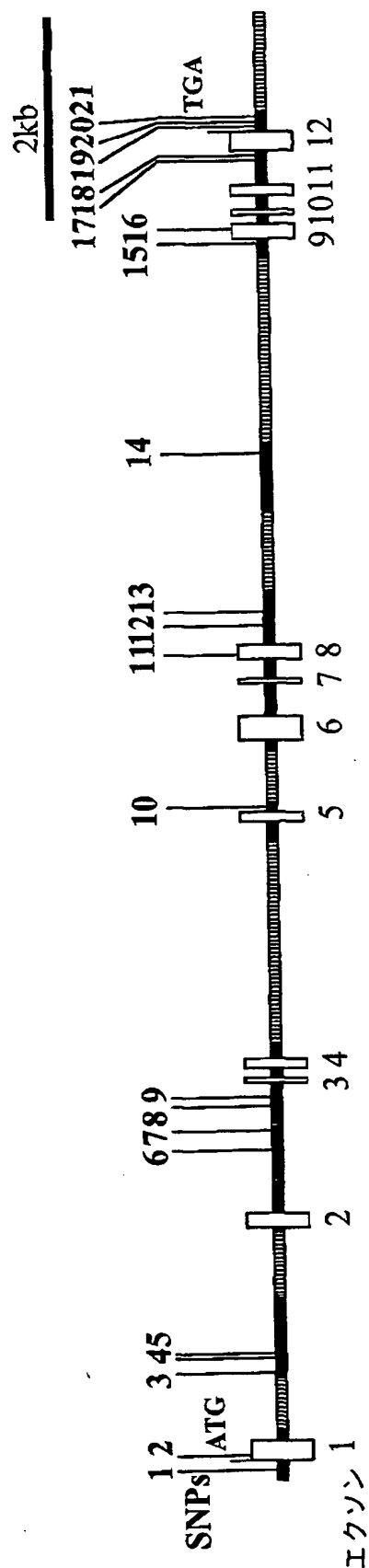
【図 151】



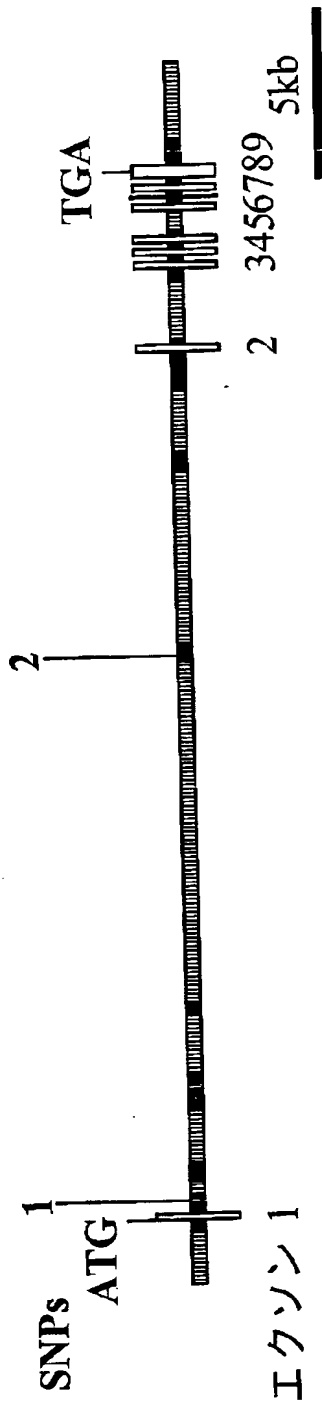
【図 152】



【図 153】



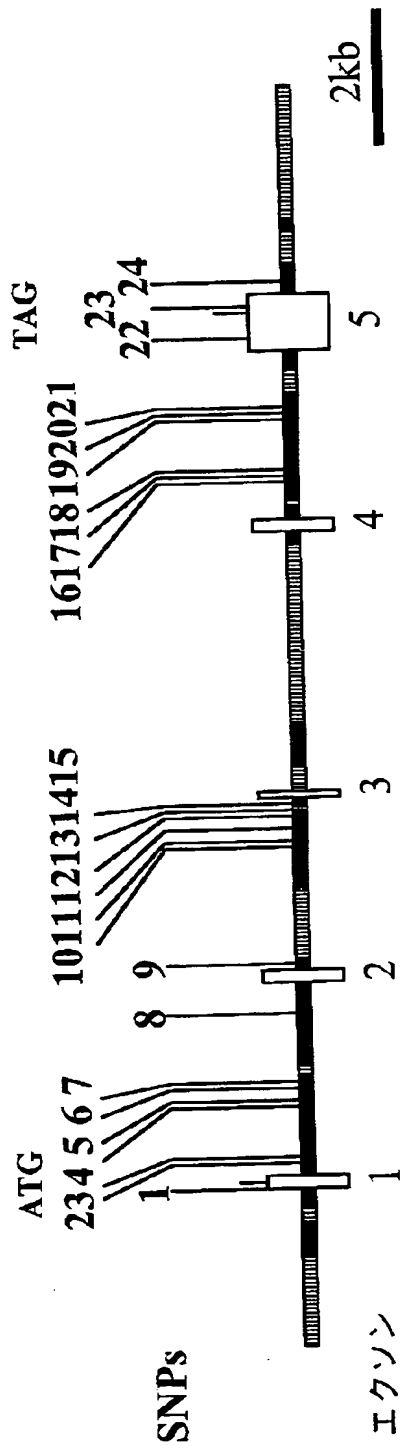
【図 154】



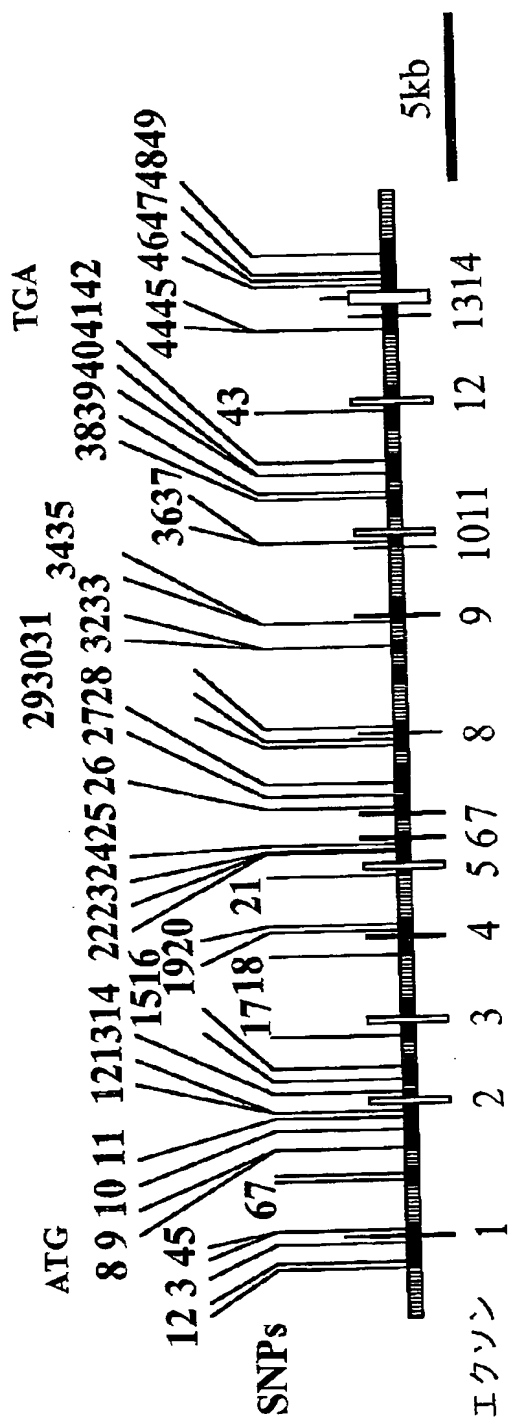
【図 155】



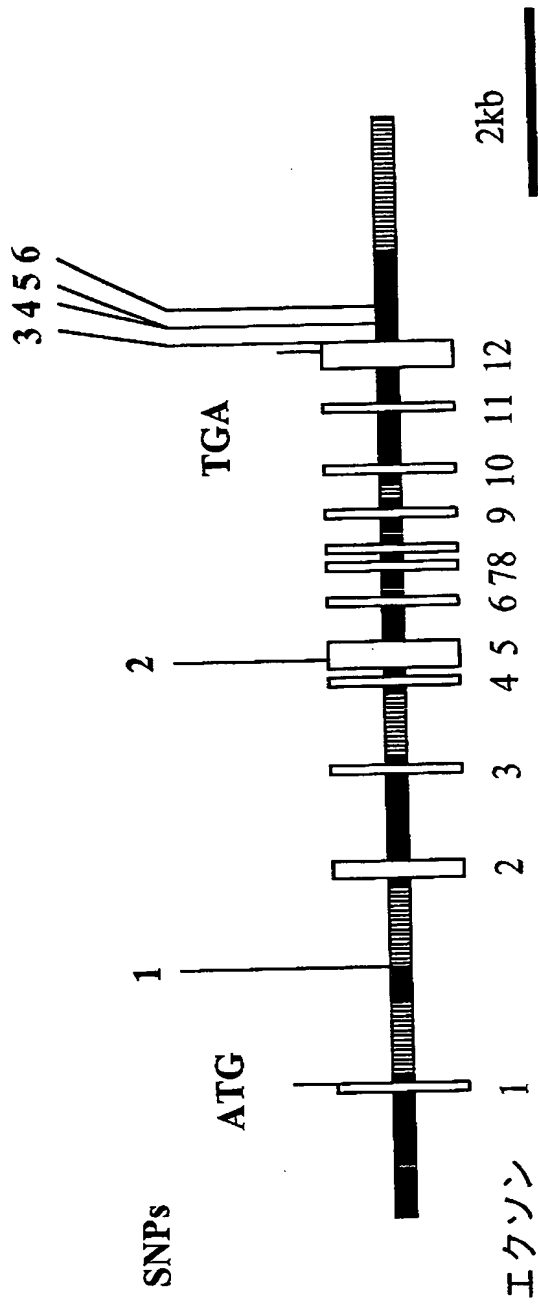
【図 156】



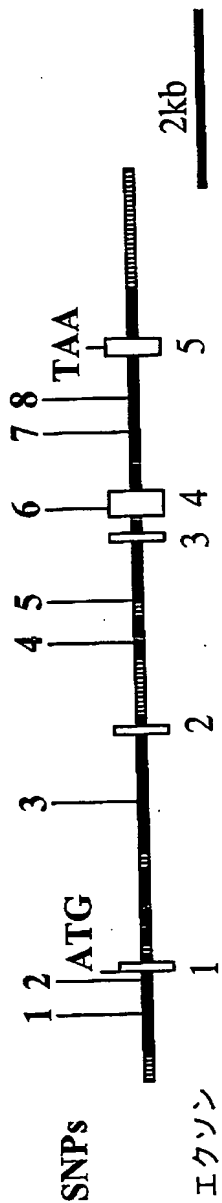
【図 157】



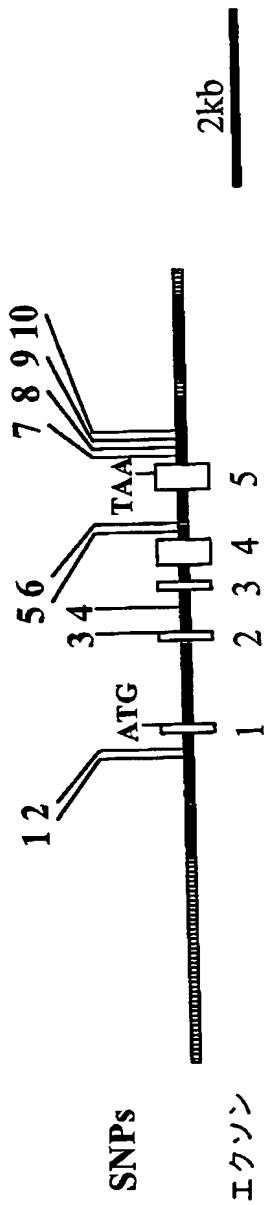
【図 158】



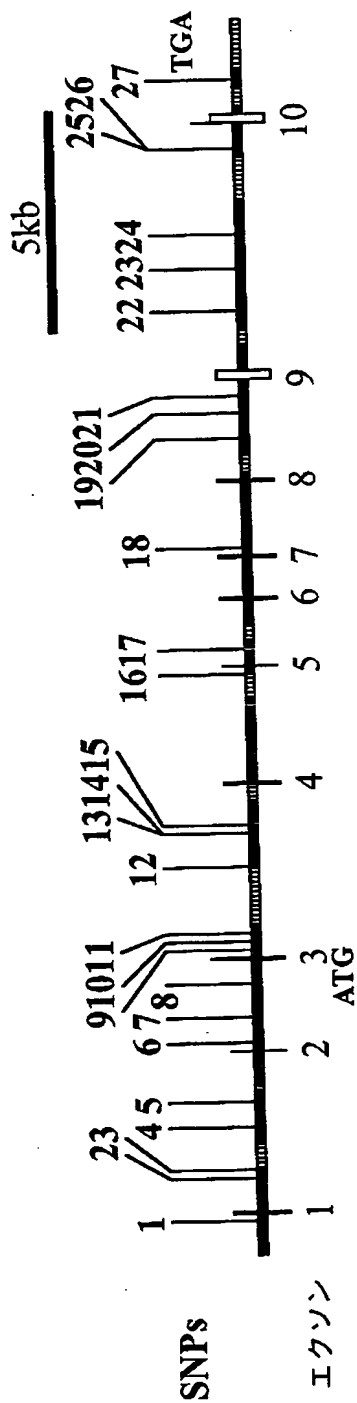
【図 159】



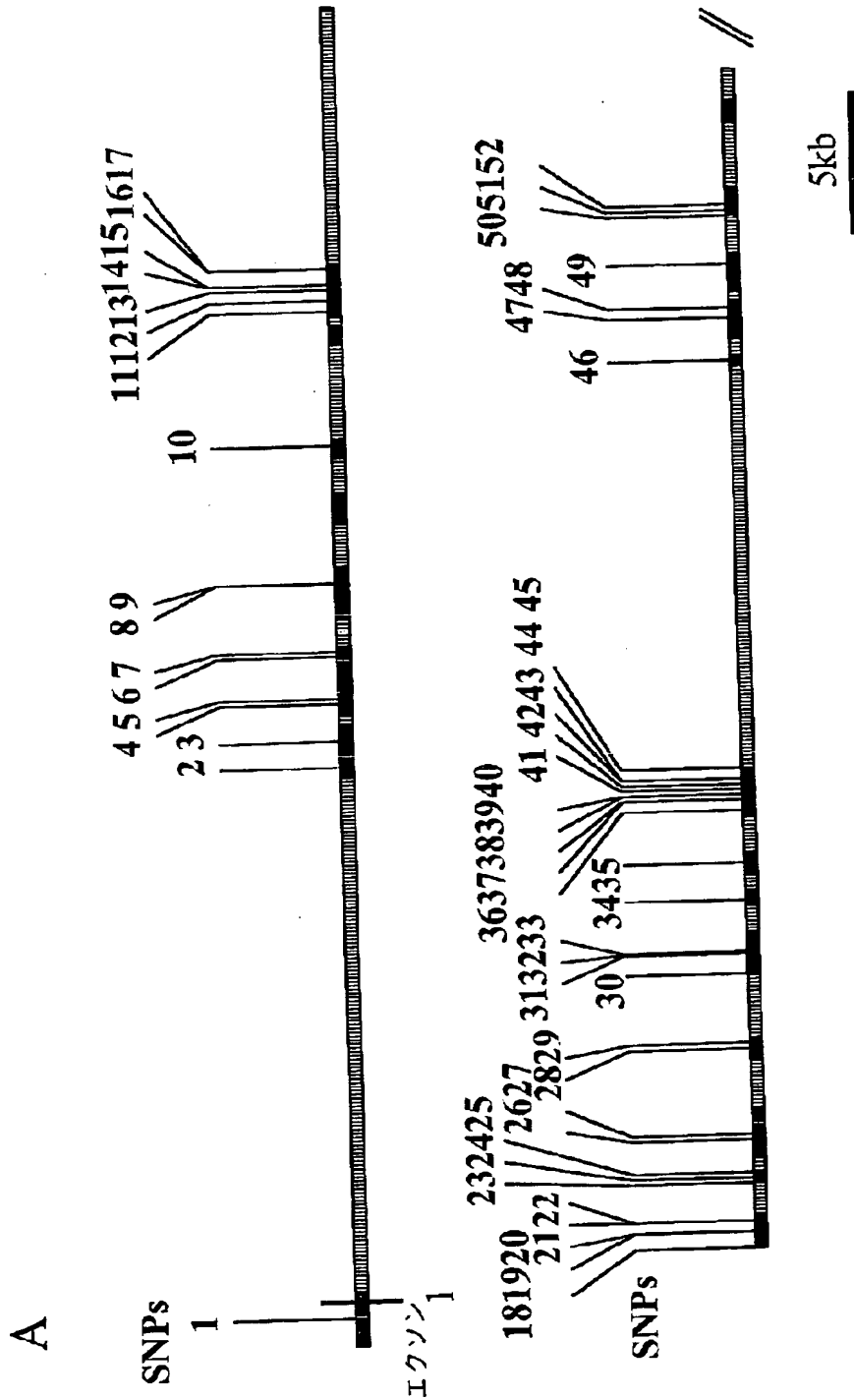
【図 160】



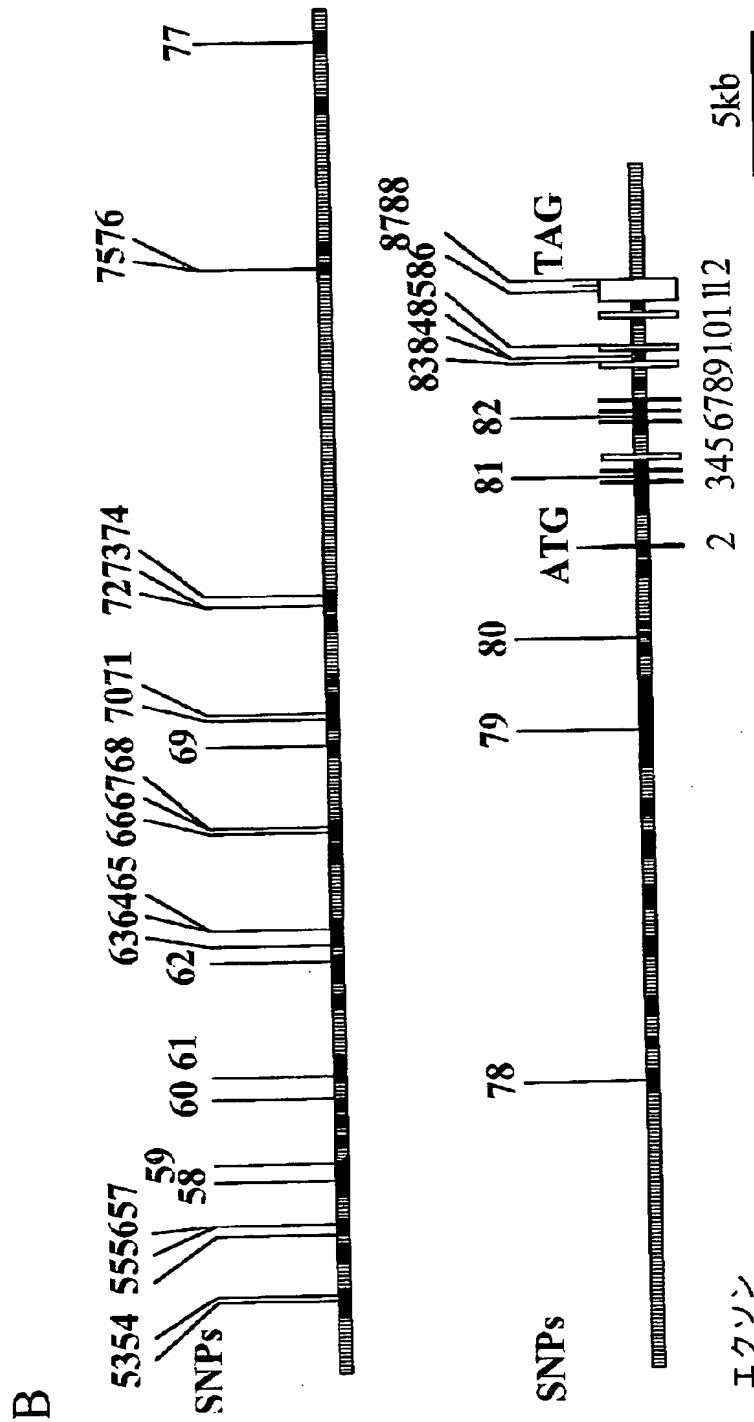
【図 161】



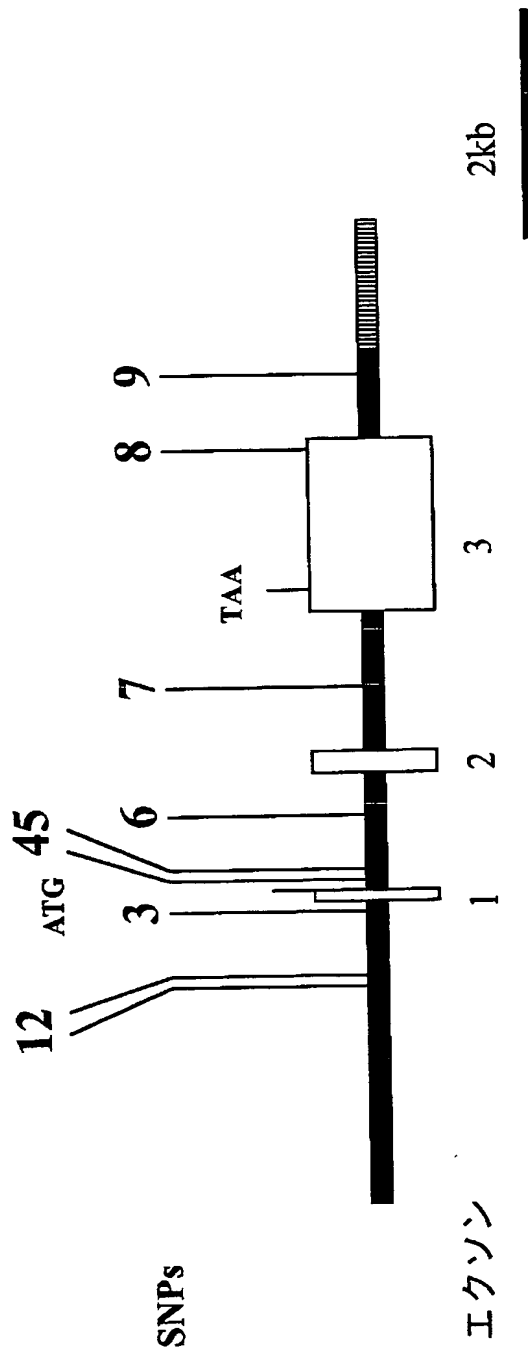
【図 162 A】



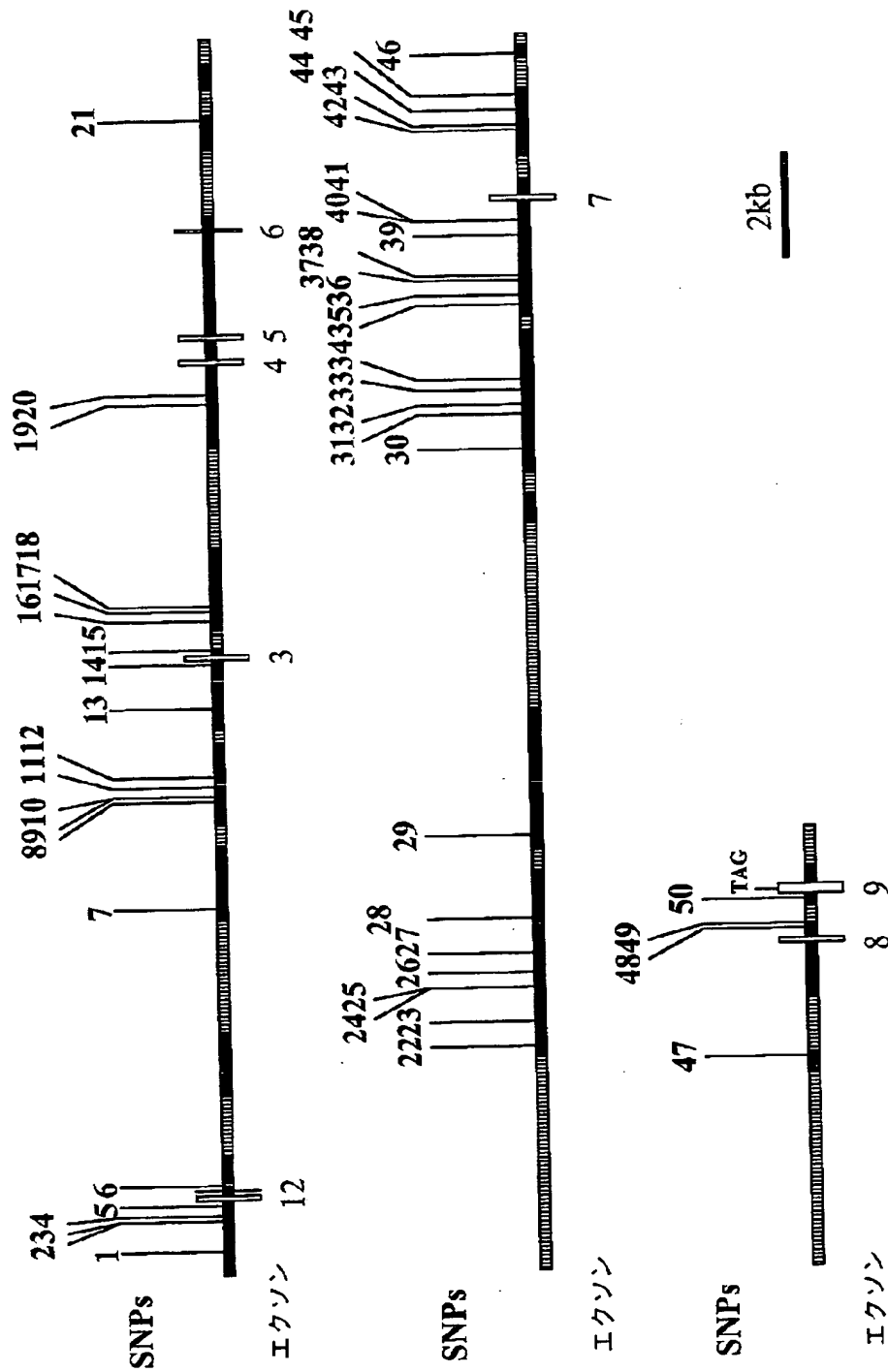
【図 162B】



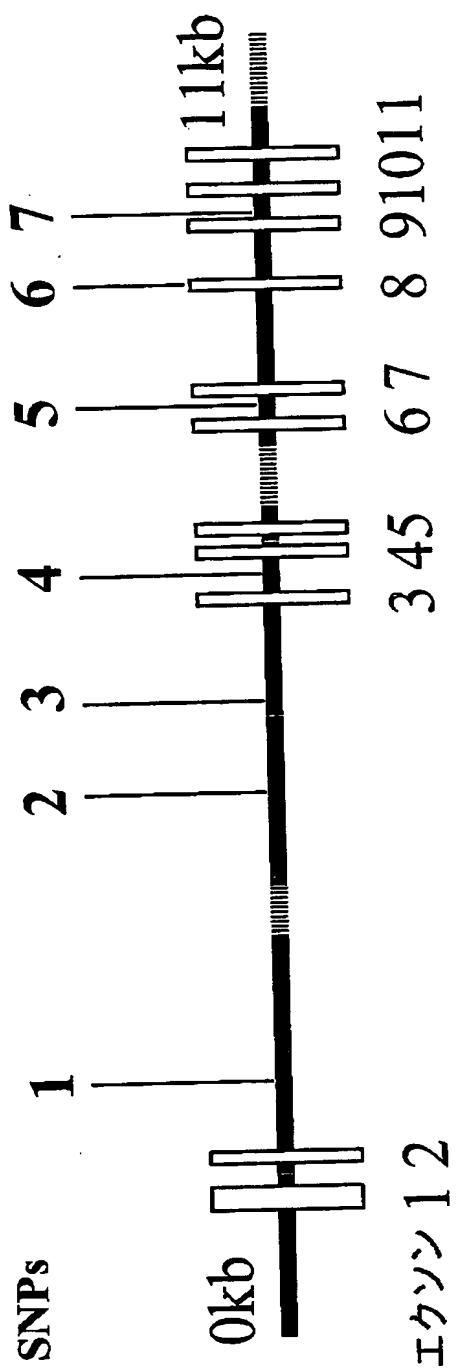
【図 163】



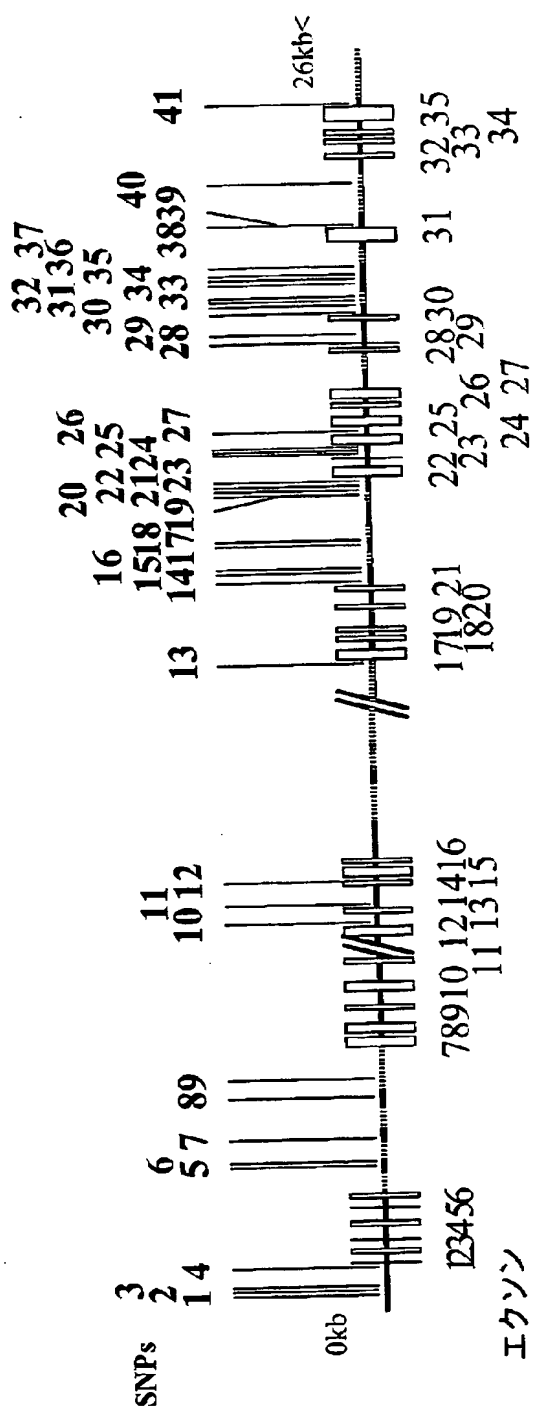
【図 164】



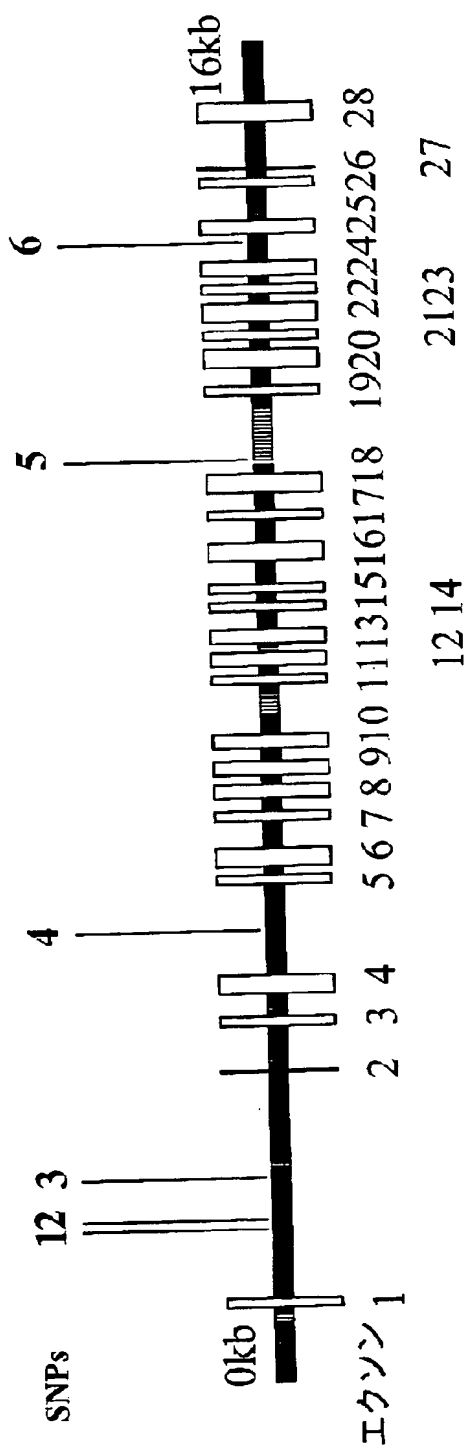
【図 165】



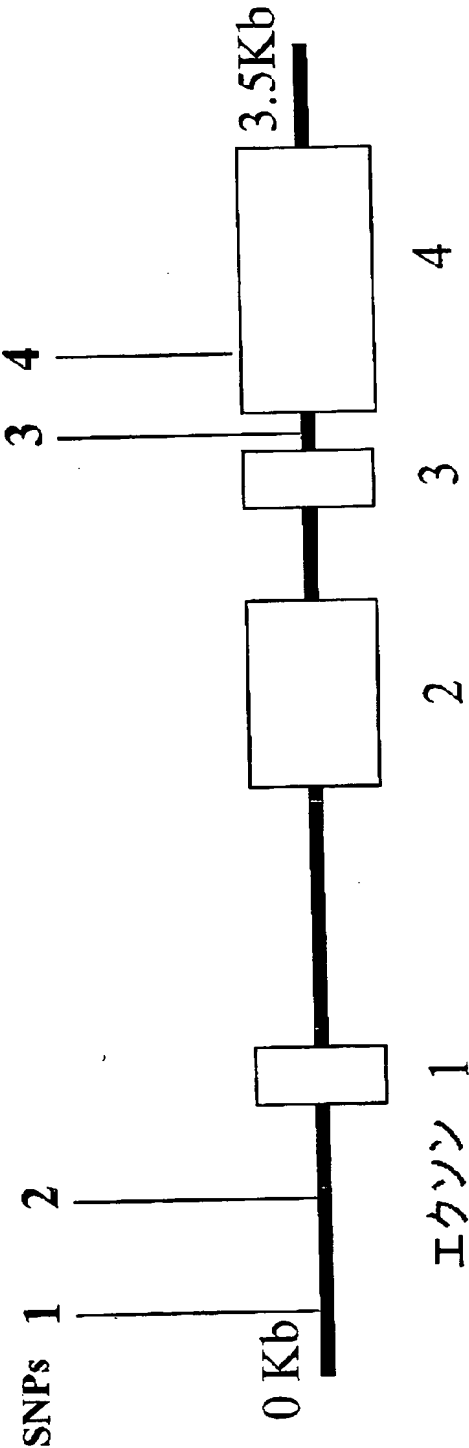
【図 166】



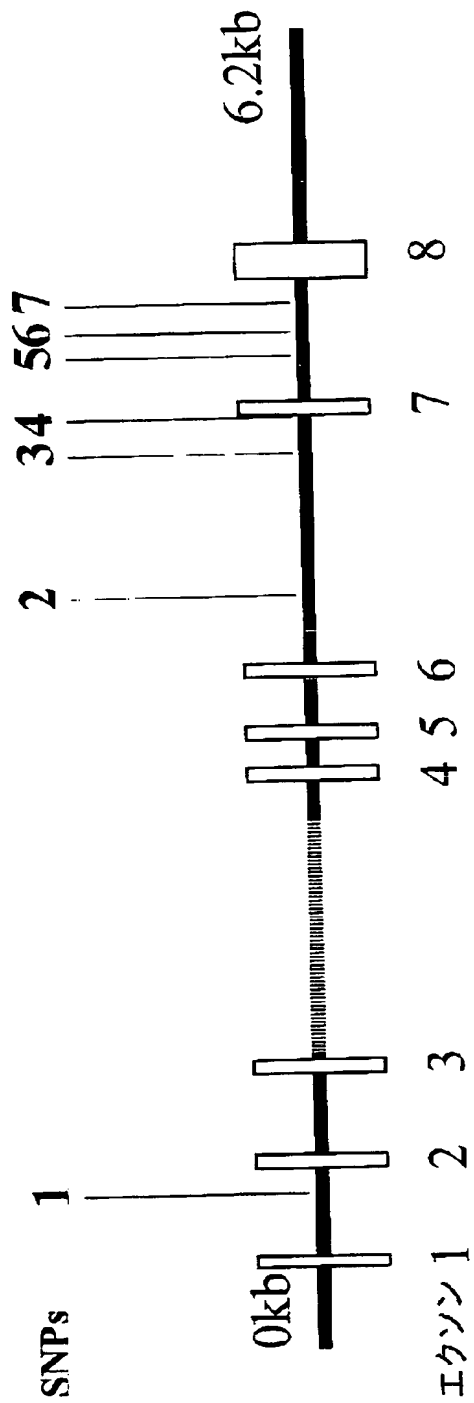
【図 167】



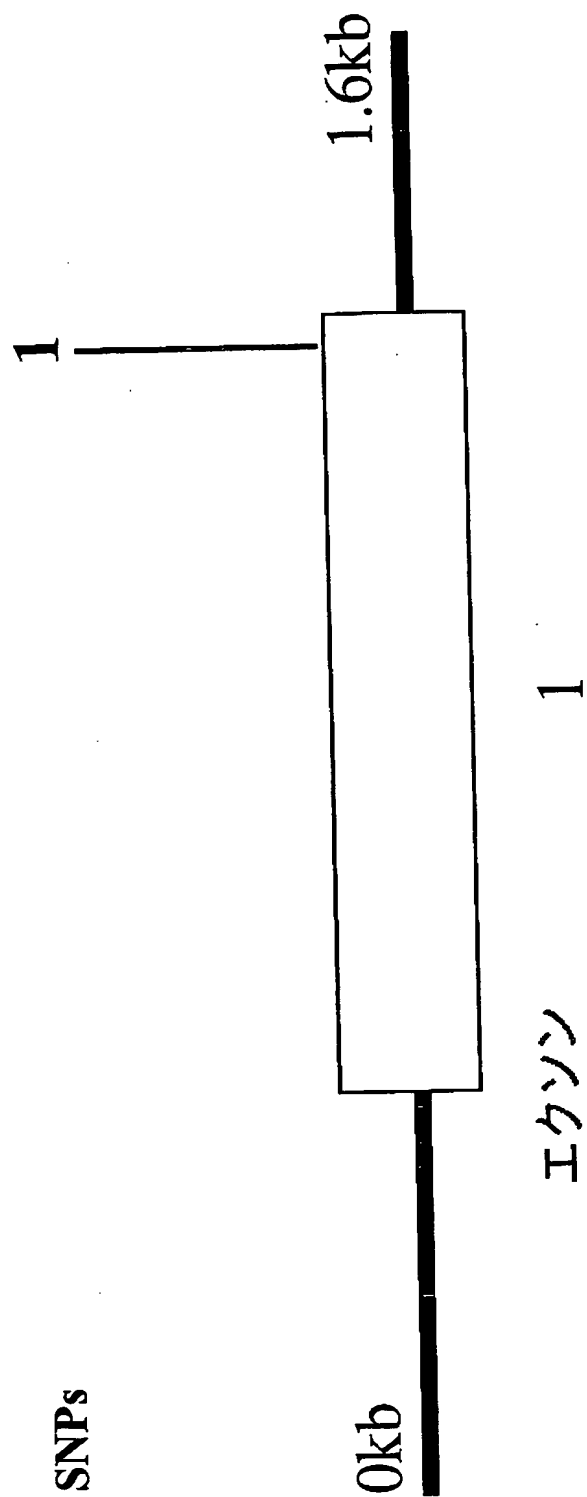
【図 168】



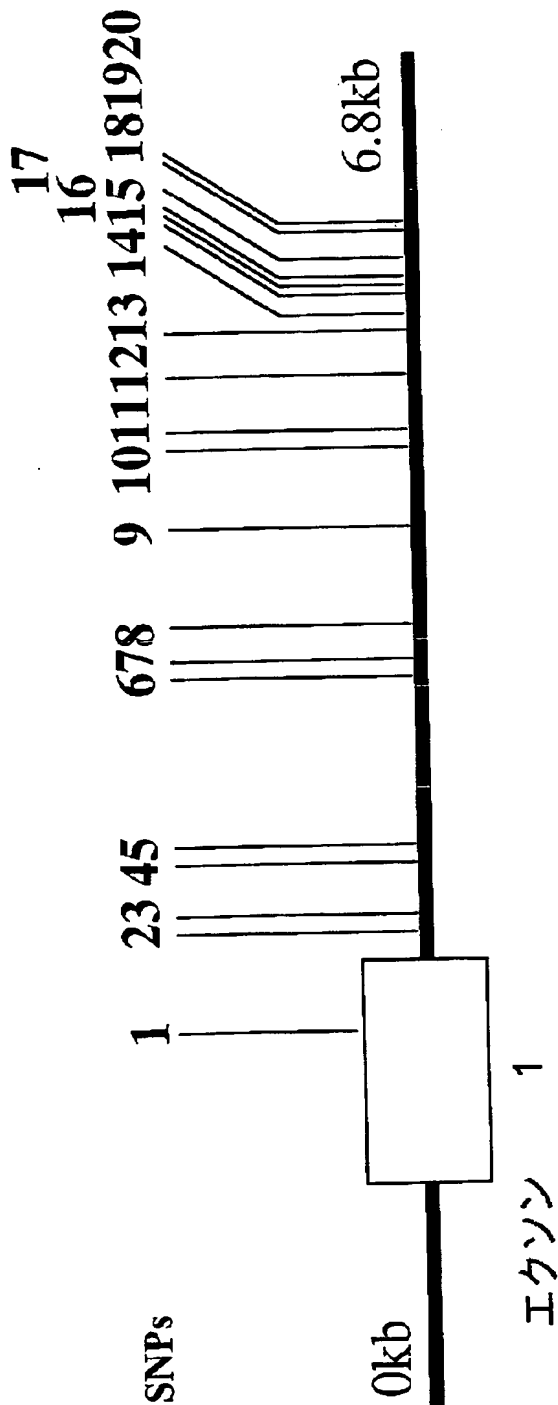
【図 169】



【図 1 7 0】



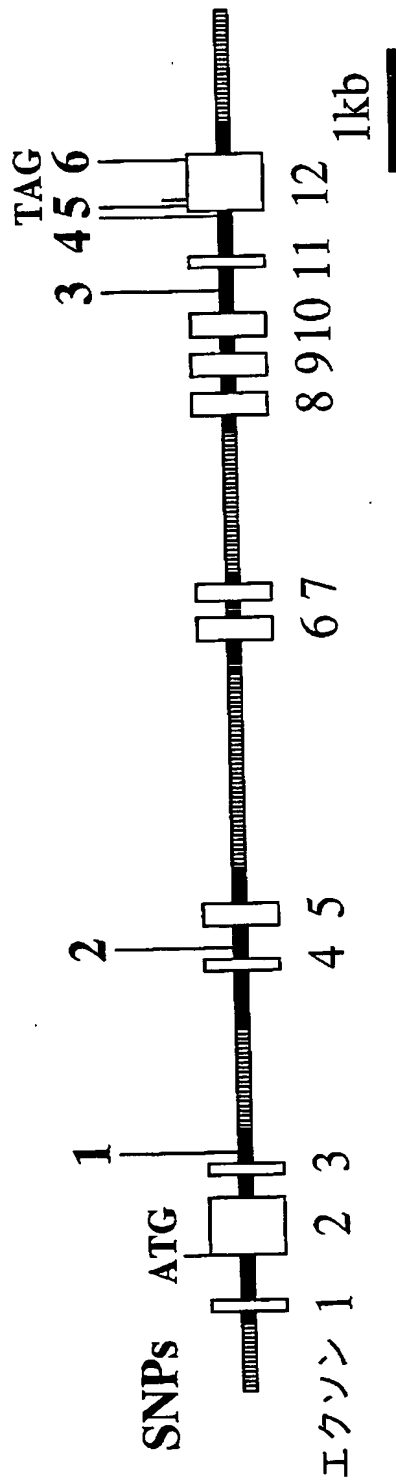
【図 171】



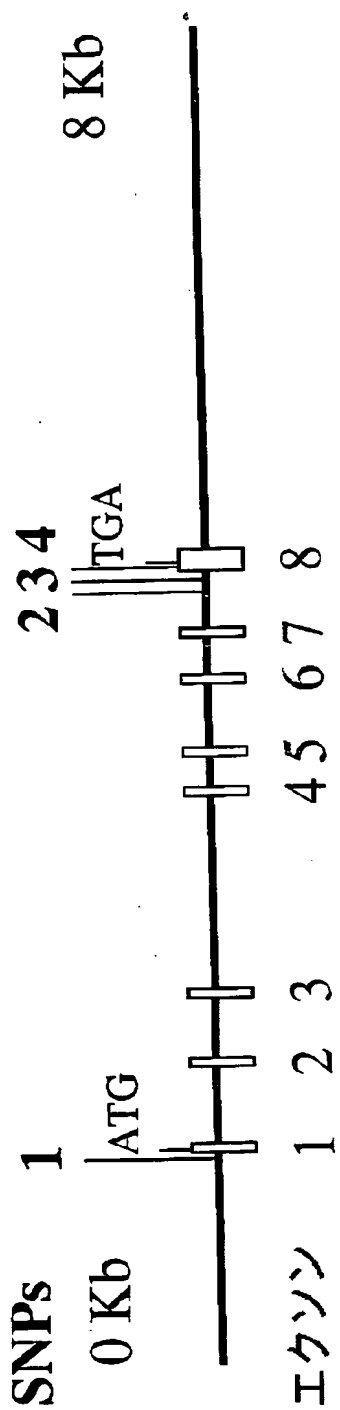
【図 172】



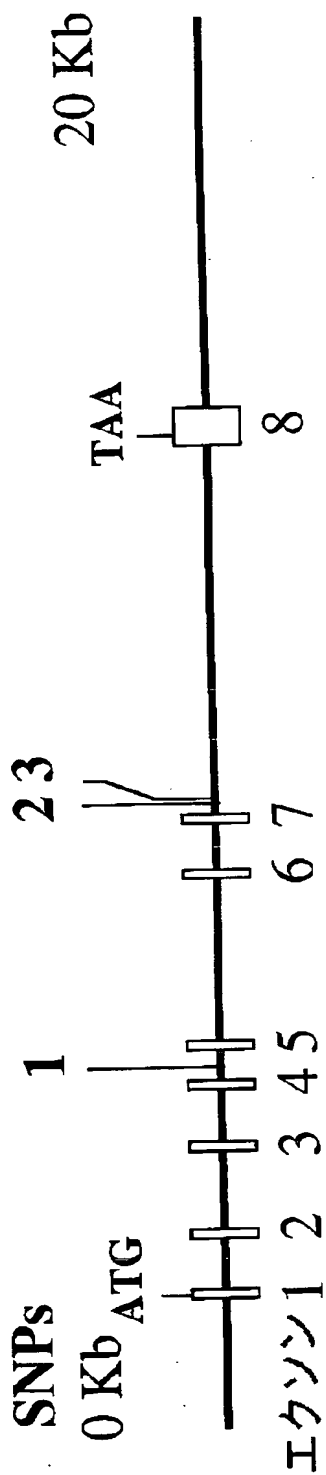
【図 173】



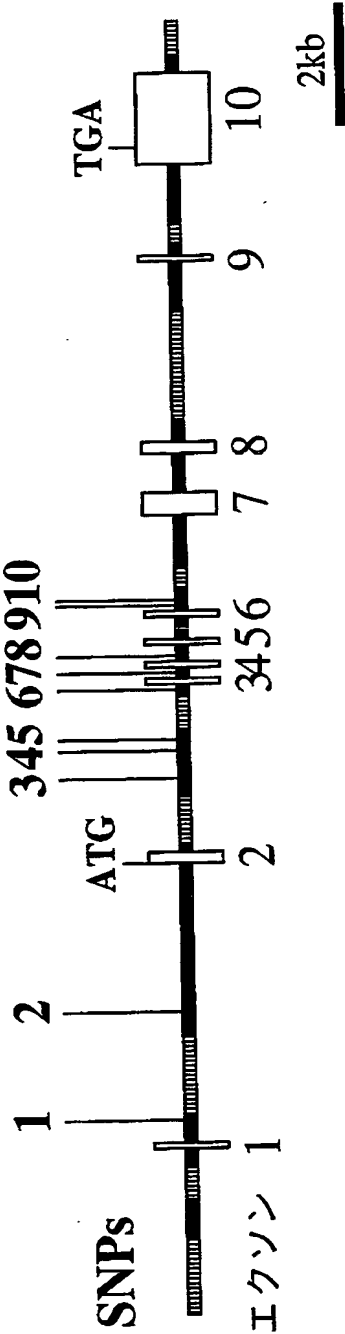
【図 1 7 4】



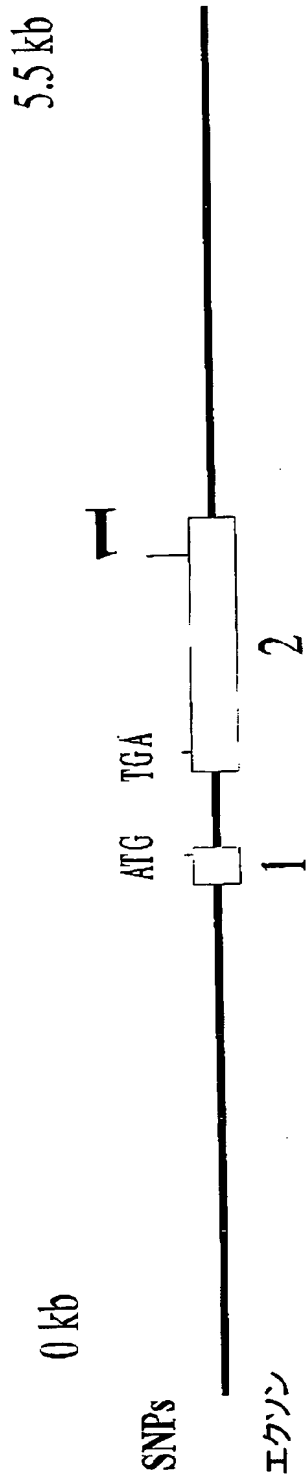
【図 175】



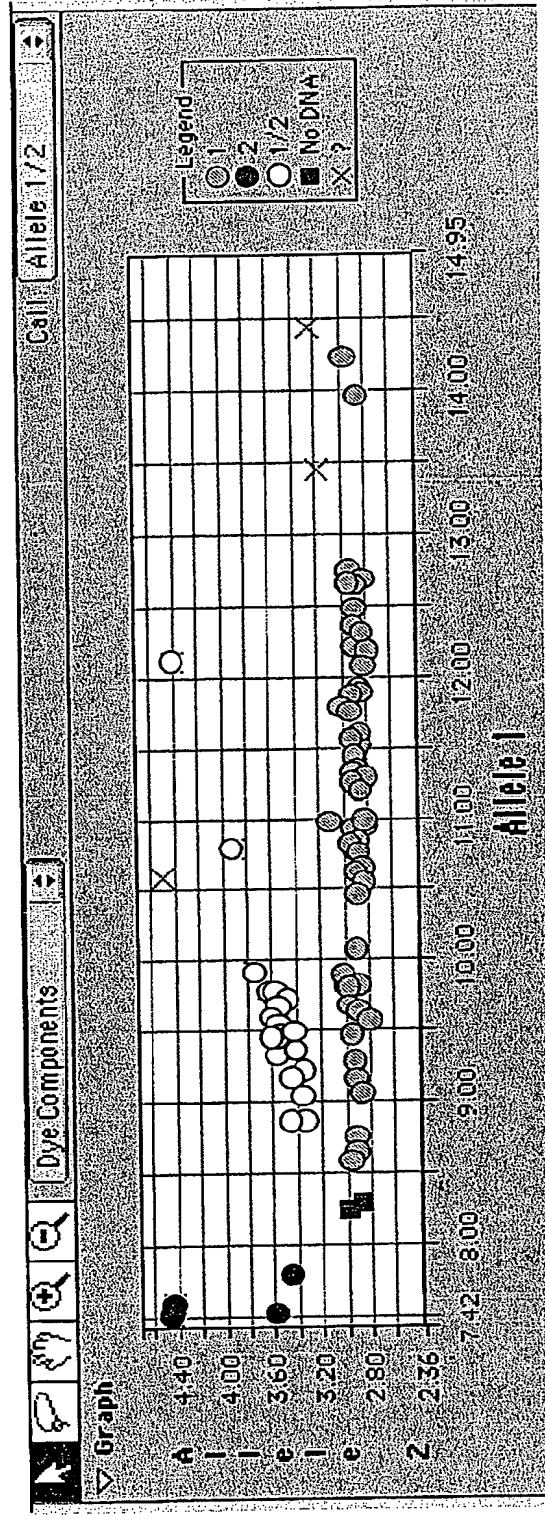
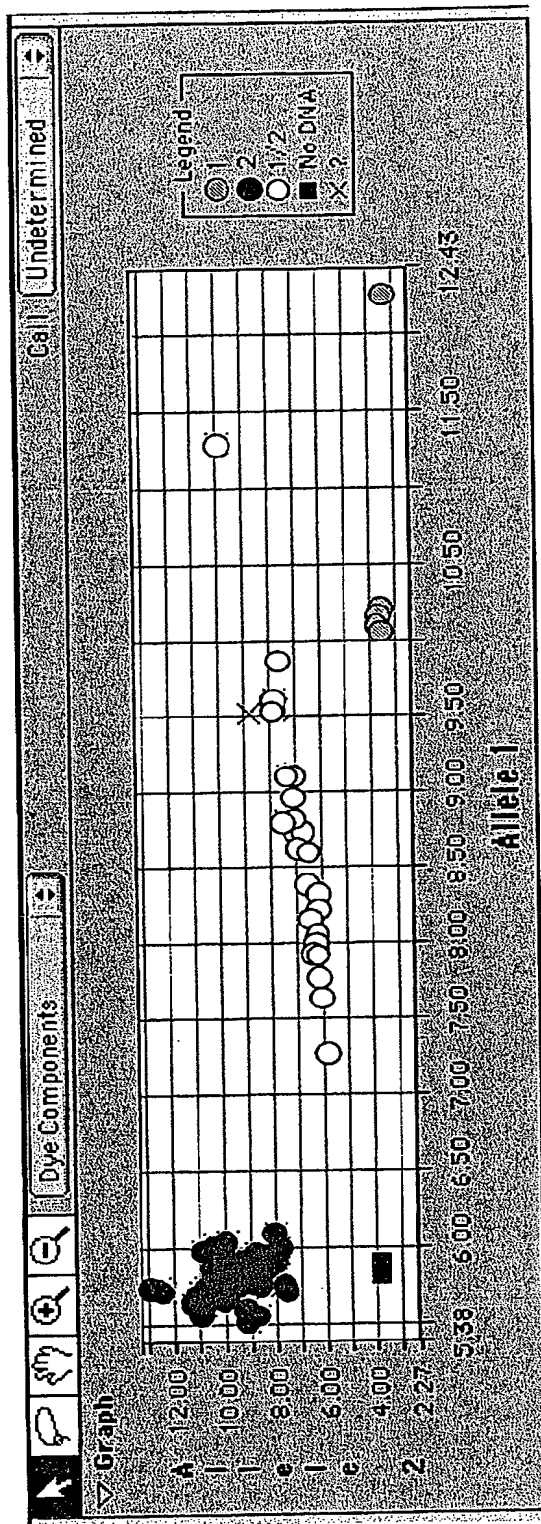
【図 176】



【図 177】



【図 178】



【書類名】 要約書

【要約】

【課題】 遺伝子多型の検出方法の提供。

【解決手段】 薬物代謝酵素をコードする遺伝子中に存在する遺伝子多型情報から、該遺伝子多型部位を含むように、又は薬物代謝酵素をコードする遺伝子を増幅したときの増幅断片中に前記遺伝子多型部位が含まれるように、オリゴヌクレオチドプローブ及び/又はオリゴヌクレオチドプライマーを作製し、得られるオリゴヌクレオチドプローブ及び/又はオリゴヌクレオチドプライマーを用いて、目的の薬物代謝酵素をコードする遺伝子中の少なくとも 1 個の遺伝子多型を検出することを特徴とする遺伝子多型の検出方法。

【選択図】 なし

【書類名】 出願人名義変更届 (一般承継)
【提出日】 平成15年12月 1日
【あて先】 特許庁長官殿
【事件の表示】
【出願番号】 特願2001-395196
【承継人】
【識別番号】 503359821
【住所又は居所】 埼玉県和光市広沢 2 番 1 号
【氏名又は名称】 独立行政法人理化学研究所
【承継人代理人】
【識別番号】 100075812
【弁理士】
【氏名又は名称】 吉武 賢次
【提出物件の目録】
【物件名】 権利の承継を証明する書面 1
【援用の表示】 平成15年11月20日提出の特許第1575167号外98件
にかか一般承継による特許権の移転登録申請書
【物件名】 登記簿謄本 1
【援用の表示】 平成15年11月20日提出の特許第1575167号外98件
にかか一般承継による特許権の移転登録申請書
【物件名】 委任状 1

【物件名】

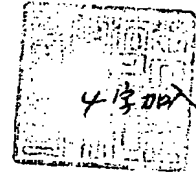
委任状

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【添付書類】



委 任 状



私は、

識別番号 100075812 弁理士 吉 武 賢 次 氏

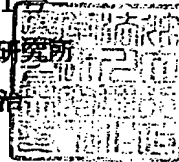
を代理人と定めて下記事項を委任する。

1. ^{954件} 別紙目録に記載の特許出願に関する出願人名義変更届をする件
2. 上記各項の手続を処理するため復代理人を選任及び解任する件

以 上

平成 / 5 年 / / 月 / 3 日

住所又は居所 埼玉県和光市広沢2番1号
氏名又は名称 独立行政法人 理化学研究所
代 表 者 理事長 野 依 良 浩



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